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A2

(54) Title: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME

(57) Abstract: Newly identified Olfactory G protein-coupled receptors (ORs), and the genes and cDNA encoding said receptors are described. Specifically, G protein-coupled receptors active in olfactory signaling, and the genes and cDNA encoding the same, are described, along with methods for isolating such genes and for isolating and expressing such receptors. Methods for representing olfactory perception of a particular odorant in a mammal are also described, as are methods for generating novel molecules or combinations of molecules that elicit a predetermined odor perception in a mammal, and methods for simulating one or more odors. Further, methods for stimulating or blocking odor perception in a mammal are also disclosed.

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HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME

Cross Reference to Related Applications

This application claims priority to the following provisional applications: U.S.

5 Ser. No. 60/188,914, filed March 13, 2000, entitled, "NOVEL OLFACTORY RECEPTORS AND GENES ENCODING SAME," to Zozulya; U.S. Ser. No. 60/192,033, filed March 24, 2000, entitled, "NOVEL OLFACTORY RECEPTORS AND GENES ENCODING SAME," to Zozulya; U.S. Ser. No. 60/198,474, filed April 12, 2000, entitled, "NOVEL OLFACTORY RECEPTORS AND GENE 10 ENCODING THE SAME to Zozulya; U.S. Ser. No. 60/199,335, filed April 24, 2000, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/207,702, filed May 26, 2000, entitled, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/213,849, filed June 23, 2000, entitled, "HUMAN OLFACTORY 15 RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/226,534, filed August 16, 2000, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/230,732, filed September 7, 2000, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; and U.S. Ser. No. 60/266,862, filed February 20, 2001, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya. All of these applications are herein incorporated by reference in their entireties.

Field of the Invention

25 The invention relates to newly identified mammalian chemosensory G protein-coupled receptors, particularly olfactory receptors, fragments thereof, classes of such receptors, genes and cDNAs encoding said receptors, vectors including said receptors, and cells that express said receptors. The invention also relates to methods of using such receptors, fragments, genes, cDNAs, vectors, and cells to identify molecules 30 involved in olfactory perception. The invention therefore has application in the selection and design of odorant compositions, as well as malodor blockers (olfactory receptor antagonists), particularly perfumes and fragrance compositions and components of deodorants and other malodor blocking compositions.

Description of the Related Art

The olfactory system provides sensory information about the chemical composition of the external world. Olfactory sensation is thought to involve distinct 5 signaling pathways. These pathways are believed to be mediated by olfactory receptors (ORs). Cells which express olfactory receptors, when exposed to certain chemical stimuli, elicit olfactory sensation by depolarizing to generate an action potential, which is believed to trigger the sensation.

As such, olfactory receptors specifically recognize molecules that elicit 10 specific olfactory sensation. These molecules are also referred to herein as "odorants." Olfactory receptors belong to the 7-transmembrane receptor superfamily (Buck *et al.*, *Cell* 65:175-87 (1991)), which are also known as G protein-coupled receptors (GPCRs). G protein-coupled receptors control many physiological 15 functions, such as endocrine function, exocrine function, heart rate, lipolysis, carbohydrate metabolism, and transmembrane signaling. The biochemical analysis and molecular cloning of a number of such receptors has revealed many basic principles regarding the function of these receptors.

For example, U. S. Patent No. 5,691,188 describes how upon a ligand binding 20 to a GPCR, the receptor presumably undergoes a conformational change leading to activation of the G protein. G proteins are comprised of three subunits: a guanyl nucleotide binding α subunit, a β subunit, and a γ subunit. G proteins cycle between two forms, depending on whether GDP or GTP is bound to the α subunit. When GDP is bound, the G protein exists as a heterotrimer: the $\text{G}\alpha\beta\gamma$ complex. When GTP is bound, the α subunit dissociates from the heterotrimer, leaving a $\text{G}\beta\gamma$ complex. When 25 a $\text{G}\alpha\beta\gamma$ complex operatively associates with an activated G protein-coupled receptor in a cell membrane, the rate of exchange of GTP for bound GDP is increased and the rate of dissociation of the bound $\text{G}\alpha$ subunit from the $\text{G}\alpha\beta\gamma$ complex increases. The free $\text{G}\alpha$ subunit and $\text{G}\beta\gamma$ complex are thus capable of transmitting a signal to downstream elements of a variety of signal transduction pathways. These events form 30 the basis for a multiplicity of different cell signaling phenomena, including for example the signaling phenomena that are identified as neurological sensory perceptions such as taste and/or smell.

Genes encoding the olfactory receptors are active primarily in olfactory neurons (Axel, *Sci. Amer.*, 273:154-59 (1995)). Individual olfactory receptor types are expressed in subsets of cells distributed in distinct zones of the olfactory epithelium (Breer, *Semin. Cell Biol.*, 5:25-32 (1994)). The human genome contains 5 approximately one thousand genes that encode a diverse repertoire of olfactory receptors (Rouquier, *Nat. Genet.*, 18:243-50 (1998); Trask, *Hum. Mol. Genet.*, 7:2007-20 (1998)). It has been demonstrated that members of the OR gene family are distributed on all but a few human chromosomes. Through fluorescence *in situ* hybridization analysis, Rouquier showed that OR sequences reside at more than 25 10 locations in the human genome. Rouquier also determined that the human genome has accumulated a striking number of dysfunctional OR copies: 72% of the analyzed sequences were found to be pseudogenes. An understanding of an animal's ability to detect and discriminate among the thousands of distinct odorants or tastants, and more particularly to distinguish, for example beneficial tastants or odorants from toxic 15 tastants or odorants, is complicated by the fact that chemosensory receptors belong to a multigene family with over a thousand members. For instance, there are up to 1,000 odorant receptors in mammals.

Moreover, each chemosensory receptor neuron may express only one or a few 20 of these receptors. With respect to odorant receptors, any given olfactory neuron can respond to a small set of odorant ligands. In addition, odorant discrimination for a given neuron may depend on the ligand specificity of the one or few receptors it expresses. To analyze odorant-receptor interactions and their effects on olfactory 25 cells, specific ligands and the olfactory receptors to which they bind are identified. This analysis requires isolation and expression of olfactory polypeptides, followed by binding assays.

Some studies suggest that OR genes can be expressed in tissues other than the olfactory epithelium, indicating potential alternative biological roles for this class of chemosensory receptors. Expression of various ORs has been reported in human and murine erythroid cells (Feingold 1999), developing rat heart (Drutel, *Receptor 30 Channels*, 3(1):33-40 (1995)), avian notochord (Nef, *PNAS*, 94(9):4766-71 (1997)) and lingual epithelium (Abe, *FES Lett.*, 316(3):253-56 (1993)). One experimentally documented case also established the existence of a large subset of mammalian ORs transcribed in testes and expressed on the surface of mature spermatozoa, thereby

suggesting a possible role of ORs in sperm chemotaxis (Parmentier, *Nature*, 355:453-55 (1992); Walensky, *Mol. Med.*, 1(2):130-41 (1998); Branscomb, *Genetics*, 156(2):785-97 (2000)). It was also hypothesized that olfactory receptors might provide molecular codes for highly specific cell-cell recognition functions in 5 development and embryogenesis (Dreyer, *PNAS*, 95(11):9072-77 (1998)).

Complete or partial sequences of numerous human and other eukaryotic chemosensory receptors are currently known. See, e.g., Pilpel, Y. and Lancet, D., *Protein Science*, 8:969-77 (1999); Mombaerts, P., *Annu. Rev. Neurosci.*, 22:487-50 (1999); see also, EP0867508A2, US 5874243, WO 92/17585, WO 95/18140, WO 10 97/17444, WO 99/67282. Due to the complexity of ligand-receptor interactions, and more particularly odorant-receptor interactions, information about ligand-receptor recognition is lacking. In part, the present invention addresses the need for better understanding of these interactions. The present invention also provides, among other things, novel chemosensory receptors, and methods for utilizing such novel 15 chemosensory receptors and the genes and cDNAs encoding such receptors, especially for identifying compounds that can be used to modulate chemosensory transduction, such as olfaction.

Summary of the Invention

20 Toward that end, it is an object of the invention to provide a new family of G protein-coupled receptors comprising over two hundred fifty olfactory G protein-coupled receptors (OR) active in olfactory perception. It is another object of the invention to provide fragments and variants of such ORs which retain odorant-binding activity.

25 It is yet another object of the invention to provide nucleic acid sequences or molecules that encode such ORs, fragments, or allelic variants.

It is still another object of the invention to provide expression vectors which 30 include nucleic acid sequences that encode such ORs, or fragments, or variants thereof, which are operably linked to at least one regulatory sequence such as a promoter, enhancer, or other sequences involved in positive or negative gene transcription and/or translation.

It is still another object of the invention to provide human or non-human cells that functionally express at least one of such ORs, or fragments, or variants thereof.

It is still another object of the invention to provide OR fusion proteins or polypeptides which include at least a fragment of at least one of such ORs.

It is another object of the invention to provide an isolated nucleic acid molecule encoding an OR comprising a nucleic acid sequence that is at least 30%, 5 more preferably at least 50%, still more preferably at least 60-70%, and still more preferably 75%, preferably 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to a nucleic acid sequence selected from the group consisting of: SEQ. ID. NO. 2, SEQ. ID. NO. 4, SEQ. ID. NO. 6, SEQ. ID. NO. 8, SEQ. ID. NO. 10, SEQ. ID. NO. 12, SEQ. ID. NO. 14, SEQ. ID. NO. 16, SEQ. ID. NO. 18, SEQ. ID. NO. 20, SEQ. ID. 10 NO. 22, SEQ. ID. NO. 24, SEQ. ID. NO. 26, SEQ. ID. NO. 28, SEQ. ID. NO. 30, SEQ. ID. NO. 32, SEQ. ID. NO. 34, SEQ. ID. NO. 36, SEQ. ID. NO. 38, SEQ. ID. NO. 40, SEQ. ID. NO. 42, SEQ. ID. NO. 44, SEQ. ID. NO. 46, SEQ. ID. NO. 48, SEQ. ID. NO. 50, SEQ. ID. NO. 52, SEQ. ID. NO. 54, SEQ. ID. NO. 56, SEQ. ID. NO. 58, SEQ. ID. NO. 60, SEQ. ID. NO. 62, SEQ. ID. NO. 64, SEQ. ID. NO. 66, 15 SEQ. ID. NO. 68, SEQ. ID. NO. 70, SEQ. ID. NO. 72, SEQ. ID. NO. 74, SEQ. ID. NO. 76, SEQ. ID. NO. 78, SEQ. ID. NO. 80, SEQ. ID. NO. 82, SEQ. ID. NO. 84, SEQ. ID. NO. 86, SEQ. ID. NO. 88, SEQ. ID. NO. 90, SEQ. ID. NO. 92, SEQ. ID. NO. 94, SEQ. ID. NO. 96, SEQ. ID. NO. 98, SEQ. ID. NO. 100, SEQ. ID. NO. 102, SEQ. ID. NO. 104, SEQ. ID. NO. 106, SEQ. ID. NO. 108, SEQ. ID. NO. 110, SEQ. 20 ID. NO. 112, SEQ. ID. NO. 114, SEQ. ID. NO. 116, SEQ. ID. NO. 118, SEQ. ID. NO. 120, SEQ. ID. NO. 122, SEQ. ID. NO. 124, SEQ. ID. NO. 126, SEQ. ID. NO. 128, SEQ. ID. NO. 130, SEQ. ID. NO. 132, SEQ. ID. NO. 134, SEQ. ID. NO. 136, SEQ. ID. NO. 138, SEQ. ID. NO. 140, SEQ. ID. NO. 142, SEQ. ID. NO. 144, SEQ. ID. NO. 146, SEQ. ID. NO. 148, SEQ. ID. NO. 150, SEQ. ID. 25 NO. 152, SEQ. ID. NO. 154, SEQ. ID. NO. 156, SEQ. ID. NO. 158, SEQ. ID. NO. 160, SEQ. ID. NO. 162, SEQ. ID. NO. 164, SEQ. ID. NO. 166, SEQ. ID. NO. 168, SEQ. ID. NO. 170, SEQ. ID. NO. 172, SEQ. ID. NO. 174, SEQ. ID. NO. 176, SEQ. ID. NO. 178, SEQ. ID. NO. 180, SEQ. ID. NO. 182, SEQ. ID. NO. 184, SEQ. ID. NO. 186, SEQ. ID. NO. 188, SEQ. ID. NO. 190, SEQ. ID. 30 NO. 192, SEQ. ID. NO. 194, SEQ. ID. NO. 196, SEQ. ID. NO. 198, SEQ. ID. NO. 200, SEQ. ID. NO. 202, SEQ. ID. NO. 204, SEQ. ID. NO. 206, SEQ. ID. NO. 208, SEQ. ID. NO. 210, SEQ. ID. NO. 212, SEQ. ID. NO. 214, SEQ. ID. NO. 216, SEQ. ID. NO. 218, SEQ. ID. NO. 220, SEQ. ID. NO. 222, SEQ. ID.

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It is a further object of the invention to provide an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a polypeptide having an amino acid sequence which is at least 40%, more preferably at least 50%, still more preferably at least 60-70%, and still more preferably 75%, 85%, 90%, 95%, 96%, 5 97%, 98%, or 99% identical to an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. 10 NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, 15 SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. 20 NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. 25 NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. 30 NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID.

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It is still a further object of the invention to provide an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a fragment of a polypeptide having an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. 5 NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, 10 SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. 15 NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. 20 NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. 25 NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID. NO. 219, SEQ. ID. 30 NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID. NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO. 241, SEQ. ID. NO. 243, SEQ. ID. NO. 245, SEQ. ID. NO. 247, SEQ. ID. NO. 249, SEQ. ID. NO. 251, SEQ. ID. NO. 253,

SEQ. ID. NO. 255, SEQ. ID. NO. 257, SEQ. ID. NO. 259, SEQ. ID. NO. 261, SEQ. ID. NO., 263, SEQ. ID. NO., 265, SEQ. ID. NO. 267, SEQ. ID. NO. 269, SEQ. ID. NO. 271, SEQ. ID. NO. 273, SEQ. ID. NO. 275, SEQ. ID. NO. 277, SEQ. ID. NO. 279, SEQ. ID. NO. 281, SEQ. ID. NO. 283, SEQ. ID. NO. 285, SEQ. ID. NO. 287, 5 SEQ. ID. NO. 289, SEQ. ID. NO. 291, SEQ. ID. NO. 293, SEQ. ID. NO. 295, SEQ. ID. NO. 297, SEQ. ID. NO. 299, SEQ. ID. NO. 301, SEQ. ID. NO. 303, SEQ. ID. NO. 305, SEQ. ID. NO. 307, SEQ. ID. NO. 309, SEQ. ID. NO. 311, SEQ. ID. NO. 313, SEQ. ID. NO. 315, SEQ. ID. NO. 317, SEQ. ID. NO. 319, SEQ. ID. NO. 321, SEQ. ID. NO. 323, SEQ. ID. NO. 325, SEQ. ID. NO. 327, SEQ. ID. NO. 329, SEQ. 10 ID. NO. 331, SEQ. ID. NO. 333, SEQ. ID. NO. 335, SEQ. ID. NO. 337, SEQ. ID. NO. 339, SEQ. ID. NO. 341, SEQ. ID. NO. 343, SEQ. ID. NO. 345, SEQ. ID. NO. 347, SEQ. ID. NO. 349, SEQ. ID. NO. 351, SEQ. ID. NO. 353, SEQ. ID. NO. 355, SEQ. ID. NO. 357, SEQ. ID. NO. 359, SEQ. ID. NO. 361, SEQ. ID. NO. 363, SEQ. ID. NO. 365, SEQ. ID. NO. 367, SEQ. ID. NO. 369, SEQ. ID. NO. 371, SEQ. ID. NO. 373, SEQ. ID. NO. 375, SEQ. ID. NO. 377, SEQ. ID. NO. 379, SEQ. ID. NO. 381, SEQ. ID. NO. 383, SEQ. ID. NO. 385, SEQ. ID. NO. 387, SEQ. ID. NO. 389, SEQ. ID. NO. 391, SEQ. ID. NO. 393, SEQ. ID. NO. 395, SEQ. ID. NO. 397, SEQ. ID. NO. 399, SEQ. ID. NO. 401, SEQ. ID. NO. 403, SEQ. ID. NO. 405, SEQ. ID. NO. 407, SEQ. ID. NO. 409, SEQ. ID. NO. 411, SEQ. ID. NO. 413, SEQ. ID. NO. 415, 20 SEQ. ID. NO. 417, SEQ. ID. NO. 419, SEQ. ID. NO. 421, SEQ. ID. NO. 423, SEQ. ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID. NO. 431, SEQ. ID. NO. 433, SEQ. ID. NO. 435, SEQ. ID. NO. 437, SEQ. ID. NO. 439, SEQ. ID. NO. 441, SEQ. ID. NO. 443, SEQ. ID. NO. 445, SEQ. ID. NO. 447, SEQ. ID. NO. 449, SEQ. ID. NO. 451, SEQ. ID. NO. 453, SEQ. ID. NO. 455, SEQ. ID. NO. 457, SEQ. 25 ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID. NO. 465, SEQ. ID. NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO. 473, SEQ. ID. NO. 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481, SEQ. ID. NO. 483, SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ. ID. NO. 491, SEQ. ID. NO. 493, SEQ. ID. NO. 495, SEQ. ID. NO. 497, SEQ. ID. NO. 499, SEQ. ID. NO. 30 501, SEQ. ID. NO. 503, SEQ. ID. NO. 505, SEQ. ID. NO. 507, SEQ. ID. NO. 509 and SEQ. ID. NO. 511, wherein the fragment is at least 10, preferably 20, 30, 50, 70, 100, or 150 amino acids in length.

It is still a further object of the invention to provide an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a variant of said fragment, wherein there is a variation in at most 10, preferably 5, 4, 3, 2, or 1 amino acid residues.

5 It is still another object of the invention to provide an isolated polypeptide comprising an amino acid sequence that is at least 40%, 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, or 99% identical to an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID.

NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID. NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO. 241, SEQ. ID. NO. 243, SEQ. ID. NO. 245, SEQ. ID. NO. 247, SEQ. ID. NO. 249, SEQ. ID. NO. 251,
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30 NO. 465, SEQ. ID. NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO. 473, SEQ. ID. NO. 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481, SEQ. ID. NO. 483, SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ. ID. NO. 491, SEQ. ID. NO. 493, SEQ. ID. NO. 495, SEQ. ID. NO. 497, SEQ. ID. NO.

499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

It is still a further object of the invention to provide an isolated polypeptide comprising a fragment of a polypeptide having an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID. NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO. 241, SEQ. ID. NO.

243, SEQ. ID. NO. 245, SEQ. ID. NO. 247, SEQ. ID. NO. 249, SEQ. ID. NO. 251,
SEQ. ID. NO. 253, SEQ. ID. NO. 255, SEQ. ID. NO. 257, SEQ. ID. NO. 259, SEQ.
ID. NO. 261, SEQ. ID. NO., 263, SEQ. ID. NO., 265, SEQ. ID. NO. 267, SEQ. ID.
NO. 269, SEQ. ID. NO. 271, SEQ. ID. NO. 273, SEQ. ID. NO. 275, SEQ. ID. NO.
5 277, SEQ. ID. NO. 279, SEQ. ID. NO. 281, SEQ. ID. NO. 283, SEQ. ID. NO. 285,
SEQ. ID. NO. 287, SEQ. ID. NO. 289, SEQ. ID. NO. 291, SEQ. ID. NO. 293, SEQ.
ID. NO. 295, SEQ. ID. NO. 297, SEQ. ID. NO. 299, SEQ. ID. NO. 301, SEQ. ID.
NO. 303, SEQ. ID. NO. 305, SEQ. ID. NO. 307, SEQ. ID. NO. 309, SEQ. ID. NO.
311, SEQ. ID. NO. 313, SEQ. ID. NO. 315, SEQ. ID. NO. 317, SEQ. ID. NO. 319,
10 SEQ. ID. NO. 321, SEQ. ID. NO. 323, SEQ. ID. NO. 325, SEQ. ID. NO. 327, SEQ.
ID. NO. 329, SEQ. ID. NO. 331, SEQ. ID. NO. 333, SEQ. ID. NO. 335, SEQ. ID.
NO. 337, SEQ. ID. NO. 339, SEQ. ID. NO. 341, SEQ. ID. NO. 343, SEQ. ID. NO.
345, SEQ. ID. NO. 347, SEQ. ID. NO. 349, SEQ. ID. NO. 351, SEQ. ID. NO. 353,
SEQ. ID. NO. 355, SEQ. ID. NO. 357, SEQ. ID. NO. 359, SEQ. ID. NO. 361, SEQ.
15 ID. NO. 363, SEQ. ID. NO. 365, SEQ. ID. NO. 367, SEQ. ID. NO. 369, SEQ. ID. NO.
371, SEQ. ID. NO. 373, SEQ. ID. NO. 375, SEQ. ID. NO. 377, SEQ. ID. NO. 379,
SEQ. ID. NO. 381, SEQ. ID. NO. 383, SEQ. ID. NO. 385, SEQ. ID. NO. 387, SEQ.
ID. NO. 389, SEQ. ID. NO. 391, SEQ. ID. NO. 393, SEQ. ID. NO. 395, SEQ. ID.
NO. 397, SEQ. ID. NO. 399, SEQ. ID. NO. 401, SEQ. ID. NO. 403, SEQ. ID. NO.
20 405, SEQ. ID. NO. 407, SEQ. ID. NO. 409, SEQ. ID. NO. 411, SEQ. ID. NO. 413,
SEQ. ID. NO. 415, SEQ. ID. NO. 417, SEQ. ID. NO. 419, SEQ. ID. NO. 421, SEQ.
ID. NO. 423, SEQ. ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID.
NO. 431, SEQ. ID. NO. 433, SEQ. ID. NO. 435, SEQ. ID. NO. 437, SEQ. ID. NO.
439, SEQ. ID. NO. 441, SEQ. ID. NO. 443, SEQ. ID. NO. 445, SEQ. ID. NO. 447,
25 SEQ. ID. NO. 449, SEQ. ID. NO. 451, SEQ. ID. NO. 453, SEQ. ID. NO. 455, SEQ.
ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID.
NO. 465, SEQ. ID. NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO.
473, SEQ. ID. NO. 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481,
SEQ. ID. NO. 483, SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ.
30 ID. NO. 491, SEQ. ID. NO. 493, SEQ. ID. NO. 495, SEQ. ID. NO. 497, SEQ. ID. NO.
499, SEQ. ID. NO. 501, SEQ. ID. NO. 503, SEQ. ID. NO. 505, SEQ. ID. NO. 507, SEQ.
ID. NO. 509 and SEQ. ID. NO. 511, wherein the fragment is at least 40, preferably 60,
80, 100, 150, 200, or 250 amino acids in length.

It is still a further object of the invention to provide an isolated polypeptide comprising a variant of said fragment, especially naturally occurring allelic variants, the expression of which may be significant in the manner by which different persons in the human population perceive odors differently, both on a qualitative and 5 quantitative level, wherein there is a variation in at most 10, preferably 5, 4, 3, 2, or 1 amino acid residues.

It is still another object of the invention to provide agonists, including inverse agonists, or antagonists of such ORs, or fragments or variants thereof.

It is yet another object of the invention to provide methods for representing the 10 perception of odor and/or for predicting the perception of odor in a mammal, including in a human. Preferably, such methods may be performed by using the ORs, or fragments or variants thereof, and genes encoding such ORs, or fragments or variants thereof, disclosed herein.

It is yet another object of the invention to provide novel molecules or combinations of 15 molecules which elicit a predetermined olfactory perception in a mammal. Such molecules or compositions can be generated by determining a value of olfactory perception in a mammal for a known molecule or combinations of molecules; determining a value of olfactory perception in a mammal for one or more unknown molecules or combinations of molecules; comparing the value of olfactory perception 20 in a mammal for one or more unknown compositions to the value of olfactory perception in a mammal for one or more known compositions; selecting a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal; and combining two or more unknown molecules or combinations of molecules to form a molecule or combination of molecules that elicits a 25 predetermined olfactory perception in a mammal. The combining step yields a single molecule or a combination of molecules that elicits a predetermined olfactory perception in a mammal.

It is still a further object of the invention to provide a method of screening one or more compounds for the presence of an odor detectable by a mammal, comprising: 30 a step of contacting said one or more compounds with the disclosed ORs, fragments or variants thereof, preferably wherein the mammal is a human.

It is another object of the invention to provided a method for simulating a fragrance, comprising: for each of a plurality of ORs, or fragments of variants thereof

disclosed herein, preferably human ORs, ascertaining the extent to which the OR interacts with the fragrance; and combining a plurality of compounds, each having a previously ascertained interaction with one or more of the ORs, in amounts that together provide a receptor-stimulation profile that mimics the profile for the
5 fragrance. Interaction of a fragrance with an OR can be determined using any of the binding or reporter assays described herein. The plurality of compounds may then be combined to form a mixture. If desired, one or more of the plurality of the compounds can be combined covalently. The combined compounds substantially stimulate at least 50%, 60%, 70%, 75%, 80% or 90% or all of the receptors that are
10 substantially stimulated by the fragrance.

In yet another aspect of the invention, a method is provided wherein a plurality of standard compounds are tested against a plurality of ORs, or fragments or variants thereof, to ascertain the extent to which the ORs each interact with each standard compound, thereby generating a receptor stimulation profile for each standard
15 compound. These receptor stimulation profiles may then be stored in a relational database on a data storage medium. The method may further comprise providing a desired receptor-stimulation profile for a scent; comparing the desired receptor stimulation profile to the relational database; and ascertaining one or more combinations of standard compounds that most closely match the desired receptor-
20 stimulation profile. The method may further comprise combining standard compounds in one or more of the ascertained combinations to simulate the scent.

It is a further object of the invention to provide a method for representing olfactory perception of a particular smell in a mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n ORs of said
25 vertebrate, where n is greater than or equal to 4, n is greater than or equal to 12; n is greater than or equal to 24, n is greater than or equal to 48; n is greater than or equal to 72; n is greater than or equal to 96; n is greater than or equal to 120; n is greater than or equal to 144; n is greater than or equal to 168; n is greater than or equal to 192; n is greater than or equal to 216, or n is greater than or equal to 256; and generating from
30 said values a quantitative representation of olfactory perception. The ORs may be an olfactory receptor disclosed herein, or fragments or variants thereof, the representation may constitutes a point or a volume in n -dimensional space, may constitutes a graph or a spectrum, and may constitutes a matrix of quantitative representations. Also, the

providing step may comprise contacting a plurality of recombinantly produced ORs, or fragments or variants thereof, with a test composition and quantitatively measuring the interaction of said composition with said receptors.

It is yet another object of the invention to provide a method for predicting the 5 olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n ORs of said vertebrate, where n is greater than or equal to 4 n is greater than or equal to 12; n is greater than or equal to 24, n is greater than or equal to 48; n is 10 greater than or equal to 72; n is greater than or equal to 96; n is greater than or equal to 120; n is greater than or equal to 144; n is greater than or equal to 168; n is greater than or equal to 192; n is greater than or equal to 216, or n is greater than or equal to 256; for one or more molecules or combinations of molecules yielding known 15 olfactory perception in a mammal; and generating from said values a quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known olfactory perception in a mammal, providing values X_1 to X_n representative of the quantitative stimulation of each of n ORs of said vertebrate, where n is greater than or equal to 4, n is greater than or equal to 12; n is greater than or equal to 24, n is greater than or equal to 48; n is greater than or equal to 72; n is greater than or equal to 96; n is greater than or equal to 120; n is greater than or equal to 144; n is greater than or equal to 168; n is greater than or equal to 192; n is greater than or equal to 216, or n is greater than or equal to 273; for one or 20 more molecules or combinations of molecules yielding unknown olfactory perception in a mammal; and generating from said values a quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal, and predicting the 25 olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal, and comparing the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal to the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known 30

olfactory perception in a mammal. The ORs used in this method may include an olfactory receptor, or fragment or variant thereof, disclosed herein.

Brief Description of the Drawings

5 Figure 1 illustrates the multiple sequence alignment derived for fifty novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty novel human olfactory receptors (hOR) proteins described herein are designated AOLFR1 through AOLFR52. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences 10 AOLFR2 through AOLFR52 were analyzed for alignment with the AOLFR1 amino acid sequence.

Figure 2 illustrates the multiple sequence alignment derived for fifty novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty novel human olfactory receptors (hOR) proteins 15 described herein are designated AOLFR54 through AOLFR109. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR55 through AOLFR109 were analyzed for alignment with the AOLFR54 amino acid sequence.

Figure 3 illustrates the multiple sequence alignment derived for fifty novel 20 ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty novel human olfactory receptors (hOR) proteins described herein are designated AOLFR110 through AOLFR163. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR111 through AOLFR163 were analyzed for alignment with the 25 AOLFR110 amino acid sequence.

Figure 4 illustrates the multiple sequence alignment derived for fifty-four novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty-four novel human olfactory receptors (hOR) proteins described herein are designated AOLFR165 through AOLFR217. The 30 alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR166 through AOLFR217 were analyzed for alignment with the AOLFR165 amino acid sequence.

Figure 5 illustrates the multiple sequence alignment derived for fifty-two novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty-two novel human olfactory receptors (hOR) proteins described herein, which are designated AOLFR218 through AOLFR328. The 5 alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR219 through AOLFR328 were analyzed for alignment with the AOLFR218 amino acid sequence.

Detailed Description of the Invention

10 The invention thus provides isolated nucleic acid molecules encoding olfactory-cell-specific G protein-coupled receptors ("GPCRs"), and the polypeptides they encode. These nucleic acid molecules and the polypeptides that they encode are members of the olfactory receptor family. Other members of the olfactory receptor family are disclosed in Krautwurst, *et al.*, *Cell*, 95:917-26 (1998), and WO 0035274, 15 the contents of which are herein incorporated by reference in their entireties.

According to one aspect of the invention, genes encoding over two hundred fifty distinct, novel human olfactory (odorant) receptors (also herein referred to ORs) have been identified in genome sequence databases. All of these receptor genes have been initially detected by computer DNA sequence analysis of genomic clones 20 (unfinished High Throughput Genomic Sequence database accession numbers AB045359, AP002532, AP002533, AL365440, AC073487, AL359636, AL359955, AP002535, AB045365, AL359218, AC002555, AB045361, AL359512, AC023255, AL358773, AL357767, AL358874, AC068380, AC025283, AP002407, AC018700, AC022289, AC006313, AC002556, AC011571, AL121944, AC007194, AP001112, 25 AC021660, AP000723, AC016856, AC018700, AP000818, AC00596, AP000916, AC011517, AP001112, AP000916, AC021427, AC021427, AC020884, AC019108, AL135841, AL133410, AF186996, AL138834, AC009237, AC025249, AC010930, AC009758, AC009642, AC009758, AC025249, AF101706, AC009642, AC025249, AC021660, AC011647, AC011711, AC09642, AC020597, AC011711, AC019088, 30 AC022882, AC011571, AL121944, AP000435, AC012616, AC010332, AC010766, AP000743, AC021809, AC011879, AC021304, AC023226, AL160314, AC021304, AC020380, AC011904, AC004977, AC021304, AP000868, AP000825, AC023080, AC022207, AC121986, AC010814, AC018700, AC021304, AC008620, AC011537,

AC010760, AC027641, AC017103, AC024729, AC024257, AC025115, AP001524, AP000916, AC010814, AL162254, AC025234, AP001521, AC026090, AC019088, AC016856, AC016787, AC009594, AC026038, AQ628489, AC025942, AL163152, AC026975, AC024654, AP001803, AP001804, AL353767, AP001884, AC026083,
5 AC018793, AP000818, AL353894, AL049734, AL355366, AC011464, AC037472, AC036111, AC019093, AC027239, AC027522, AC009545, AC021333, AC036216, AC021935, AC022762, AL356019, AC055861, AC018375, AC072059, AC068339, AC022891, AL357039, AP002345, AC044810, AC073113, AC024399, AC023564, AL390860, AC074365, AP002826, AL359636, AL391534, AC055731, AC076959,
10 AP002826, AC019088, AC009779, AL445307, AP002512, AP000818, AC079190) by virtue of their sequence homology to some of the known human and other mammalian olfactory receptor genes.

15 Alternatively, nucleic acids encoding the olfactory receptors (ORs) and polypeptides of the invention can be isolated from a variety of sources, genetically engineered, amplified, synthesized, and/or expressed recombinantly according to the methods disclosed in WO 0035374, which is herein incorporated by reference in its entirety.

20 These nucleic acids provide valuable probes for the identification of olfactory cells, as the nucleic acids are specifically expressed in olfactory cells. They can also serve as tools for the generation of sensory topographical maps that elucidate the relationship between olfactory cells and olfactory sensory neurons leading to olfactory centers in the brain. Furthermore, the nucleic acids and the polypeptides they encode can be used as probes to elucidate olfactory-induced behaviors.

25 The invention also provides methods of screening for modulators, *e.g.*, activators, inhibitors, stimulators, enhancers, agonists, inverse agonists and antagonists, of the ORs, or fragments or variants thereof, of the invention. Such modulators of olfactory transduction are useful for pharmacological and genetic modulation of olfactory signaling pathways. These methods of screening can be used to identify high affinity agonists and antagonists of olfactory cell activity. These 30 modulator compounds can then be used in the food, pharmaceutical, and cosmetic industries to customize odors and fragrances.

Thus, the invention provides assays for olfactory modulation, where the ORs, or fragments or variants thereof, of the invention act as direct or indirect reporter

molecules for the effect of modulators on olfactory transduction. The ORs, or fragments or variants thereof, can be used in assays, *e.g.*, to measure changes in ion concentration, membrane potential, current flow, ion flux, transcription, signal transduction, receptor-ligand interaction, second messenger concentrations, *in vitro*, *in vivo* and *ex vivo*. In one embodiment, the ORs, or fragments or variants thereof, can be used as an indirect reporters via attachment to second reporter molecules, such as green fluorescent protein (*see, e.g.*, Mistili *et al.*, *Nature Biotech.*, 15:961-64 (1997)). In another embodiment, the ORs, or fragments or variants thereof, can be expressed in host cells, and modulation of olfactory transduction via OR activity can be assayed by measuring changes in Ca^{2+} levels.

Methods of assaying for modulators of olfactory transduction include *in vitro* ligand binding assays using the ORs of the invention, or fragments or variants thereof. More particularly, such assays can use the ORs; portions thereof such as the extracellular or transmembrane domains; chimeric proteins comprising one or more of such domains; oocyte receptor expression; tissue culture cell receptor expression; transcriptional activation of the receptor; G protein binding to the receptor; ligand binding assays; voltage, membrane potential and conductance changes; ion flux assays; changes in intracellular second messengers such as cAMP and inositol triphosphate; changes in intracellular Ca^{2+} levels; and neurotransmitter release.

The invention also provides for methods of detecting olfactory nucleic acid and protein expression, allowing for the investigation of olfactory transduction regulation and specific identification of olfactory receptor cells. The ORs, fragments, and variants of the invention can also be used to generate monoclonal and polyclonal antibodies useful for identifying olfactory receptor cells. Olfactory receptor cells can be identified using techniques such as reverse transcription and amplification of mRNA, isolation of total RNA or poly A^+ RNA, northern blotting, dot blotting, *in situ* hybridization, RNase protection, S1 digestion, probing DNA microchip arrays, western blots, and the like.

A. Identification and Characterization of Olfactory Receptors

The amino acid sequences of the ORs and polypeptides of the invention can be identified by putative translation of the coding nucleic acid sequences. These various

amino acid sequences and the coding nucleic acid sequences may be compared to one another or to other sequences according to a number of methods.

For example, in sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program parameters can be used, as described below for the BLASTN and BLASTP programs, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window," as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of: from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well known in the art. Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *PNAS*, 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (*see, e.g.*, *Current Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 supplement)).

A preferred example of an algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, *Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al.*, *J Mol. Biol.* 215:403-410 (1990), respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued

threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, Altschul *et al.*, *Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al.*, *J Mol. Biol.* 215:403-410 (1990)). These initial neighborhood word hits act as seeds for initiating 5 searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a 10 scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and 15 X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) or 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, *PNAS*, 89:10915 (1989)) 20 alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

Another example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments to show relationship and percent sequence identity. It also plots a so-called “tree” or “dendrogram” showing the clustering relationships used to create the 25 alignment (see, e.g., Figure 2). PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, *J Mol. Evol.* 35:351-60 (1987). The method used is similar to the method described by Higgins & Sharp, CABIOS 5:151-153 (1989). The program can align up to 300 sequences, each of a maximum length of 30 5,000 nucleotides or amino acids. The multiple alignment procedure begins with the pairwise alignment of the two most similar sequences, producing a cluster of two aligned sequences. This cluster is then aligned to the next most related sequence or cluster of aligned sequences. Two clusters of sequences are aligned by a simple

extension of the pairwise alignment of two individual sequences. The final alignment is achieved by a series of progressive, pairwise alignments. The program is run by designating specific sequences and their amino acid or nucleotide coordinates for regions of sequence comparison and by designating the program parameters. Using 5 PILEUP, a reference sequence is compared to other test sequences to determine the percent sequence identity relationship using the following parameters: default gap weight (3.00), default gap length weight (0.10), and weighted end gaps. PILEUP can be obtained from the GCG sequence analysis software package, *e.g.*, version 7. 0 (Devereaux *et al.*, *Nuc. Acids Res.* 12:387-395 (1984) encoded by the genes were 10 derived by conceptual translation of the corresponding open reading frames. Comparison of these protein sequences to all known proteins in the public sequence databases using BLASTP algorithm revealed their strong homology to the members of the mammalian olfactory receptor family, each of the odorant receptor sequences having at least 50%, and preferably at least 55%, at least 60%, at least 65%, and most 15 preferably at least 70%, amino acid identity to at least one known member of the family.

The nucleic acid molecules of the present invention are typically intronless and encode putative OR proteins generally having lengths of approximately 290 to approximately 400 amino acid residues that contain seven transmembrane domains, as 20 predicted by hydrophobicity plotting analysis, indicating that they belong to the G protein-coupled receptor 7-transmembrane (7TM) superfamily, which includes the subset of taste and olfactory receptors. In addition to the overall structural similarity, each of the ORs identified herein has a characteristic sequence signature of an olfactory receptor. In particular, all the identified sequences contain very close 25 matches to the following consensus amino acid motifs (Mombaerts, 1999, Pilpel 1999): EFILL (SEQ ID NO: 513) before transmembrane domain 1, LHTPMY (SEQ ID No: 514) in intracellular loop 1, MAYDRYVAIC (SEQ ID NO: 510) at the end of transmembrane domain 3 and the beginning of intracellular loop 2, SY at the end of transmembrane domain 5, FSTCSSH (SEQ ID NO: 516) in the beginning of 30 transmembrane domain 6, and PMLNPF (SEQ ID NO: 517) in transmembrane domain 7. Combination of all the above-mentioned structural features of the identified genes and encoded proteins strongly suggests that they represent novel members of the human olfactory receptor family.

As noted above, complete or partial sequences of numerous human and other eukaryotic olfactory receptors are currently known. The novel human receptors have amino acid sequences distinctly different from the previously known human olfactory receptors, which suggests their different specificity in odorant recognition. Therefore, 5 these novel receptors and their genes can be used, alone or in combination with known olfactory receptors, in developing detection systems and assays for chemically distinct types of odorants not recognized by the known receptors, as well as for diagnostic and research purposes.

B. Definitions

10 As used herein, the following terms have the meanings ascribed to them unless specified otherwise.

“OR” refers to one or more members of a family of G protein-coupled receptors that are expressed in olfactory cells. Olfactory receptor cells can also be identified on the basis of morphology (*see, e.g., Roper, supra*), or by the expression of 15 proteins specifically expressed in olfactory cells. OR family members may have the ability to act as receptors for olfactory transduction.

“OR” nucleic acids encode a family of GPCRs with seven transmembrane regions that have “G protein-coupled receptor activity,” *e.g.*, they may bind to G proteins in response to extracellular stimuli and promote production of second 20 messengers such as IP3, cAMP, cGMP, and Ca²⁺ via stimulation of enzymes such as phospholipase C and adenylate cyclase (for a description of the structure and function of GPCRs, *see, e.g., Fong, supra, and Baldwin, supra*). A single olfactory cell may contain many distinct OR polypeptides.

Topologically, certain chemosensory GPCRs have an “N-terminal domain;” 25 “extracellular domains;” “transmembrane domains” comprising seven transmembrane regions, and corresponding cytoplasmic, and extracellular loops; “cytoplasmic domains,” and a “C-terminal domain” (*see, e.g., Hoon et al., Cell, 96:541-51 (1999); Buck & Axel, Cell, 65:175-87 (1991)*). These domains can be structurally identified using methods known to those of skill in the art, such as sequence analysis programs 30 that identify hydrophobic and hydrophilic domains (*see, e.g., Stryer, Biochemistry, (3rd ed. 1988); see also any of a number of Internet based sequence analysis programs, such as those found at dot.ingen.bcm.tmc.edu*). Such domains are useful

for making chimeric proteins and for in vitro assays of the invention, *e.g.*, ligand binding assays.

“Extracellular domains” therefore refers to the domains of OR polypeptides that protrude from the cellular membrane and are exposed to the extracellular face of the cell. Such domains generally include the “N terminal domain” that is exposed to the extracellular face of the cell, and optionally can include portions of the extracellular loops of the transmembrane domain that are exposed to the extracellular face of the cell, *i.e.*, the loops between transmembrane regions 2 and 3, between transmembrane regions 4 and 5, and between transmembrane regions 6 and 7.

10 The “N terminal domain” region starts at the N-terminus and extends to a region close to the start of the transmembrane domain. “Transmembrane domain,” which comprises the seven “transmembrane regions,” refers to the domain of OR polypeptides that lies within the plasma membrane, and may also include the corresponding cytoplasmic (intracellular) and extracellular loops. The seven 15 transmembrane regions and extracellular and cytoplasmic loops can be identified using standard methods, as described in Kyte & Doolittle, *J. Mol. Biol.*, 157:105-32 (1982)), or in Stryer, *supra*. The general secondary and tertiary structure of transmembrane domains, in particular the seven transmembrane domains of 7-transmembrane receptors such as olfactory receptors, are well known in the art. Thus, 20 primary structure sequence can be designed or predicted based on known transmembrane domain sequences, as described in detail below. These transmembrane domains are useful for *in vitro* ligand-binding assays, both soluble and solid phase.

“Cytoplasmic domains” refers to the domains of OR polypeptides that face the 25 inside of the cell, *e.g.*, the “C terminal domain” and the intracellular loops of the transmembrane domain, *e.g.*, the intracellular loop between transmembrane regions 1 and 2, the intracellular loop between transmembrane regions 3 and 4, and the intracellular loop between transmembrane regions 5 and 6. “C terminal domain” refers to the region that spans the end of the last transmembrane domain and the C- 30 terminus of the protein, and which is normally located within the cytoplasm.

The term “ligand-binding region” or “ligand-binding domain” refers to sequences derived from a chemosensory receptor, particularly an olfactory receptor,

that substantially incorporates at least transmembrane domains II to VII. The ligand-binding region may be capable of binding a ligand, and more particularly, an odorant.

The phrase "functional effects" in the context of assays for testing compounds that modulate OR family member mediated olfactory transduction includes the 5 determination of any parameter that is indirectly or directly under the influence of the receptor, *e.g.*, functional, physical and chemical effects. It includes ligand binding, changes in ion flux, membrane potential, current flow, transcription, G protein binding, GPCR phosphorylation or dephosphorylation, signal transduction, receptor-ligand interactions, second messenger concentrations (*e.g.*, cAMP, cGMP, 10 IP3, or intracellular Ca^{2+}), *in vitro*, *in vivo*, and *ex vivo* and also includes other physiologic effects such increases or decreases of neurotransmitter or hormone release.

By "determining the functional effect" in the context of assays is meant assays for a compound that increases or decreases a parameter that is indirectly or directly 15 under the influence of an OR family member, *e.g.*, functional, physical and chemical effects. Such functional effects can be measured by any means known to those skilled in the art, *e.g.*, changes in spectroscopic characteristics (*e.g.*, fluorescence, absorbance, refractive index), hydrodynamic (*e.g.*, shape), chromatographic, or solubility properties, patch clamping, voltage-sensitive dyes, whole cell currents, 20 radioisotope efflux, inducible markers, oocyte OR gene expression; tissue culture cell OR expression; transcriptional activation of OR genes; ligand-binding assays; voltage, membrane potential and conductance changes; ion flux assays; changes in intracellular second messengers such as cAMP, cGMP, and inositol triphosphate (IP3); changes in intracellular calcium levels; neurotransmitter release, and the like.

25 "Inhibitors," "activators," and "modulators" of OR genes or proteins are used interchangeably to refer to inhibitory, activating, or modulating molecules identified using *in vitro* and *in vivo* assays for olfactory transduction, *e.g.*, ligands, agonists, antagonists, and their homologs and mimetics. Inhibitors are compounds that, *e.g.*, bind to, partially or totally block stimulation, decrease, prevent, delay activation, 30 inactivate, desensitize, or down regulate olfactory transduction, *e.g.*, antagonists. Activators are compounds that, *e.g.*, bind to, stimulate, increase, open, activate, facilitate, enhance activation, sensitize, or up regulate olfactory transduction, *e.g.*, agonists. Modulators include compounds that, *e.g.*, alter the interaction of a receptor

with: extracellular proteins that bind activators or inhibitor (*e.g.*, ebnerin and other members of the hydrophobic carrier family); G proteins; kinases (*e.g.*, homologs of rhodopsin kinase and beta adrenergic receptor kinases that are involved in deactivation and desensitization of a receptor); and arrestins, which also deactivate and desensitize receptors. Modulators can include genetically modified versions of OR family members, *e.g.*, with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, small chemical molecules and the like. Such assays for inhibitors and activators include, *e.g.*, expressing OR family members in cells or cell membranes, applying putative modulator compounds, in the presence or absence of tastants, *e.g.*, sweet tastants, and then determining the functional effects on olfactory transduction, as described above. Samples or assays comprising OR family members that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of modulation. Control samples (untreated with modulators) are assigned a relative OR activity value of 100%. Inhibition of a OR is achieved when the OR activity value relative to the control is about 80%, optionally 50% or 25-0%. Activation of an OR is achieved when the OR activity value relative to the control is 110%, optionally 150%, optionally 200-500%, or 1000-3000% higher.

The terms “purified,” “substantially purified,” and “isolated” as used herein refer to the state of being free of other, dissimilar compounds with which the compound of the invention is normally associated in its natural state, so that the “purified,” “substantially purified,” and “isolated” subject comprises at least 0.5%, 1%, 5%, 10%, or 20%, and most preferably at least 50% or 75% of the mass, by weight, of a given sample. In one preferred embodiment, these terms refer to the compound of the invention comprising at least 95% of the mass, by weight, of a given sample. As used herein, the terms “purified,” “substantially purified,” and “isolated” “isolated,” when referring to a nucleic acid or protein, of nucleic acids or proteins, also refers to a state of purification or concentration different than that which occurs naturally in the mammalian, especially human, body. Any degree of purification or concentration greater than that which occurs naturally in the mammalian, especially human, body, including (1) the purification from other associated structures or compounds or (2) the association with structures or compounds to which it is not normally associated in the mammalian, especially human, body, are within the

meaning of "isolated." The nucleic acid or protein or classes of nucleic acids or proteins, described herein, may be isolated, or otherwise associated with structures or compounds to which they are not normally associated in nature, according to a variety of methods and processes known to those of skill in the art.

5 As used herein, the term "isolated," when referring to a nucleic acid or polypeptide refers to a state of purification or concentration different than that which occurs naturally in the mammalian, especially human, body. Any degree of purification or concentration greater than that which occurs naturally in the body, including (1) the purification from other naturally-occurring associated structures or 10 compounds, or (2) the association with structures or compounds to which it is not normally associated in the body are within the meaning of "isolated" as used herein. The nucleic acids or polypeptides described herein may be isolated or otherwise associated with structures or compounds to which they are not normally associated in nature, according to a variety of methods and processes known to those of skill in the 15 art.

As used herein, the terms "amplifying" and "amplification" refer to the use of any suitable amplification methodology for generating or detecting recombinant or naturally expressed nucleic acid, as described in detail, below. For example, the invention provides methods and reagents (e.g., specific degenerate oligonucleotide 20 primer pairs) for amplifying (e.g., by polymerase chain reaction, PCR) naturally expressed (e.g., genomic or mRNA) or recombinant (e.g., cDNA) nucleic acids of the invention (e.g., tastant-binding sequences of the invention) *in vivo* or *in vitro*.

The term "7- transmembrane receptor" means a polypeptide belonging to a superfamily of transmembrane proteins that have seven domains that span the plasma 25 membrane seven times (thus, the seven domains are called "transmembrane" or "TM" domains TM I to TM VII). The families of olfactory and certain taste receptors each belong to this super-family. 7-transmembrane receptor polypeptides have similar and characteristic primary, secondary and tertiary structures, as discussed in further detail below.

30 The term "library" means a preparation that is a mixture of different nucleic acid or polypeptide molecules, such as the library of recombinantly generated chemosensory, particularly olfactory receptor ligand-binding domains generated by amplification of nucleic acid with degenerate primer pairs, or an isolated collection of

vectors that incorporate the amplified ligand-binding domains, or a mixture of cells each randomly transfected with at least one vector encoding an olfactory receptor.

The term "nucleic acid" or "nucleic acid sequence" refers to a deoxy-ribonucleotide or ribonucleotide oligonucleotide in either single- or double-stranded form. The term encompasses nucleic acids, i.e., oligonucleotides, containing known analogs of natural nucleotides. The term also encompasses nucleic-acid-like structures with synthetic backbones (see e.g., *Oligonucleotides and Analogues, a Practical Approach*, ed. F. Eckstein, Oxford Univ. Press (1991); *Antisense Strategies, Annals of the N.Y. Acad. of Sci.*, Vol. 600, Eds. Baserga *et al.* (NYAS 1992); Milligan 5 *J. Med. Chem.* 36:1923-1937 (1993); *Antisense Research and Applications* (1993, CRC Press), WO 97/03211; WO 96/39154; Mata, *Toxicol. Appl. Pharmacol.* 144:189-197 (1997); Strauss-Soukup, *Biochemistry* 36:8692-8698 (1997); Samstag, 10 *Antisense Nucleic Acid Drug Dev.*, 6:153-156 (1996)).

Unless otherwise indicated, a particular nucleic acid sequence also implicitly 15 encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions) and complementary sequences, as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating, e.g., sequences in which the third position of one or more selected codons is substituted with mixed-base and/or deoxyinosine residues (Batzer *et al.*, *Nucleic 20 Acid Res.*, 19:5081 (1991); Ohtsuka *et al.*, *J. Biol. Chem.*, 260:2605-08 (1985); Rossolini *et al.*, *Mol. Cell. Probes*, 8:91-98 (1994)). The term nucleic acid is used 25 interchangeably with gene, cDNA, mRNA, oligonucleotide, and polynucleotide.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid 25 polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers and non-naturally occurring amino acid polymer.

The term "plasma membrane translocation domain" or simply "translocation domain" means a polypeptide domain that, when incorporated into the amino terminus 30 of a polypeptide coding sequence, can with great efficiency "chaperone" or "translocate" the hybrid ("fusion") protein to the cell plasma membrane. For instance, a "translocation domain" may be derived from the amino terminus of the bovine rhodopsin receptor polypeptide. In one embodiment, the translocation domain may be

functionally equivalent to an exemplary translocation domain (5'-MNGTEGPNFYVPFSNKTGVV; SEQ ID NO: 518). However, rhodopsin from any mammal may be used, as can other translocation facilitating sequences. Thus, the translocation domain is particularly efficient in translocating 7-transmembrane fusion 5 proteins to the plasma membrane, and a protein (e.g., an olfactory receptor polypeptide) comprising an amino terminal translocating domain will be transported to the plasma membrane more efficiently than without the domain. However, if the N-terminal domain of the polypeptide is active in binding, the use of other translocation domains may be preferred.

10 "Functional equivalency" means the domain's ability and efficiency in translocating newly translated proteins to the plasma membrane as efficiently as exemplary SEQ ID NO: 518 under similar conditions; relatively efficiencies can be measured (in quantitative terms) and compared, as described herein. Domains falling within the scope of the invention can be determined by routine screening for their 15 efficiency in translocating newly synthesized polypeptides to the plasma membrane in a cell (mammalian, *Xenopus*, and the like) with the same efficiency as the twenty amino acid long translocation domain SEQ ID NO: 518, as described in detail below.

The "translocation domain," "ligand-binding domain", and chimeric receptors compositions described herein also include "analogs," or "conservative variants" and 20 "mimetics" ("peptidomimetics") with structures and activity that substantially correspond to the exemplary sequences. Thus, the terms "conservative variant" or "analog" or "mimetic" refer to a polypeptide which has a modified amino acid sequence, such that the change(s) do not substantially alter the polypeptide's (the conservative variant's) structure and/or activity, as defined herein. These include 25 conservatively modified variations of an amino acid sequence, *i.e.*, amino acid substitutions, additions or deletions of those residues that are not critical for protein activity, or substitution of amino acids with residues having similar properties (e.g., acidic, basic, positively or negatively charged, polar or non-polar, *etc.*) such that the substitutions of even critical amino acids does not substantially alter structure and/or 30 activity. Conservative substitution tables providing functionally similar amino acids are well known in the art.

More particularly, "conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences,

conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids 5 encode any given protein.

For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded polypeptide.

10 Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes every possible silent variation of the nucleic acid. One of skill will recognize that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only 15 codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, each silent variation of a nucleic acid which encodes a polypeptide is implicit in each described sequence.

20 Conservative substitution tables providing functionally similar amino acids are well known in the art. For example, one exemplary guideline to select conservative substitutions includes (original residue followed by exemplary substitution): ala/gly or ser; arg/lys; asn/gln or his; asp/glu; cys/ser; gln/asn; gly/asp; gly/ala or pro; his/asn or gln; ile/leu or val; leu/ile or val; lys/arg or gln or glu; met/leu or tyr or ile; phe/met or leu or tyr; ser/thr; thr/ser; trp/tyr; tyr/trp or phe; val/ile or leu. An alternative exemplary guideline uses the following six groups, each containing amino acids that 25 are conservative substitutions for one another: 1) Alanine (A), Serine (S), Threonine (T); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (I); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); and 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); (*see also, e.g., Creighton, Proteins, W.H. Freeman and Company (1984); Schultz and Schimer, Principles of Protein Structure, Springer-Verlag (1979)*). One of skill in the art will appreciate that the above-identified substitutions are not the only possible conservative substitutions. For example, for some purposes, one may regard all charged amino acids as 30 conservative substitutions for each other whether they are positive or negative. In

addition, individual substitutions, deletions or additions that alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence can also be considered "conservatively modified variations."

The terms "mimetic" and "peptidomimetic" refer to a synthetic chemical compound that has substantially the same structural and/or functional characteristics of the polypeptides, *e.g.*, translocation domains, ligand-binding domains, or chimeric receptors of the invention. The mimetic can be either entirely composed of synthetic, non-natural analogs of amino acids, or may be a chimeric molecule of partly natural peptide amino acids and partly non-natural analogs of amino acids. The mimetic can also incorporate any amount of natural amino acid conservative substitutions as long as such substitutions also do not substantially alter the mimetic's structure and/or activity.

As with polypeptides of the invention which are conservative variants, routine experimentation will determine whether a mimetic is within the scope of the invention, *i.e.*, that its structure and/or function is not substantially altered. Polypeptide mimetic compositions can contain any combination of non-natural structural components, which are typically from three structural groups: a) residue linkage groups other than the natural amide bond ("peptide bond") linkages; b) non-natural residues in place of naturally occurring amino acid residues; or c) residues which induce secondary structural mimicry, *i.e.*, to induce or stabilize a secondary structure, *e.g.*, a beta turn, gamma turn, beta sheet, alpha helix conformation, and the like. A polypeptide can be characterized as a mimetic when all or some of its residues are joined by chemical means other than natural peptide bonds. Individual peptidomimetic residues can be joined by peptide bonds, other chemical bonds or coupling means, such as, *e.g.*, glutaraldehyde, N-hydroxysuccinimide esters, bifunctional maleimides, N,N'-dicyclohexylcarbodiimide (DCC) or N,N'-diisopropylcarbodiimide (DIC). Linking groups that can be an alternative to the traditional amide bond ("peptide bond") linkages include, *e.g.*, ketomethylene (*e.g.*, -C(=O)-CH₂- for -C(=O)-NH-), aminomethylene (CH₂-NH), ethylene, olefin (CH=CH), ether (CH₂-O), thioether (CH₂-S), tetrazole (CN₄), thiazole, retroamide, thioamide, or ester (*see, e.g.*, Spatola, *Chemistry and Biochemistry of Amino Acids, Peptides and Proteins*, 7:267-357, "Peptide Backbone Modifications," Marcell Dekker, NY (1983)). A polypeptide can also be characterized as a mimetic by

containing all or some non-natural residues in place of naturally occurring amino acid residues; non-natural residues are well described in the scientific and patent literature.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, or chemical means. For 5 example, useful labels include ^{32}P , fluorescent dyes, electron-dense reagents, enzymes (*e.g.*, as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins which can be made detectable, *e.g.*, by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either 10 covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe.

As used herein a "nucleic acid probe or oligonucleotide" is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence 15 through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (*i.e.*, A, G, C, or T) or modified bases (7-deazaguanosine, inosine, *etc.*). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, for 20 example, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. It will be understood by one of skill in the art that probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are optionally directly labeled as with isotopes, 25 chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence.

The term "heterologous" when used with reference to portions of a nucleic 30 acid indicates that the nucleic acid comprises two or more subsequences that are not found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences from unrelated genes arranged to make a new functional nucleic acid, *e.g.*, a promoter from one

source and a coding region from another source. Similarly, a heterologous protein indicates that the protein comprises two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is defined as an array of nucleic acid sequences that direct 5 transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter 10 that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, wherein the 15 expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

As used herein, "recombinant" refers to a polynucleotide synthesized or otherwise manipulated *in vitro* (e.g., "recombinant polynucleotide"), to methods of using recombinant polynucleotides to produce gene products in cells or other 20 biological systems, or to a polypeptide ("recombinant protein") encoded by a recombinant polynucleotide. "Recombinant means" also encompass the ligation of nucleic acids having various coding regions or domains or promoter sequences from different sources into an expression cassette or vector for expression of, e.g., inducible or constitutive expression of a fusion protein comprising a translocation domain of the 25 invention and a nucleic acid sequence amplified using a primer of the invention.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

30 The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acid, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer

sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Techniques in Biochemistry and Molecular Biology - Hybridisation with Nucleic Probes*, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent 5 conditions are selected to be about 5-10° C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength pH. The Tm is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at Tm, 50% of the probes are occupied at 10 equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the 15 addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least two times background, optionally 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42°C, or, 5x SSC, 1% SDS, incubating at 65°C, with wash in 0.2x SSC, and 0.1 % SDS at 65°C. Such 20 hybridizations and wash steps can be carried out for, e.g., 1, 2, 5, 10, 15, 30, 60; or more minutes.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially related if the polypeptides that they encode are substantially related. This occurs, for example, when a copy of a nucleic acid is created using the maximum 25 codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 1x SSC at 45°C. Such hybridizations and wash steps can be carried out for, e.g., 1, 2, 5, 10, 15, 30, 60, or 30 more minutes. A positive hybridization is at least twice background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency.

“Antibody” refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad 5 immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair 10 having one “light” (about 25 kDa) and one “heavy” chain (about 50-70 kDa). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (VL) and variable heavy chain (VH) refer to these light and heavy chains respectively.

A “chimeric antibody” is an antibody molecule in which (a) the constant 15 region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, *e.g.*, an enzyme, toxin, hormone, growth factor, drug, *etc.*; or (b) the variable region, or a portion thereof, is altered, replaced or 20 exchanged with a variable region having a different or altered antigen specificity.

An “anti-OR” antibody is an antibody or antibody fragment that specifically binds a polypeptide encoded by a OR gene, cDNA, or a subsequence thereof.

The term “immunoassay” is an assay that uses an antibody to specifically bind 25 an antigen. The immunoassay is characterized by the use of specific binding properties of a particular antibody to isolate, target, and/or quantify the antigen.

The phrase “specifically (or selectively) binds” to an antibody or, “specifically (or selectively) immunoreactive with,” when referring to a protein or peptide, refers to a binding reaction that is determinative of the presence of the protein in a heterogeneous population of proteins and other biologics. Thus, under designated 30 immunoassay conditions, the specified antibodies bind to a particular protein at least two times the background and do not substantially bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions may require an antibody that is selected for its specificity for a particular

protein. For example, polyclonal antibodies raised to an OR family member from specific species such as rat, mouse, or human can be selected to obtain only those polyclonal antibodies that are specifically immunoreactive with the OR polypeptide or an immunogenic portion thereof and not with other proteins, except for orthologs or 5 polymorphic variants and alleles of the OR polypeptide. This selection may be achieved by subtracting out antibodies that cross-react with OR molecules from other species or other OR molecules. Antibodies can also be selected that recognize only OR GPCR family members but not GPCRs from other families. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive 10 with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select antibodies specifically immunoreactive with a protein (see, e.g., Harlow & Lane, *Antibodies, A Laboratory Manual*, (1988), for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity). Typically a specific or selective reaction will be at least twice 15 background signal or noise and more typically more than 10 to 100 times background.

The phrase "selectively associates with" refers to the ability of a nucleic acid to "selectively hybridize" with another as defined above, or the ability of an antibody to "selectively (or specifically) bind to a protein, as defined above.

The term "expression vector" refers to any recombinant expression system for 20 the purpose of expressing a nucleic acid sequence of the invention *in vitro* or *in vivo*, constitutively or inducibly, in any cell, including prokaryotic, yeast, fungal, plant, insect or mammalian cell. The term includes linear or circular expression systems. The term includes expression systems that remain episomal or integrate into the host 25 cell genome. The expression systems can have the ability to self-replicate or not, i.e., drive only transient expression in a cell. The term includes recombinant expression "cassettes which contain only the minimum elements needed for transcription of the recombinant nucleic acid.

By "host cell" is meant a cell that contains an expression vector and supports 30 the replication or expression of the expression vector. Host cells may be prokaryotic cells such as E. coli, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, HEK-293, and the like, e.g., cultured cells, explants, and cells *in vivo*.

C. Isolation and Expression of Olfactory Receptors

Isolation and expression of the ORs, or fragments or variants thereof, of the invention can be performed as described below. PCR primers can be used for the amplification of nucleic acids encoding olfactory receptor ligand-binding regions and 5 libraries of these nucleic acids can thereby be generated. Libraries of expression vectors can then be used to infect or transfect host cells for the functional expression of these libraries. These genes and vectors can be made and expressed *in vitro* or *in vivo*. One of skill will recognize that desired phenotypes for altering and controlling nucleic acid expression can be obtained by modulating the expression or activity of 10 the genes and nucleic acids (e.g., promoters, enhancers and the like) within the vectors of the invention. Any of the known methods described for increasing or decreasing expression or activity can be used. The invention can be practiced in conjunction with any method or protocol known in the art, which are well described in the scientific and patent literature.

15 The nucleic acid sequences of the invention and other nucleic acids used to practice this invention, whether RNA, cDNA, genomic DNA, vectors, viruses or hybrids thereof, may be isolated from a variety of sources, genetically engineered, amplified, and/or expressed recombinantly. Any recombinant expression system can be used, including, in addition to mammalian cells, e.g., bacterial, yeast, insect or 20 plant systems.

25 Alternatively, these nucleic acids can be synthesized *in vitro* by well-known chemical synthesis techniques, as described in, e.g., Carruthers, *Cold Spring Harbor Symp. Quant. Biol.* 47:411-418 (1982); Adams, *Am. Chem. Soc.* 105:661 (1983); Belousov, *Nucleic Acids Res.* 25:3440-3444 (1997); Frenkel, *Free Radic. Biol. Med.* 19:373-380 (1995); Blommers, *Biochemistry* 33:7886-7896 (1994); Narang, *Meth. Enzymol.* 68:90 (1979); Brown, *Meth. Enzymol.* 68:109 (1979); Beaucage, *Tetra. Lett.* 22:1859 (1981); U.S. Patent No. 4,458,066. Double-stranded DNA fragments may then be obtained either by synthesizing the complementary strand and annealing the strands together under appropriate conditions, or by adding the complementary strand 30 using DNA polymerase with an appropriate primer sequence..

Techniques for the manipulation of nucleic acids, such as, for example, for generating mutations in sequences, subcloning, labeling probes, sequencing, hybridization and the like are well described in the scientific and patent literature.

See, e.g., Sambrook, ed., Molecular Cloning: a Laboratory manual (2nd ed.), Vols. 1-3, Cold Spring Harbor Laboratory (1989); Current Protocols in Molecular Biology, Ausubel, ed. John Wiley & Sons, Inc., New York (1997); Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I, 5 Theory and Nucleic Acid Preparation, Tijssen, ed. Elsevier, N.Y. (1993).

Nucleic acids, vectors, capsids, polypeptides, and the like can be analyzed and quantified by any of a number of general means well known to those of skill in the art. These include, e.g., analytical biochemical methods such as NMR, spectrophotometry, radiography, electrophoresis, capillary electrophoresis, high performance liquid 10 chromatography (HPLC), thin layer chromatography (TLC), and hyperdiffusion chromatography, various immunological methods, e.g., fluid or gel precipitin reactions, immunodiffusion, immuno-electrophoresis, radioimmunoassays (RIAs), enzyme-linked immunosorbent assays (ELISAs), immuno-fluorescent assays, Southern analysis, Northern analysis, dot-blot analysis, gel electrophoresis (e.g., SDS-PAGE), RT-PCR, quantitative PCR, other nucleic acid or target or signal 15 amplification methods, radiolabeling, scintillation counting, and affinity chromatography.

Oligonucleotide primers are used to amplify nucleic acid encoding an olfactory receptor ligand-binding region. The nucleic acids described herein can also be cloned 20 or measured quantitatively using amplification techniques. Using exemplary degenerate primer pair sequences, (see below), the skilled artisan can select and design suitable oligonucleotide amplification primers. Amplification methods are also well known in the art, and include, e.g., polymerase chain reaction, PCR (PCR Protocols, a Guide to Methods and Applications, ed. Innis. Academic Press, N.Y. 25 (1990) and PCR Strategies, ed. Innis, Academic Press, Inc., N.Y. (1995), ligase chain reaction (LCR) (see, e.g., Wu, *Genomics* 4:560 (1989); Landegren, *Science* 241:1077,(1988); Barringer, *Gene* 89:117 (1990)); transcription amplification (see, e.g., Kwoh, *PNAS*, 86:1173 (1989)); and, self-sustained sequence replication (see, e.g., Guatelli, *PNAS*, 87:1874 (1990)); Q Beta replicase amplification (see, e.g., 30 Smith, *J. Clin. Microbiol.* 35:1477-1491 (1997)); automated Q-beta replicase amplification assay (see, e.g., Burg, *Mol. Cell. Probes* 10:257-271 (1996)) and other RNA polymerase mediated techniques (e.g., NASBA, Cangene, Mississauga, Ontario); see also Berger, *Methods Enzymol.* 152:307-316 (1987); Sambrook;

Ausubel; U.S. Patent Nos. 4,683,195 and 4,683,202; Sooknanan, *Biotechnology* 13:563-564 (1995).

Once amplified, the nucleic acids, either individually or as libraries, may be cloned according to methods known in the art, if desired, into any of a variety of vectors using routine molecular biological methods; methods for cloning *in vitro* amplified nucleic acids are described, *e.g.*, U.S. Pat. No. 5,426,039. To facilitate cloning of amplified sequences, restriction enzyme sites can be "built into" the PCR primer pair. For example, Pst I and Bsp E1 sites were designed into the exemplary primer pairs of the invention. These particular restriction sites have a sequence that, 5 when ligated, are "in-frame" with respect to the 7-membrane receptor "donor" coding sequence into which they are spliced (the ligand-binding region coding sequence is internal to the 7-membrane polypeptide, thus, if it is desired that the construct be translated downstream of a restriction enzyme splice site, out of frame results should be avoided; this may not be necessary if the inserted ligand-binding domain comprises 10 substantially most of the transmembrane VII region). The primers can be designed to retain the original sequence of the "donor" 7-membrane receptor (the Pst I and Bsp E1 sequence in the primers of the invention generate an insert that, when ligated into the Pst I/Bsp E1 cut vector, encode residues found in the "donor" mouse olfactory receptor M4 sequence). Alternatively, the primers can encode amino acid residues 15 that are conservative substitutions (*e.g.*, hydrophobic for hydrophobic residue, see above discussion) or functionally benign substitutions (*e.g.*, do not prevent plasma membrane insertion, cause cleavage by peptidase, cause abnormal folding of receptor, 20 and the like).

The primer pairs are designed to selectively amplify ligand-binding regions of 25 olfactory receptor proteins. These domain regions may vary for different ligands, and more particularly odorants; thus, what may be a minimal binding region for one ligand, and more particularly odorants, may be too limiting for a second potential ligand. Thus, domain regions of different sizes comprising different domain structures may be amplified; for example, transmembrane (TM) domains II through 30 VII, III through VII, III through VI or II through VI, or variations thereof (*e.g.*, only a subsequence of a particular domain, mixing the order of the domains, and the like), of a 7-transmembrane OR.

As domain structures and sequence of many 7-membrane proteins, particularly olfactory receptors, are known, the skilled artisan can readily select domain-flanking and internal domain sequences as model sequences to design degenerate amplification primer pairs. For example, a nucleic acid sequence encoding domain regions II through VII can be generated by PCR amplification using a primer pair. To amplify a nucleic acid comprising transmembrane domain I (TM I) sequence, a degenerate primer can be designed from a nucleic acid that encodes the amino acid sequence LFLLYL3' (SEQ ID NO: 519). Such a degenerate primer can be used to generate a binding domain incorporating TM I through TM III, TM I through TM IV, TM I through TM V, TM I through TM VI or TM I through TM VII.

To amplify a nucleic acid comprising a transmembrane domain III (TM III) sequence, a degenerate primer (of at least about 17 residues) can be designed from a nucleic acid that encodes the amino acid sequence M(A/G)(Y/F)DRYVAI 3' (SEQ ID NO: 520) (encoded by a nucleic acid sequence such as 5'-ATGG(G/C)CT(A/T)TGACCG(C/A/T)T(AT)(C/T)GT-3' (SEQ ID NO: 521)). Such a degenerate primer can be used to generate a binding domain incorporating TM III through TM IV, TM III through TM V, TM III through TM VI or TM III through TM VII.

To amplify transmembrane domain VI (TM VI) sequence, a degenerate primer (of at least about 17 residues) can be designed from nucleic acid encoding an amino acid sequence TC(G/A)SHL (SEQ ID NO: 522), encoded by a sequence such as 5'-AG(G/A)TGN(G/C)(T/A)N(G/C)C(G/A)CANGT-3' 3' (SEQ ID NO: 522). Such a degenerate primer can be used to generate a binding domain incorporating TM I through TM VI, TM II through TM VI, TM III through TM VI or TM IV through TM VI.

Paradigms to design degenerate primer pairs are well known in the art. For example, a COnsensus-DEgenerate Hybrid Oligonucleotide Primer (CODEHOP) (SEQ ID NO: 523) strategy computer program is accessible as <http://blocks.fhcrc.org/codehop.html>, and is directly linked from the BlockMaker multiple sequence alignment site for hybrid primer prediction beginning with a set of related protein sequences, as known olfactory receptor ligand-binding regions (see, e.g., Rose, *Nucleic Acids Res.* 26:1628-1635 (1998); Singh, *Biotechniques*, 24:318-19 (1998)).

Means to synthesize oligonucleotide primer pairs are well known in the art. "Natural" base pairs or synthetic base pairs can be used. For example, use of artificial nucleobases offers a versatile approach to manipulate primer sequence and generate a more complex mixture of amplification products. Various families of artificial nucleobases are capable of assuming multiple hydrogen bonding orientations through internal bond rotations to provide a means for degenerate molecular recognition. Incorporation of these analogs into a single position of a PCR primer allows for generation of a complex library of amplification products. *See, e.g., Hoops, Nucleic Acids Res. 25:4866-4871 (1997).* Nonpolar molecules can also be used to mimic the shape of natural DNA bases. A non-hydrogen-bonding shape mimic for adenine can replicate efficiently and selectively against a nonpolar shape mimic for thymine (*see, e.g., Morales, Nat. Struct. Biol. 5:950-954 (1998)*). For example, two degenerate bases can be the pyrimidine base 6H, 8H-3,4-dihydropyrimido[4,5-c][1,2]oxazin-7-one or the purine base N6-methoxy-2,6-diaminopurine (*see, e.g., Hill, PNAS, 95:4258-63 (1998)*). Exemplary degenerate primers of the invention incorporate the nucleobase analog 5'-Dimethoxytrityl-N-benzoyl-2'-deoxy-Cytidine,3'-(2-cyanoethyl)-(N,N-diisopropyl)]-phosphoramidite (the term "P" in the sequences, see above). This pyrimidine analog hydrogen bonds with purines, including A and G residues.

Exemplary primer pairs for amplification of olfactory receptor transmembrane domains II through VII include:

- (a) 5'-GGGGTCCGGAG(A/G)(C/G)(A/G)TA(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-3' (SEQ ID NO: 524) and
5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3' (SEQ ID NO: 525).
- (b) 5'-GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-3' (SEQ ID NO: 526); and
5'-GGGGCTGCAGACACC(AC/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3' (SEQ ID NO: 527)
- (c) 5'-GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/C/T)A(A/G/C/T)(A/G/C/T)GG-3' (SEQ ID NO: 528) and
5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3' (SEQ ID NO: 558)

Nucleic acids that encode ligand-binding regions of olfactory receptors may be generated by amplification (*e.g., PCR*) of appropriate nucleic acid sequences using

degenerate primer pairs. The amplified nucleic acid can be genomic DNA from any cell or tissue or mRNA or cDNA derived from olfactory receptor-expressing cells, *e.g.*, olfactory neurons or olfactory epithelium.

Isolation from olfactory receptor-expressing cells is well known in the art
5 (cells expressing naturally or inducibly expressing olfactory receptors can be used to express the hybrid olfactory receptors of the invention to screen for potential odorants and odorant effect on cell physiology, as described below). For example, cells can be identified by olfactory marker protein (OMP), an abundant cytoplasmic protein expressed almost exclusively in mature olfactory sensory neurons (*see, e.g.*, Buiakova,
10 *PNAS*, 93:9858-63 (1996)). Shirley, *Eur. J. Biochem.* 32:485-494 (1983), describes a rat olfactory preparation suitable for biochemical studies *in vitro* on olfactory mechanisms. Cultures of adult rat olfactory receptor neurons are described by Vargas,
15 *Chem. Senses* 24:211-216 (1999). Because these cultured neurons exhibit typical voltage-gated currents and are responsive to application of odorants, they can also be used to express the hybrid olfactory receptors of the invention for odorant screening (endogenous olfactory receptor can be initially blocked, if desired, by, *e.g.*, antisense, knockout, and the like). U.S. Patent No. 5,869,266 describes culturing human
19 olfactory neurons for neurotoxicity tests and screening. Murrell, *J. Neurosci.* 19:8260-8270 (1999), describes differentiated olfactory receptor-expressing cells in culture that respond to odorants, as measured by an influx of calcium.
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In one embodiment, hybrid protein-coding sequences comprising nucleic acids ORs fused to the translocation sequences described herein may be constructed. Also provided are hybrid ORs comprising the translocation motifs and ligand-binding domains of olfactory receptors. These nucleic acid sequences can be operably linked
25 to transcriptional or translational control elements, *e.g.*, transcription and translation initiation sequences, promoters and enhancers, transcription and translation terminators, polyadenylation sequences, and other sequences useful for transcribing DNA into RNA. In construction of recombinant expression cassettes, vectors, transgenics, and a promoter fragment can be employed to direct expression of the
30 desired nucleic acid in all tissues. Olfactory cell-specific transcriptional elements can also be used to express the fusion polypeptide receptor, including, *e.g.*, a 6.7 kb region upstream of the M4 olfactory receptor coding region. This region was sufficient to direct expression in olfactory epithelium with wild type zonal restriction and

distributed neuronal expression for endogenous olfactory receptors (Qasba, *J. Neurosci.* 18:227-236 (1998)). Receptor genes are normally expressed in a small subset of neurons throughout a zonally restricted region of the sensory epithelium. The transcriptional or translational control elements can be isolated from natural sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

In another embodiment, fusion proteins, either having C-terminal or, more preferably, N-terminal translocation sequences, may also comprise the translocation motif described herein. However, these fusion proteins can also comprise additional elements for, *e.g.*, protein detection, purification, or other applications. Detection and purification facilitating domains include, *e.g.*, metal chelating peptides such as polyhistidine tracts or histidine-tryptophan modules or other domains that allow purification on immobilized metals; maltose binding protein; protein A domains that allow purification on immobilized immunoglobulin; or the domain utilized in the 15 FLAG extension/affinity purification system (Immunex Corp, Seattle WA).

The inclusion of a cleavable linker sequences such as Factor Xa (*see, e.g.*, Ottavi, *Biochimie* 80:289-293 (1998)), subtilisin protease recognition motif (*see, e.g.*, Polyak, *Protein Eng.* 10:615-619 (1997)); enterokinase (Invitrogen, San Diego, CA), and the like, between the translocation domain (for efficient plasma membrane 20 expression) and the rest of the newly translated polypeptide may be useful to facilitate purification. For example, one construct can include a polypeptide-encoding nucleic acid sequence linked to six histidine residues followed by a thioredoxin, an enterokinase cleavage site (*see, e.g.*, Williams, *Biochemistry* 34:1787-1797 (1995)), and an amino terminal translocation domain. The histidine residues facilitate 25 detection and purification while the enterokinase cleavage site provides a means for purifying the desired protein(s) from the remainder of the fusion protein. Technology pertaining to vectors encoding fusion proteins and application of fusion proteins are well described in the scientific and patent literature (*see, e.g.*, Kroll, *DNA Cell. Biol.* 12:441-53 (1993)).

30 Expression vectors, either as individual expression vectors or as libraries of expression vectors, comprising the olfactory binding domain-encoding sequences may be introduced into a genome or into the cytoplasm or a nucleus of a cell and expressed by a variety of conventional techniques, well described in the scientific and patent

literature (see, e.g., Roberts, *Nature* 328:731 (1987); Berger *supra*; Schneider, *Protein Expr. Purif.* 6435:10 (1995); Sambrook; Tijssen; Ausubel). Product information from manufacturers of biological reagents and experimental equipment also provide information regarding known biological methods. The vectors can be isolated from 5 natural sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

The nucleic acids can be expressed in expression cassettes, vectors or viruses which are stably or transiently expressed in cells (e.g., episomal expression systems). Selection markers can be incorporated into expression cassettes and vectors to confer 10 a selectable phenotype on transformed cells and sequences. For example, selection markers can code for episomal maintenance and replication such that integration into the host genome is not required. For example, the marker may encode antibiotic resistance (e.g., chloramphenicol, kanamycin, G418, bleomycin, hygromycin) or herbicide resistance (e.g., chlorosulfuron or Basta) to permit selection of those cells 15 transformed with the desired DNA sequences (see, e.g., Blondelet-Rouault, *Gene* 190:315-17 (1997); Aubrecht, *J. Pharmacol. Exp. Ther.*, 281:992-97 (1997)). Because selectable marker genes conferring resistance to substrates like neomycin or hygromycin can only be utilized in tissue culture, chemoresistance genes are also used 20 as selectable markers *in vitro* and *in vivo*.

20 A chimeric nucleic acid sequence may encode a ligand-binding domain within any 7-transmembrane polypeptide. 7-transmembrane receptors belong to a superfamily of transmembrane (TM) proteins having seven domains that traverse a plasma membrane seven times. Each of the seven domains spans the plasma membrane (TM I to TM VII). Because 7-transmembrane receptor polypeptides have 25 similar primary sequences and secondary and tertiary structures, structural domains (e.g., TM domains) can be readily identified by sequence analysis. For example, homology modeling, Fourier analysis and helical periodicity detection can identify and characterize the seven domains with a 7-transmembrane receptor sequence. Fast Fourier Transform (FFT) algorithms can be used to assess the dominant periods that 30 characterize profiles of the hydrophobicity and variability of analyzed sequences. To predict TM domains and their boundaries and topology, a "neural network algorithm" by "PHD server" can be used, as done by Pilpel, *Protein Science* 8:969-977 (1999); Rost, *Protein Sci.* 4:521-533 (1995). Periodicity detection enhancement and alpha

helical periodicity index can be done as by, *e.g.*, Donnelly, *Protein Sci.* 2:55-70 (1993). Other alignment and modeling algorithms are well known in the art, *see, e.g.*, Peitsch, *Receptors Channels* 4:161-164 (1996); Cronet, *Protein Eng.* 6:59-64 (1993) (homology and "discover modeling"); <http://bioinfo.weizmann.ac.il/>.

5 The library sequences include receptor sequences that correspond to TM ligand-binding domains, including, *e.g.*, TM II to VII, TM II to VI, TM III to VII, and TM III to VII, that have been amplified (*e.g.*, PCR) from mRNA or cDNA derived from, *e.g.*, olfactory receptor-expressing neurons or genomic DNA.

10 Libraries of olfactory receptor ligand-binding TM domain sequences can include a various TM domains or variations thereof, as described above. These sequences can be derived from any 7-transmembrane receptor. Because these polypeptides have similar primary sequences and secondary and tertiary structures, the seven domains can be identified by various analyses well known in the art, including, *e.g.*, homology modeling, Fourier analysis and helical periodicity (*see, e.g.*, Pilpel 15 *supra*), as described above. Using this information sequences flanking the seven domains can be identified and used to design degenerate primers for amplification of various combinations of TM regions and subsequences.

20 The present invention also includes not only the DNA and proteins having the specified amino acid sequences, but also DNA fragments, particularly fragments of, for example, 40, 60, 80, 100, 150, 200, or 250 nucleotides, or more, as well as protein fragments of, for example, 10, 20, 30, 50, 70, 100, or 150 amino acids, or more.

Also contemplated are chimeric proteins, comprising at least 10, 20, 30, 50, 70, 100, or 150 amino acids, or more, of one of at least one of the olfactory receptors described herein, coupled to additional amino acids representing all or part of another 25 G protein receptor, preferably a member of the 7TM superfamily. These chimeras can be made from the instant receptors and a G protein receptor described herein, or they can be made by combining two or more of the present proteins. In one preferred embodiment, one portion of the chimera corresponds to and is derived from one or more of the domains of the seven transmembrane protein described herein, and the 30 remaining portion or portions come from another G protein-coupled receptor. Chimeric receptors are well known in the art, and the techniques for creating them and the selection and boundaries of domains or fragments of G protein-coupled receptors for incorporation therein are also well known. Thus, this knowledge of those skilled

in the art can readily be used to create such chimeric receptors. The use of such chimeric receptors can provide, for example, an olfactory selectivity characteristic of one of the receptors specifically disclosed herein, coupled with the signal transduction characteristics of another receptor, such as a well known receptor used in prior art
5 assay systems.

For example, a domain such as a ligand-binding domain, an extracellular domain, a transmembrane domain (*e.g.*, one comprising seven transmembrane regions and corresponding extracellular and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, etc., can be
10 covalently linked to a heterologous protein. For instance, an extracellular domain can be linked to a heterologous GPCR transmembrane domain, or a heterologous GPCR extracellular domain can be linked to a transmembrane domain. Other heterologous proteins of choice can include, *e.g.*, green fluorescent protein, β -gal, glutamate receptor, and the rhodopsin presequence.

15 Polymorphic variants, alleles, and interspecies homologs that are substantially identical to an olfactory receptor disclosed herein can be isolated using the nucleic acid probes described above. It is hypothesized that allelic differences in receptors may explain why there is a difference in olfactory sensation in different human subjects. Accordingly, the identification of such alleles may be significant, especially
20 with respect to producing receptor libraries that adequately represent the olfactory capability of the human population, *i.e.*, which take into account allelic differences in different individuals. Alternatively, expression libraries can be used to clone olfactory receptors and polymorphic variants, alleles, and interspecies homologs thereof, by detecting expressed homologs immunologically with antisera or purified antibodies
25 made against an olfactory polypeptide, which also recognize and selectively bind to the olfactory receptor homolog.

Also within the scope of the invention are host cells for expressing the ORs, fragments, or variants of the invention. To obtain high levels of expression of a cloned gene or nucleic acid, such as cDNAs encoding the olfactory receptors, fragments, or variants of the invention, one of skill typically subclones the nucleic acid sequence of interest into an expression vector that contains a strong promoter to direct transcription, a transcription/translation terminator, and if for a nucleic acid encoding a protein, a ribosome binding site for translational initiation. Suitable
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bacterial promoters are well known in the art and described, *e.g.*, in Sambrook *et al.* However, bacterial or eukaryotic expression systems can be used.

Any of the well-known procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, polybrene, protoplast fusion, electroporation, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (*see, e.g.*, Sambrook *et al.*) It is only necessary that the particular genetic engineering procedure used be capable of successfully introducing at least one gene into the host cell capable of expressing the olfactory receptor, fragment, or variant of interest.

After the expression vector is introduced into the cells, the transfected cells are cultured under conditions favoring expression of the receptor, fragment, or variant of interest, which is then recovered from the culture using standard techniques. Examples of such techniques are well known in the art. *See, e.g.*, WO 00/06593, which is incorporated by reference in a manner consistent with this disclosure.

D. Immunological Detection of OR Polypeptides

In addition to the detection of OR genes and gene expression using nucleic acid hybridization technology, one can also use immunoassays to detect ORs, *e.g.*, to identify olfactory receptor cells, and variants of OR family members. Immunoassays can be used to qualitatively or quantitatively analyze the ORs. A general overview of the applicable technology can be found in Harlow & Lane, *Antibodies: A Laboratory Manual* (1988).

1. Antibodies to OR family members

Methods of producing polyclonal and monoclonal antibodies that react specifically with a OR family member are known to those of skill in the art (*see, e.g.*, Coligan, *Current Protocols in Immunology* (1991); Harlow & Lane, *supra*; Goding, *Monoclonal Antibodies: Principles and Practice* (2d ed. 1986); and Kohler & Milstein, *Nature*, 256:495-97 (1975)). Such techniques include antibody preparation by selection of antibodies from libraries of recombinant antibodies in phage or similar vectors, as well as preparation of polyclonal and monoclonal antibodies by

immunizing rabbits or mice (see, e.g., Huse *et al.*, *Science*, 246:1275-81 (1989); Ward *et al.*, *Nature*, 341:544-46 (1989)).

A number of OR-comprising immunogens may be used to produce antibodies specifically reactive with a OR family member. For example, a recombinant OR 5 protein, or an antigenic fragment thereof, can be isolated as described herein. Suitable antigenic regions include, e.g., the conserved motifs that are used to identify members of the OR family. Recombinant proteins can be expressed in eukaryotic or prokaryotic cells as described above, and purified as generally described above. Recombinant protein is the preferred immunogen for the production of monoclonal or 10 polyclonal antibodies. Alternatively, a synthetic peptide derived from the sequences disclosed herein and conjugated to a carrier protein can be used an immunogen. Naturally occurring protein may also be used either in pure or impure form. The product is then injected into an animal capable of producing antibodies. Either monoclonal or polyclonal antibodies may be generated, for subsequent use in 15 immunoassays to measure the protein.

Methods of production of polyclonal antibodies are known to those of skill in the art. For example, an inbred strain of mice (e.g., BALB/C mice) or rabbits may be immunized with the protein using a standard adjuvant, such as Freund's adjuvant, and a standard immunization protocol. The animal's immune response to the immunogen 20 preparation is monitored by taking test bleeds and determining the titer of reactivity to the OR. When appropriately high titers of antibody to the immunogen are obtained, blood is collected from the animal and antisera are prepared. Further fractionation of the antisera to enrich for antibodies reactive to the protein can be done if desired (see Harlow & Lane, *supra*).

Monoclonal antibodies may be obtained by various techniques familiar to 25 those skilled in the art. Briefly, spleen cells from an animal immunized with a desired antigen may be immortalized, commonly by fusion with a myeloma cell (see Kohler & Milstein, *Eur. J. Immunol.*, 6:511-19 (1976)). Alternative methods of immortalization include transformation with Epstein Barr Virus, oncogenes, or retroviruses, or other 30 methods well known in the art. Colonies arising from single immortalized cells are screened for production of antibodies of the desired specificity and affinity for the antigen, and yield of the monoclonal antibodies produced by such cells may be enhanced by various techniques, including injection into the peritoneal cavity of a

vertebrate host. Alternatively, one may isolate DNA sequences which encode a monoclonal antibody or a binding fragment thereof by screening a DNA library from human B cells according to the general protocol outlined by Huse *et al.*, *Science*, 246:1275-1281 (1989).

5 Monoclonal antibodies and polyclonal sera are collected and titered against the immunogen protein in an immunoassay, for example, a solid phase immunoassay with the immunogen immobilized on a solid support. Typically, polyclonal antisera with a titer of 10⁹ or greater are selected and tested for their cross reactivity against non-OR proteins, or even other OR family members or other related proteins from other
10 organisms, using a competitive binding immunoassay. Specific polyclonal antisera and monoclonal antibodies will usually bind with a K_d of at least about 0.1 mM, more usually at least about 1 pM, optionally at least about 0.1 pM or better, and optionally 0.01 pM or better.

15 Once OR family member specific antibodies are available, individual OR proteins can be detected by a variety of immunoassay methods. For a review of immunological and immunoassay procedures, see *Basic and Clinical Immunology* (Stites & Terr eds., 7th ed. 1991). Moreover, the immunoassays of the present invention can be performed in any of several configurations, which are reviewed extensively in Enzyme Immunoassay (Maggio, ed., 1980); and Harlow & Lane, *supra*.

20 2. Immunological binding assays

25 OR proteins can be detected and/or quantified using any of a number of well recognized immunological binding assays (see, e.g., U.S. Patents 4,366,241; 4,376,110; 4,517,288; and 4,837,168). For a review of the general immunoassays, see also *Methods in Cell Biology: Antibodies in Cell Biology*, volume 37 (Asai, ed. 1993); *Basic and Clinical Immunology* (Stites & Terr, eds., 7th ed. 1991). Immunological binding assays (or immunoassays) typically use an antibody that specifically binds to a protein or antigen of choice (in this case an OR family member or an antigenic subsequence thereof). The antibody (e.g., anti-OR) may be produced by any of a number of means well known to those of skill in the art and as described above.

30 Immunoassays also often use a labeling agent to specifically bind to and label the complex formed by the antibody and antigen. The labeling agent may itself be one of the moieties comprising the antibody/antigen complex. Thus, the labeling agent may be a labeled OR polypeptide or a labeled anti-OR antibody. Alternatively, the

labeling agent may be a third moiety, such a secondary antibody that specifically binds to the antibody/OR complex (a secondary antibody is typically specific to antibodies of the species from which the first antibody is derived). Other proteins capable of specifically binding immunoglobulin constant regions, such as protein A or protein G

5 may also be used as the label agent. These proteins exhibit a strong non-immunogenic reactivity with immunoglobulin constant regions from a variety of species (*see, e.g.,* Kronval *et al.*, *J. Immunol.*, 111:1401-1406 (1973); Akerstrom *et al.*, *J. Immunol.*, 135:2589-2542 (1985)). The labeling agent can be modified with a detectable moiety, such as biotin, to which another molecule can specifically bind, such as streptavidin.

10 A variety of detectable moieties are well known to those skilled in the art.

Throughout the assays, incubation and/or washing steps may be required after each combination of reagents. Incubation steps can vary from about 5 seconds to several hours, optionally from about 5 minutes to about 24 hours. However, the incubation time will depend upon the assay format, antigen, volume of solution, 15 concentrations, and the like. Usually, the assays will be carried out at ambient temperature, although they can be conducted over a range of temperatures, such as 10°C to 40°C.

a. Non-competitive assay formats

Immunoassays for detecting an OR protein in a sample may be either 20 competitive or noncompetitive. Noncompetitive immunoassays are assays in which the amount of antigen is directly measured. In one preferred "sandwich" assay, for example, the anti-OR antibodies can be bound directly to a solid substrate on which they are immobilized. These immobilized antibodies then capture the OR protein present in the test sample. The OR protein is thus immobilized is then bound by a 25 labeling agent, such as a second OR antibody bearing a label. Alternatively, the second antibody may lack a label, but it may, in turn, be bound by a labeled third antibody specific to antibodies of the species from which the second antibody is derived. The second or third antibody is typically modified with a detectable moiety, such as biotin, to which another molecule specifically binds, *e.g.*, streptavidin, to 30 provide a detectable moiety.

b. Competitive assay formats

In competitive assays, the amount of OR protein present in the sample is measured indirectly by measuring the amount of a known, added (exogenous) OR

protein displaced (competed away) from an anti-OR antibody by the unknown OR protein present in a sample. In one competitive assay, a known amount of OR protein is added to a sample and the sample is then contacted with an antibody that specifically binds to the OR. The amount of exogenous OR protein bound to the antibody is inversely proportional to the concentration of OR protein present in the sample. In a particularly preferred embodiment, the antibody is immobilized on a solid substrate. The amount of OR protein bound to the antibody may be determined either by measuring the amount of OR protein present in a OR/antibody complex, or alternatively by measuring the amount of remaining uncomplexed protein. The amount of OR protein may be detected by providing a labeled OR molecule.

A hapten inhibition assay is another preferred competitive assay. In this assay the known OR protein is immobilized on a solid substrate. A known amount of anti-OR antibody is added to the sample, and the sample is then contacted with the immobilized OR. The amount of anti-OR antibody bound to the known immobilized OR protein is inversely proportional to the amount of OR protein present in the sample. Again, the amount of immobilized antibody may be detected by detecting either the immobilized fraction of antibody or the fraction of the antibody that remains in solution. Detection may be direct where the antibody is labeled or indirect by the subsequent addition of a labeled moiety that specifically binds to the antibody as described above.

c. Cross-reactivity determinations

Immunoassays in the competitive binding format can also be used for cross-reactivity determinations. For example, a protein at least partially encoded by the nucleic acid sequences disclosed herein can be immobilized to a solid support. Proteins (*e.g.*, OR proteins and homologs) are added to the assay that compete for binding of the antisera to the immobilized antigen. The ability of the added proteins to compete for binding of the antisera to the immobilized protein is compared to the ability of the OR polypeptide encoded by the nucleic acid sequences disclosed herein to compete with itself. The percent cross-reactivity for the above proteins is calculated, using standard calculations. Those antisera with less than 10% cross-reactivity with each of the added proteins listed above are selected and pooled. The cross-reacting antibodies are optionally removed from the pooled antisera by immunoabsorption with the added considered proteins, *e.g.*, distantly related

homologs. In addition, peptides comprising amino acid sequences representing conserved motifs that are used to identify members of the OR family can be used in cross-reactivity determinations.

The immunoabsorbed and pooled antisera are then used in a competitive 5 binding immunoassay as described above to compare a second protein, thought to be perhaps an allele or polymorphic variant of a OR family member, to the immunogen protein (*i.e.*, OR protein encoded by the nucleic acid sequences disclosed herein). In order to make this comparison, the two proteins are each assayed at a wide range of concentrations and the amount of each protein required to inhibit 50% of the binding 10 of the antisera to the immobilized protein is determined. If the amount of the second protein required to inhibit 50% of binding is less than 10 times the amount of the protein encoded by nucleic acid sequences disclosed herein required to inhibit 50% of binding, then the second protein is said to specifically bind to the polyclonal antibodies generated to a OR immunogen.

15 Antibodies raised against OR conserved motifs can also be used to prepare antibodies that specifically bind only to GPCRs of the OR family, but not to GPCRs from other families.

20 Polyclonal antibodies that specifically bind to a particular member of the OR family, *e.g.*, AOLFR1, can be make by subtracting out cross-reactive antibodies using other OR family members. Species-specific polyclonal antibodies can be made in a similar way. For example, antibodies specific to human AOLFR1 can be made by, subtracting out antibodies that are cross-reactive with orthologous sequences, *e.g.*, rat OR1 or mouse OR1.

d. Other assay formats

25 Western blot (immunoblot) analysis is used to detect and quantify the presence of OR protein in the sample. The technique generally comprises separating sample proteins by gel electrophoresis on the basis of molecular weight, transferring the separated proteins to a suitable solid support, (such as a nitrocellulose filter, a nylon filter, or derivatized nylon filter), and incubating the sample with the antibodies that 30 specifically bind the OR protein. The anti-OR polypeptide antibodies specifically bind to the OR polypeptide on the solid support. These antibodies may be directly labeled or alternatively may be subsequently detected using labeled antibodies (*e.g.*, labeled sheep anti-mouse antibodies) that specifically bind to the anti-OR antibodies.

Other, assay formats include liposome immunoassays (LIA), which use liposomes designed to bind specific molecules (e.g., antibodies) and release encapsulated reagents or markers. The released chemicals are then detected according to standard techniques (see Monroe *et al.*, *Amer. Clin. Prod. Rev.*, 5:34-41 (1986)).

5 e. Reduction of non-specific binding

One of skill in the art will appreciate that it is often desirable to minimize non-specific binding in immunoassays. Particularly, where the assay involves an antigen or antibody immobilized on a solid substrate it is desirable to minimize the amount of non-specific binding to the substrate. Means of reducing such non-specific 10 binding are well known to those of skill in the art. Typically, this technique involves coating the substrate with a proteinaceous composition. In particular, protein compositions such as bovine serum albumin (BSA), nonfat powdered milk, and gelatin are widely used with powdered milk being most preferred.

15 f. Labels

15 The particular label or detectable group used in the assay is not a critical aspect of the invention, as long as it does not significantly interfere with the specific binding of the antibody used in the assay. The detectable group can be any material having a detectable physical or chemical property. Such detectable labels have been well-developed in the field of immunoassays and, in general, most any label useful in such 20 methods can be applied to the present invention. Thus, a label is any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include magnetic beads (e.g., DYNABEADSTM) (SEQ ID NO: 529), fluorescent dyes (e.g., fluorescein isothiocyanate, Texas red, rhodamine, and the like), radiolabels (e.g., ³H, ¹²⁵I, ³⁵S, ¹⁴C, 25 or ³²P), enzymes (e.g., horseradish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and colorimetric labels such as colloidal gold or colored glass or plastic beads (e.g., polystyrene, polypropylene, latex, *etc.*).

30 The label may be coupled directly or indirectly to the desired component of the assay according to methods well known in the art. As indicated above, a wide variety of labels may be used, with the choice of label depending on sensitivity required, ease of conjugation with the compound, stability requirements, available instrumentation, and disposal provisions.

Non-radioactive labels are often attached by indirect means. Generally, a ligand molecule (*e.g.*, biotin) is covalently bound to the molecule. The ligand then binds to another molecules (*e.g.*, streptavidin) molecule, which is either inherently detectable or covalently bound to a signal system, such as a detectable enzyme, a 5 fluorescent compound, or a chemiluminescent compound. The ligands and their targets can be used in any suitable combination with antibodies that recognize a OR protein, or secondary antibodies that recognize anti-OR.

The molecules can also be conjugated directly to signal generating compounds, *e.g.*, by conjugation with an enzyme or fluorophore. Enzymes of interest 10 as labels will primarily be hydrolases, particularly phosphatases, esterases and glycosidases, or oxidotases, particularly peroxidases. Fluorescent compounds include fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone, *etc.* Chemiluminescent compounds include luciferin, and 2,3-dihydrophthalazinediones, *e.g.*, luminol. For a review of various labeling or 15 signal producing systems that may be used, *see* U.S. Patent No. 4,391,904.

Means of detecting labels are well known to those of skill in the art. Thus, for example, where the label is a radioactive label, means for detection include a scintillation counter or photographic film as in autoradiography. Where the label is a fluorescent label, it may be detected by exciting the fluorochrome with the appropriate 20 wavelength of light and detecting the resulting fluorescence. The fluorescence may be detected visually, by means of photographic film, by the use of electronic detectors such as charge coupled devices (CCDs) or photomultipliers and the like. Similarly, enzymatic labels may be detected by providing the appropriate substrates for the enzyme and detecting the resulting reaction product. Finally simple colorimetric 25 labels may be detected simply by observing the color associated with the label. Thus, in various dipstick assays, conjugated gold often appears pink, while various conjugated beads appear the color of the bead.

Some assay formats do not require the use of labeled components. For instance, agglutination assays can be used to detect the presence of the target 30 antibodies. In this case, antigen-coated particles are agglutinated by samples comprising the target antibodies. In this format, none of the components need be labeled and the presence of the target antibody is detected by simple visual inspection.

E. Detection of Olfactory Modulators

Methods and compositions for determining whether a test compound specifically binds to a mammalian chemosensory, and more particularly, an olfactory receptor of the invention, both *in vitro* and *in vivo* are described below. Many aspects 5 of cell physiology can be monitored to assess the effect of ligand-binding to a naturally-occurring or chimeric olfactory receptor. These assays may be performed on intact cells expressing an olfactory receptor, on permeabilized cells or on membrane fractions produced by standard methods.

Olfactory receptors are normally located on the specialized cilia of olfactory 10 neurons. These receptors bind odorants and initiate the transduction of chemical stimuli into electrical signals. An activated or inhibited G protein will in turn alter the properties of target enzymes, channels, and other effector proteins. Some examples include the activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G protein, phospholipase C by Gq and other 15 cognate G proteins, and modulation of diverse channels by Gi and other G proteins. Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

The OR protein of the assay will typically be selected from a polypeptide having a sequence selected from SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, 20 SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. 25 NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, 30 SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID.

NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. 5 NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. 10 NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID. NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO. 15 NO. 241, SEQ. ID. NO. 243, SEQ. ID. NO. 245, SEQ. ID. NO. 247, SEQ. ID. NO. 249, SEQ. ID. NO. 251, SEQ. ID. NO. 253, SEQ. ID. NO. 255, SEQ. ID. NO. 257, SEQ. ID. NO. 259, SEQ. ID. NO. 261, SEQ. ID. NO. 263, SEQ. ID. NO. 265, SEQ. ID. NO. 267, SEQ. ID. NO. 269, SEQ. ID. NO. 271, SEQ. ID. NO. 273, SEQ. ID. NO. 275, SEQ. ID. NO. 277, SEQ. ID. NO. 279, SEQ. ID. NO. 281, SEQ. ID. NO. 283, 20 SEQ. ID. NO. 285, SEQ. ID. NO. 287, SEQ. ID. NO. 289, SEQ. ID. NO. 291, SEQ. ID. NO. 293, SEQ. ID. NO. 295, SEQ. ID. NO. 297, SEQ. ID. NO. 299, SEQ. ID. NO. 301, SEQ. ID. NO. 303, SEQ. ID. NO. 305, SEQ. ID. NO. 307, SEQ. ID. NO. 309, SEQ. ID. NO. 311, SEQ. ID. NO. 313, SEQ. ID. NO. 315, SEQ. ID. NO. 317, SEQ. ID. NO. 319, SEQ. ID. NO. 321, SEQ. ID. NO. 323, SEQ. ID. NO. 325, SEQ. 25 ID. NO. 327, SEQ. ID. NO. 329, SEQ. ID. NO. 331, SEQ. ID. NO. 333, SEQ. ID. NO. 335, SEQ. ID. NO. 337, SEQ. ID. NO. 339, SEQ. ID. NO. 341, SEQ. ID. NO. 343, SEQ. ID. NO. 345, SEQ. ID. NO. 347, SEQ. ID. NO. 349, SEQ. ID. NO. 351, SEQ. ID. NO. 353, SEQ. ID. NO. 355, SEQ. ID. NO. 357, SEQ. ID. NO. 359, SEQ. ID. NO. 361, SEQ. ID. NO. 363, SEQ. ID. NO. 365, SEQ. ID. NO. 367, SEQ. ID. 30 NO. 369, SEQ. ID. NO. 371, SEQ. ID. NO. 373, SEQ. ID. NO. 375, SEQ. ID. NO. 377, SEQ. ID. NO. 379, SEQ. ID. NO. 381, SEQ. ID. NO. 383, SEQ. ID. NO. 385, SEQ. ID. NO. 387, SEQ. ID. NO. 389, SEQ. ID. NO. 391, SEQ. ID. NO. 393, SEQ. ID. NO. 395, SEQ. ID. NO. 397, SEQ. ID. NO. 399, SEQ. ID. NO. 401, SEQ. ID.

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15 Alternatively, the OR protein of the assay can be derived from a eukaryote host cell and can include an amino acid subsequence having at least about 30-40% amino acid sequence identity to SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, 20 SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. 25 NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. 30 NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID.

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ID. NO. 423, SEQ. ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID. NO. 431, SEQ. ID. NO. 433, SEQ. ID. NO. 435, SEQ. ID. NO. 437, SEQ. ID. NO. 439, SEQ. ID. NO. 441, SEQ. ID. NO. 443, SEQ. ID. NO. 445, SEQ. ID. NO. 447, SEQ. ID. NO. 449, SEQ. ID. NO. 451, SEQ. ID. NO. 453, SEQ. ID. NO. 455, SEQ.

5 ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID. NO. 465, SEQ. ID. NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO. 473, SEQ. ID. NO. 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481, SEQ. ID. NO. 483, SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ.

10 ID. NO. 491, SEQ. ID. NO. 493, SEQ. ID. NO. 495, SEQ. ID. NO. 497, SEQ. ID. NO. 499, SEQ. ID. NO. 501, SEQ. ID. NO. 503, SEQ. ID. NO. 505, SEQ. ID. NO. 507, SEQ. ID. NO. 509 and SEQ. ID. NO. 511.

Preferably, the amino acid sequence identity will be at least 50-75% preferably 85%, 90%, 95%, 96%, 97%, 98%, or 99%. Optionally, the polypeptide of the assays can comprise a domain of an OR protein, such as an extracellular domain, 15 transmembrane region, transmembrane domain, cytoplasmic domain, ligand-binding domain, subunit association domain, active site, and the like. Either the OR protein or a domain thereof can be covalently linked to a heterologous protein to create a chimeric protein used in the assays described herein. As discussed *infra*, the family of ORs provided herein exhibits substantial sequence similarity at both the DNA and 20 protein level, but also significant dissimilarity. In particular, the members possess an average percentage sequence identity to other members of the family when determined over the full length of the gene by about 30%. Moreover, different members of the genes at the protein level exhibit an average on the order of about 40% sequence identity to other members of the family when the full length protein sequences are 25 compared. However, while there exist differences, there are characteristic similarities, e.g. the consensus sequence already mentioned, which further define members of this novel genus of receptors.

Modulators of OR activity can be tested using OR polypeptides as described above, either recombinant or naturally occurring. The protein can be isolated, 30 expressed in a cell, expressed in a membrane derived from a cell, expressed in tissue or in an animal, either recombinant or naturally occurring. Modulation can be tested using one of the *in vitro* or *in vivo* assays described herein.

1. In vitro binding assays

Olfactory transduction can also be examined *in vitro* with soluble or solid state reactions, using a full-length OR or a chimeric molecule such as an extracellular domain or transmembrane region, or combination thereof, of a OR covalently linked 5 to a heterologous signal transduction domain, or a heterologous extracellular domain and/or transmembrane region covalently linked to the transmembrane and/or cytoplasmic domain of an OR. Furthermore, ligand-binding domains of the protein of interest can be used *in vitro* in soluble or solid state reactions to assay for ligand binding. In numerous embodiments, a chimeric receptor will be made that comprises 10 all or part of a OR polypeptide, as well an additional sequence that facilitates the localization of the OR to the membrane, such as a rhodopsin, *e.g.*, an N-terminal fragment of a rhodopsin protein, *e.g.* bovine or another mammalian rhodopsin.

Ligand binding to a OR protein, a domain, or chimeric protein can be tested in solution, in a bilayer membrane, attached to a solid phase, in a lipid monolayer, or in 15 vesicles. Binding of a modulator can be tested using, *e.g.*, changes in spectroscopic characteristics (*e.g.*, fluorescence, absorbence, refractive index) hydrodynamic (*e.g.*, shape), chromatographic, or solubility properties.

Receptor-G protein interactions can also be examined. For example, binding 20 of the G protein to the receptor or its release from the receptor can be examined. For example, in the absence of GTP, an activator will lead to the formation of a tight complex of a G protein (all three subunits) with the receptor. This complex can be detected in a variety of ways, as noted above. Such an assay can be modified to search for inhibitors, *e.g.*, by adding an activator to the receptor and G protein in the absence of GTP, which form a tight complex, and then screen for inhibitors by 25 looking at dissociation of the receptor-G protein complex. In the presence of GTP, release of the alpha subunit of the G protein from the other two G protein subunits serves as a criterion of activation.

An activated or inhibited G protein will in turn alter the properties of target 30 enzymes, channels, and other effector proteins. The classic examples are the activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G protein, phospholipase C by Gq and other cognate G proteins, and modulation of diverse channels by Gi and other G proteins.

Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

In another embodiment of the invention, a GTP γ S assay may be used. As described above, upon activation of a GPCR, the G α subunit of the G protein complex 5 is stimulated to exchange bound GDP for GTP. Ligand-mediated stimulation of G protein exchange activity can be measured in a biochemical assay measuring the binding of added radioactively-labeled GTP γ ³⁵S to the G protein in the presence of a putative ligand. Typically, membranes containing the chemosensory receptor of interest are mixed with a complex of G proteins. Potential inhibitors and/or activators 10 and GTP γ S are added to the assay, and binding of GTP γ S to the G protein is measured. Binding can be measured by liquid scintillation counting or by any other means known in the art, including scintillation proximity assays (SPA). In other assays formats, fluorescently-labeled GTP γ S can be utilized.

2. Fluorescence Polarization Assays

15 In another embodiment, Fluorescence Polarization ("FP") based assays may be used to detect and monitor odorant binding. Fluorescence polarization is a versatile laboratory technique for measuring equilibrium binding, nucleic acid hybridization, and enzymatic activity. Fluorescence polarization assays are homogeneous in that they do not require a separation step such as centrifugation, filtration, 20 chromatography, precipitation or electrophoresis. These assays are done in real time, directly in solution and do not require an immobilized phase. Polarization values can be measured repeatedly and after the addition of reagents since measuring the polarization is rapid and does not destroy the sample. Generally, this technique can be used to measure polarization values of fluorophores from low picomolar to 25 micromolar levels. This section describes how fluorescence polarization can be used in a simple and quantitative way to measure the binding of odorants to the olfactory receptors of the invention.

When a fluorescently labeled molecule is excited with plane polarized light, it 30 emits light that has a degree of polarization that is inversely proportional to its molecular rotation. Large fluorescently labeled molecules remain relatively stationary during the excited state (4 nanoseconds in the case of fluorescein) and the polarization of the light remains relatively constant between excitation and emission. Small fluorescently labeled molecules rotate rapidly during the excited state and the

polarization changes significantly between excitation and emission. Therefore, small molecules have low polarization values and large molecules have high polarization values. For example, a single-stranded fluorescein-labeled oligonucleotide has a relatively low polarization value but when it is hybridized to a complementary strand, 5 it has a higher polarization value. When using FP to detect and monitor odorant-binding which may activate or inhibit the olfactory receptors of the invention, fluorescence-labeled odorants or auto-fluorescent odorants may be used.

Fluorescence polarization (P) is defined as:

$$P = \frac{Int_{\parallel} - Int_{\perp}}{Int_{\parallel} + Int_{\perp}}$$

10 Where \parallel is the intensity of the emission light parallel to the excitation light plane and $Int \perp$ is the intensity of the emission light perpendicular to the excitation light plane. P, being a ratio of light intensities, is a dimensionless number. For example, the Beacon ® and Beacon 2000 ™ System may be used in connection with these assays. Such systems typically express polarization in millipolarization units (1
15 Polarization Unit = 1000 mP Units).

The relationship between molecular rotation and size is described by the Perrin equation and the reader is referred to Jolley, M. E. (1991) in Journal of Analytical Toxicology, pp. 236-240, which gives a thorough explanation of this equation. Summarily, the Perrin equation states that polarization is directly proportional to the 20 rotational relaxation time, the time that it takes a molecule to rotate through an angle of approximately 68.5°. Rotational relaxation time is related to viscosity (η), absolute temperature (T), molecular volume (V), and the gas constant (R) by the following equation:

$$Rotational\ Relaxation\ Time = \frac{3\eta V}{RT}$$

25 The rotational relaxation time is small (\approx 1 nanosecond) for small molecules (e.g. fluorescein) and large (\approx 100 nanoseconds) for large molecules (e.g. immunoglobulins). If viscosity and temperature are held constant, rotational relaxation time, and therefore polarization, is directly related to the molecular volume. Changes in molecular volume may be due to interactions with other molecules, 30 dissociation, polymerization, degradation, hybridization, or conformational changes of the fluorescently labeled molecule. For example, fluorescence polarization has been

used to measure enzymatic cleavage of large fluorescein labeled polymers by proteases, DNases, and RNases. It also has been used to measure equilibrium binding for protein/protein interactions, antibody/antigen binding, and protein/DNA binding.

3. Solid state and soluble high throughput assays

5 In yet another embodiment, the invention provides soluble assays using molecules such as a domain such as ligand-binding domain, an extracellular domain, a transmembrane domain (e.g., one comprising seven transmembrane regions and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, etc.; a domain that is covalently linked to a heterologous 10 protein to create a chimeric molecule; an OR protein; or a cell or tissue expressing an OR protein, either naturally occurring or recombinant. In another embodiment, the invention provides solid phase based in vitro assays in a high throughput format, where the domain, chimeric molecule, OR protein, or cell or tissue expressing the OR is attached to a solid phase substrate.

15 In the high throughput assays of the invention, it is possible to screen up to several thousand different modulators or ligands in a single day. In particular, each well of a microtiter plate can be used to run a separate assay against a selected potential modulator, or, if concentration or incubation time effects are to be observed, every 5-10 wells can test a single modulator. Thus, a single standard microtiter plate 20 can assay about 100 (e.g., 96) modulators. If 1536 well plates are used, then a single plate can easily assay from about 1000 to about 1500 different compounds. It is also possible to assay multiple compounds in each plate well. Further, it is possible to assay several different plates per day; assay screens for up to about 6,000-20,000 different compounds is possible using the integrated systems of the invention. More 25 recently, microfluidic approaches to reagent manipulation have been developed.

The molecule of interest can be bound to the solid state component, directly or indirectly, via covalent or non covalent linkage, e.g., via a tag. The tag can be any of a variety of components. In general, a molecule which binds the tag (a tag binder) is fixed to a solid support, and the tagged molecule of interest (e.g., the olfactory 30 transduction molecule of interest) is attached to the solid support by interaction of the tag and the tag binder.

A number of tags and tag binders can be used, based upon known molecular interactions well described in the literature. For example, where a tag has a natural

binder, for example, biotin, protein A, or protein G, it can be used in conjunction with appropriate tag binders (avidin, streptavidin, neutravidin, the Fc region of an immunoglobulin, *etc.*). Antibodies to molecules with natural binders such as biotin are also widely available and appropriate tag binders (*see*, SIGMA Immunochemicals 5 1998 catalogue SIGMA, St. Louis MO).

Similarly, any haptenic or antigenic compound can be used in combination with an appropriate antibody to form a tag/tag binder pair. Thousands of specific antibodies are commercially available and many additional antibodies are described in the literature. For example, in one common configuration, the tag is a first antibody 10 and the tag binder is a second antibody which recognizes the first antibody. In addition to antibody-antigen interactions, receptor-ligand interactions are also appropriate as tag and tag-binder pairs. For example, agonists and antagonists of cell membrane receptors (*e.g.*, cell receptor-ligand interactions such as transferrin, c-kit, viral receptor ligands, cytokine receptors, chemokine receptors, interleukin receptors, 15 immunoglobulin receptors and antibodies, the cadherein family, the integrin family, the selectin family, and the like; *see, e.g.*, Pigott & Power, *The Adhesion Molecule Facts Book I* (1993)). Similarly, toxins and venoms, viral epitopes, hormones (*e.g.*, opiates, steroids, *etc.*), intracellular receptors (*e.g.*, which mediate the effects of various small ligands, including steroids, thyroid hormone, retinoids and vitamin D; 20 peptides), drugs, lectins, sugars, nucleic acids (both linear and cyclic polymer configurations), oligosaccharides, proteins, phospholipids and antibodies can all interact with various cell receptors.

Synthetic polymers, such as polyurethanes, polyesters, polycarbonates, polyureas, polyamides, polyethyleneimines, polyarylene sulfides, polysiloxanes, 25 polyimides, and polyacetates can also form an appropriate tag or tag binder. Many other tag/tag binder pairs are also useful in assay systems described herein, as would be apparent to one of skill upon review of this disclosure.

Common linkers such as peptides, polyethers, and the like can also serve as tags, and include polypeptide sequences, such as poly gly sequences of between about 30 5 and 200 amino acids. Such flexible linkers are known to persons of skill in the art. For example, poly(ethylene glycol) linkers are available from Shearwater Polymers, Inc. Huntsville, Alabama. These linkers optionally have amide linkages, sulfhydryl linkages, or heterofunctional linkages.

Tag binders are fixed to solid substrates using any of a variety of methods currently available. Solid substrates are commonly derivatized or functionalized by exposing all or a portion of the substrate to a chemical reagent that fixes a chemical group to the surface which is reactive with a portion of the tag binder. For example, 5 groups that are suitable for attachment to a longer chain portion would include amines, hydroxyl, thiol, and carboxyl groups. Aminoalkylsilanes and hydroxyalkylsilanes can be used to functionalize a variety of surfaces, such as glass surfaces. The construction of such solid phase biopolymer arrays is well described in the literature. *See, e.g.*, Merrifield, *J. Am. Chem. Soc.*, 85:2149-54 (1963) (describing 10 solid phase synthesis of, *e.g.*, peptides); Geysen *et al.*, *J. Immun. Meth.*, 102:259-74 (1987) (describing synthesis of solid phase components on pins); Frank & Doring, *Tetrahedron*, 44:60316040 (1988) (describing synthesis of various peptide sequences on cellulose disks); Fodor *et al.*, *Science*, 251:767-77 (1991); Sheldon *et al.*, *Clinical Chemistry*, 39(4):718-19 (1993); and Kozal *et al.*, *Nature Medicine*, 2(7):753759 (1996) (all describing arrays of biopolymers fixed to solid substrates). Non-chemical 15 approaches for fixing tag binders to substrates include other common methods, such as heat, cross-linking by UV radiation, and the like.

4. Computer-based assays

Yet another assay for compounds that modulate OR protein activity involves 20 computer assisted compound design, in which a computer system is used to generate a three-dimensional structure of an OR protein based on the structural information encoded by its amino acid sequence. The input amino acid sequence interacts directly and actively with a preestablished algorithm in a computer program to yield secondary, tertiary, and quaternary structural models of the protein. The models of the 25 protein structure are then examined to identify regions of the structure that have the ability to bind, *e.g.*, ligands. These regions are then used to identify ligands that bind to the protein.

The three-dimensional structural model of the protein is generated by entering 30 protein amino acid sequences of at least 10 amino acid residues or corresponding nucleic acid sequences encoding a OR polypeptide into the computer system. The nucleotide sequence encoding the polypeptide, or the amino acid sequence thereof, can be any of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID

NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID 5 NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, 10 SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID 15 NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, 20 SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID 25 NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, 30 SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,

SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359,
5 SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449,
10 SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511, and conservatively modified versions thereof.

The amino acid sequence represents the primary sequence or subsequence of the protein, which encodes the structural information of the protein. At least 10 residues of the amino acid sequence (or a nucleotide sequence encoding 10 amino acids) are entered into the computer system from computer keyboards, computer readable substrates that include, but are not limited to, electronic storage media (e.g., magnetic diskettes, tapes, cartridges, and chips), optical media (e.g., CD ROM), information distributed by internet sites, and by RAM. The three-dimensional structural model of the protein is then generated by the interaction of the amino acid sequence and the computer system, using software known to those of skill in the art.

The amino acid sequence represents a primary structure that encodes the information necessary to form the secondary, tertiary and quaternary structure of the

protein of interest. The software looks at certain parameters encoded by the primary sequence to generate the structural model. These parameters are referred to as "energy terms," and primarily include electrostatic potentials, hydrophobic potentials, solvent accessible surfaces, and hydrogen bonding. Secondary energy terms include van der 5 Waals potentials. Biological molecules form the structures that minimize the energy terms in a cumulative fashion. The computer program is therefore using these terms encoded by the primary structure or amino acid sequence to create the secondary structural model.

10 The tertiary structure of the protein encoded by the secondary structure is then formed on the basis of the energy terms of the secondary structure. The user at this point can enter additional variables such as whether the protein is membrane bound or soluble, its location in the body, and its cellular location, *e.g.*, cytoplasmic, surface, or nuclear. These variables along with the energy terms of the secondary structure are used to form the model of the tertiary structure. In modeling the tertiary structure, the 15 computer program matches hydrophobic faces of secondary structure with like, and hydrophilic faces of secondary structure with like.

Once the structure has been generated, potential ligand-binding regions are identified by the computer system. Three-dimensional structures for potential ligands are generated by entering amino acid or nucleotide sequences or chemical formulas of 20 compounds, as described above. The three-dimensional structure of the potential ligand is then compared to that of the OR protein to identify ligands that bind to the protein. Binding affinity between the protein and ligands is determined using energy terms to determine which ligands have an enhanced probability of binding to the protein.

25 Computer systems are also used to screen for mutations, polymorphic variants, alleles and interspecies homologs of OR genes. Such mutations can be associated with disease states or genetic traits. As described above, GeneChip™ and related technology can also be used to screen for mutations, polymorphic variants, alleles and interspecies homologs. Once the variants are identified, diagnostic assays can be used 30 to identify patients having such mutated genes. Identification of the mutated OR genes involves receiving input of a first nucleic acid or amino acid sequence of a OR gene, or conservatively modified versions thereof. The sequence is entered into the computer system as described above. The first nucleic acid or amino acid sequence is

then compared to a second nucleic acid or amino acid sequence that has substantial identity to the first sequence. The second sequence is entered into the computer system in the manner described above. Once the first and second sequences are compared, nucleotide or amino acid differences between the sequences are identified.

5 Such sequences can represent allelic differences in various OR genes, and mutations associated with disease states and genetic traits.

5. Cell-based binding assays

In a preferred embodiment, an OR polypeptide is expressed in a eukaryotic cell as a chimeric receptor with a heterologous, chaperone sequence that facilitates its 10 maturation and targeting through the secretory pathway. In a preferred embodiment, the heterologous sequence is a rhodopsin sequence, such as an N-terminal fragment of a rhodopsin. Such chimeric OR receptors can be expressed in any eukaryotic cell, such as HEK-293 cells. Preferably, the cells comprise a functional G protein, *e.g.*, G α 15, that is capable of coupling the chimeric receptor to an intracellular signaling 15 pathway or to a signaling protein such as phospholipase C. Activation of such chimeric receptors in such cells can be detected using any standard method, such as by detecting changes in intracellular calcium by detecting FURA-2 dependent fluorescence in the cell.

Activated GPCR receptors become substrates for kinases that phosphorylate 20 the C-terminal tail of the receptor (and possibly other sites as well). Thus, activators will promote the transfer of 32 P from gamma-labeled GTP to the receptor, which can be assayed with a scintillation counter. The phosphorylation of the C-terminal tail will promote the binding of arrestin-like proteins and will interfere with the binding of 25 G proteins. The kinase/arrestin pathway plays a key role in the desensitization of many GPCR receptors. For example, compounds that modulate the duration an olfactory receptor stays active would be useful as a means of prolonging a desired odor or cutting off an unpleasant one. For a general review of GPCR signal transduction and methods of assaying signal transduction, *see, e.g.*, *Methods in Enzymology*, vols. 237 and 238 (1994) and volume 96 (1983); Bourne *et al.*, *Nature*, 30 10:349:117-27 (1991); Bourne *et al.*, *Nature*, 348:125-32 (1990); Pitcher *et al.*, *Annu. Rev. Biochem.*, 67:653-92 (1998).

OR modulation may be assayed by comparing the response of an OR polypeptide treated with a putative OR modulator to the response of an untreated

control sample. Such putative OR modulators can include odorants that either inhibit or activate OR polypeptide activity. In one embodiment, control samples (untreated with activators or inhibitors) are assigned a relative OR activity value of 100. Inhibition of an OR polypeptide is achieved when the OR activity value relative to the 5 control is about 90%, optionally 50%, optionally 25-0%. Activation of an OR polypeptide is achieved when the OR activity value relative to the control is 110%, optionally 150%, 200-500%, or 1000-2000%.

Changes in ion flux may be assessed by determining changes in polarization (i.e., electrical potential) of the cell or membrane expressing a OR protein. One 10 means to determine changes in cellular polarization is by measuring changes in current (thereby measuring changes in polarization) with voltage-clamp and patch-clamp techniques, *e.g.*, the “cell-attached” mode, the “inside-out” mode, and the “whole cell” mode (*see, e.g.*, Ackerman *et al.*, *New Engl. J Med.*, 336:1575-1595 15 (1997)). Whole cell currents are conveniently determined using the standard. Other known assays include: radiolabeled ion flux assays and fluorescence assays using 20 voltage-sensitive dyes (*see, e.g.*, Vestergaard-Bogind *et al.*, *J. Membrane Biol.*, 88:67-75 (1988); Gonzales & Tsien, *Chem. Biol.*, 4:269277 (1997); Daniel *et al.*, *J. Pharmacol. Meth.*, 25:185-193 (1991); Holevinsky *et al.*, *J. Membrane Biology*, 137:59-70 (1994)). Generally, the compounds to be tested are present in the range from 1 pM to 100 mM.

The effects of the test compounds upon the function of the polypeptides can be measured by examining any of the parameters described above. Any suitable physiological change that affects GPCR activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional 25 consequences are determined using intact cells or animals, one can also measure a variety of effects such as transmitter release, hormone release, transcriptional changes to both known and uncharacterized genetic markers (*e.g.*, northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as Ca^{2+} , IP3, cGMP, or cAMP.

Preferred assays for GPCRs include cells that are loaded with ion or voltage sensitive dyes to report receptor activity. Assays for determining activity of such receptors can also use known agonists and antagonists for other G protein coupled receptors as negative or positive controls to assess activity of tested compounds. In 30

assays for identifying modulatory compounds (e.g., agonists, antagonists), changes in the level of ions in the cytoplasm or membrane voltage will be monitored using an ion sensitive or membrane voltage fluorescent indicator, respectively. Among the ion-sensitive indicators and voltage probes that may be employed are those disclosed 5 in the Molecular Probes 1997 Catalog. For G protein coupled receptors, promiscuous G proteins such as G α 15 and G α 16 can be used in the assay of choice (Wilkie *et al.*, *PNAS*, 88:10049-53 (1991)). Such promiscuous G proteins allow coupling of a wide range of receptors.

Receptor activation typically initiates subsequent intracellular events, *e.g.*, 10 increases in second messengers such as IP3, which releases intracellular stores of calcium ions. Activation of some G protein coupled receptors stimulates the formation of inositol triphosphate (IP3) through phospholipase C-mediated hydrolysis of phosphatidylinositol (Berridge & Irvine, *Nature*, 312:315-21 (1984)). IP3 in turn stimulates the release of intracellular calcium ion stores. Thus, a change in 15 cytoplasmic calcium ion levels, or a change in second messenger levels such as IP3 can be used to assess G protein coupled receptor function. Cells expressing such G protein coupled receptors may exhibit increased cytoplasmic calcium levels as a result of contribution from both intracellular stores and via activation of ion channels, in which case it may be desirable although not necessary to conduct such assays in 20 calcium-free buffer, optionally supplemented with a chelating agent such as EGTA, to distinguish fluorescence response resulting from calcium release from internal stores.

Other assays can involve determining the activity of receptors which, when activated, result in a change in the level of intracellular cyclic nucleotides, *e.g.*, cAMP or cGMP, by activating or inhibiting enzymes such as adenylate cyclase. There are 25 cyclic nucleotide-gated ion channels, *e.g.*, rod photoreceptor cell channels and olfactory neuron channels that are permeable to cations upon activation by binding of cAMP or cGMP (*see, e.g.*, Altenhofen *et al.*, *PNAS*, 88:9868-72 (1991) and Dhallan *et al.*, *Nature*, 347:184-187 (1990)). In cases where activation of the receptor results in a decrease in cyclic nucleotide levels, it may be preferable to expose the cells to agents 30 that increase intracellular cyclic nucleotide levels, *e.g.*, forskolin, prior to adding a receptor-activating compound to the cells in the assay. Cells for this type of assay can be made by co-transfection of a host cell with DNA encoding a cyclic nucleotide-crated ion channel, GPCR phosphatase and DNA encoding a receptor (*e.g.*,

certain glutamate receptors, muscarinic acetylcholine receptors, dopamine receptors, serotonin receptors, and the like), which, when activated, causes a change in cyclic nucleotide levels in the cytoplasm.

In a preferred embodiment, OR protein activity is measured by expressing a 5 OR gene in a heterologous cell with a promiscuous G protein that links the receptor to a phospholipase C signal transduction pathway (see Offermanns & Simon, *J. Biol. Chem.*, 270:15175-15180 (1995)). Optionally the cell line is HEK-293 (which does not naturally express OR genes) and the promiscuous G protein is G α 15/G α 16 (Offermanns & Simon, *supra*). Modulation of olfactory transduction is assayed by 10 measuring changes in intracellular Ca²⁺ levels, which change in response to modulation of the OR signal transduction pathway via administration of a molecule that associates with a OR protein. Changes in Ca²⁺ levels are optionally measured using fluorescent Ca²⁺ indicator dyes and fluorometric imaging.

In one embodiment, the changes in intracellular cAMP or cGMP can be 15 measured using immunoassays. The method described in Offermanns & Simon, *J. Bio. Chem.*, 270:15175-15180 (1995), may be used to determine the level of cAMP. Also, the method described in Felley-Bosco *et al.*, *Am. J. Resp. Cell and Mol. Biol.*, 11:159-164 (1994), may be used to determine the level of cGMP. Further, an assay 20 kit for measuring cAMP and/or cGMP is described in U.S. Patent 4,115,538, herein incorporated by reference.

In another embodiment, phosphatidyl inositol (PI) hydrolysis can be analyzed according to U.S. Patent 5,436,128, herein incorporated by reference. Briefly, the assay involves labeling of cells with ³H-myoinositol for 48 or more hrs. The labeled cells are treated with a test compound for one hour. The treated cells are lysed and 25 extracted in chloroform-methanol-water after which the inositol phosphates were separated by ion exchange chromatography and quantified by scintillation counting. Fold stimulation is determined by calculating the ratio of cpm in the presence of agonist, to cpm in the presence of buffer control. Likewise, fold inhibition is determined by calculating the ratio of cpm in the presence of antagonist, to cpm in the 30 presence of buffer control (which may or may not contain an agonist).

In another embodiment, transcription levels can be measured to assess the effects of a test compound on signal transduction. A host cell containing an OR protein of interest is contacted with a test compound for a sufficient time to effect any

interactions, and then the level of gene expression is measured. The amount of time to effect such interactions may be empirically determined, such as by running a time course and measuring the level of transcription as a function of time. The amount of transcription may be measured by using any method known to those of skill in the art

5 to be suitable. For example, mRNA expression of the protein of interest may be detected using northern blots or their polypeptide products may be identified using immunoassays. Alternatively, transcription based assays using reporter gene may be used as described in U.S. Patent 5,436,128, herein incorporated by reference. The reporter genes can be, e.g., chloramphenicol acetyltransferase, luciferase,

10 '3-galactosidase and alkaline phosphatase. Furthermore, the protein of interest can be used as an indirect reporter via attachment to a second reporter such as green fluorescent protein (see, e.g., Mistili & Spector, *Nature Biotechnology*, 15:961-64 (1997)).

The amount of transcription is then compared to the amount of transcription in

15 either the same cell in the absence of the test compound, or it may be compared with the amount of transcription in a substantially identical cell that lacks the OR protein of interest. A substantially identical cell may be derived from the same cells from which the recombinant cell was prepared but which had not been modified by introduction of heterologous DNA. Any difference in the amount of transcription indicates that the

20 test compound has in some manner altered the activity of the OR protein of interest.

6. Transgenic non-human animals expressing olfactory receptors

Non-human animals expressing one or more olfactory receptor sequences of the invention, particularly human olfactory receptor sequences, can also be used for receptor assays. Such expression can be used to determine whether a test compound

25 specifically binds to a mammalian olfactory transmembrane receptor polypeptide *in vivo* by contacting a non-human animal stably or transiently transfected with a nucleic acid encoding an olfactory receptor or ligand-binding region thereof with a test compound and determining whether the animal reacts to the test compound by specifically binding to the receptor polypeptide.

30 Use of the translocation domains of the invention in the fusion polypeptides generates a cell expressing high levels of olfactory receptor. Animals transfected or infected with the vectors of the invention are particularly useful for assays to identify and characterize odorants/ligands that can bind to a specific or sets of receptors. Such

vector-infected animals expressing libraries of human olfactory sequences can be used for *in vivo* screening of odorants and their effect on, *e.g.*, cell physiology (*e.g.*, on olfactory neurons), on the CNS (*e.g.*, olfactory bulb activity), or behavior.

Means to infect/express the nucleic acids and vectors, either individually or as 5 libraries, are well known in the art. A variety of individual cell, organ or whole animal parameters can be measured by a variety of means. For example, recording of stimulant-induced waves (bulbar responses) from the main olfactory bulb or accessory olfactory bulb is a useful tool for measuring quantitative stable olfactory responses. When electrodes are located on the olfactory bulb surface it is possible to record stable 10 responses over a period of several days (*see, e.g.*, Kashiwayanagi, *Brain Res. Protoc.* 1:287-291 (1997)). In this study, electroolfactogram recordings were made with a four-electrode assembly from the olfactory epithelium overlying the endoturbinate bones facing the nasal septum. Four electrodes were fixed along the dorsal-to-ventral axis of one turbinate bone or were placed in corresponding positions on four turbinate 15 bones and moved together up toward the top of the bone. *See also*, Scott, *J. Neurophysiol.* 77:1950-1962 (1997); Scott, *J. Neurophysiol.* 75:2036-2049 (1996); Ezeh, *J. Neurophysiol.* 73:2207-2220 (1995). In other systems, fluorescence changes in nasal epithelium can be measured using the dye di-4-ANEPPS, which is applied on the rat's nasal septum and medial surface of the turbinates (*see, e.g.*, Youngentob, *J. 20 Neurophysiol.* 73:387-398 (1995)). Extracellular potassium activity (aK) measurements can also be carried out in *in vivo*. An increase in aK can be measured in the mucus and the proximal part of the nasal epithelium (*see, e.g.*, Khayari, *Brain Res.* 539:1-5 (1991)).

The OR sequences of the invention can be for example expressed in animal 25 nasal epithelium by delivery with an infecting agent, *e.g.*, adenovirus expression vector. Recombinant adenovirus-mediated expression of a recombinant gene in olfactory epithelium using green fluorescent protein as a marker is described by, *e.g.*, Touhara, *PNAS*, 96:4040-45 (1999).

The endogenous olfactory receptor genes can remain functional and wild-type 30 (native) activity can still be present. In other situations, where it is desirable that all olfactory receptor activity is by the introduced exogenous hybrid receptor, use of a knockout line is preferred. Methods for the construction of non-human transgenic

animals, particularly transgenic mice, and the selection and preparation of recombinant constructs for generating transformed cells are well known in the art.

Construction of a "knockout" cell and animal is based on the premise that the level of expression of a particular gene in a mammalian cell can be decreased or 5 completely abrogated by introducing into the genome a new DNA sequence that serves to interrupt some portion of the DNA sequence of the gene to be suppressed. Also, "gene trap insertion" can be used to disrupt a host gene, and mouse embryonic stem (ES) cells can be used to produce knockout transgenic animals (see, e.g., Holzschu, *Transgenic Res.* 6:97-106 (1997)). The insertion of the exogenous is 10 typically by homologous recombination between complementary nucleic acid sequences. The exogenous sequence is some portion of the target gene to be modified, such as exonic, intronic or transcriptional regulatory sequences, or any genomic sequence which is able to affect the level of the target gene's expression; or a combination thereof. Gene targeting via homologous recombination in pluripotential 15 embryonic stem cells allows one to modify precisely the genomic sequence of interest. Any technique can be used to create, screen for, propagate, a knockout animal, e.g., see Bijvoet, *Hum. Mol. Genet.* 7:53-62 (1998); Moreadith, *J. Mol. Med.* 75:208-216 (1997); Tojo, *Cytotechnology* 19:161-165 (1995); Mudgett, *Methods Mol. Biol.* 48:167-184 (1995); Longo, *Transgenic Res.* 6:321-328 (1997); U.S. Patents Nos. 20 5,616,491; 5,464,764; 5,631,153; 5,487,992; 5,627,059; 5,272,071; WO 91/09955; WO 93/09222; WO 96/29411; WO 95/31560; WO 91/12650.

The nucleic acid libraries of the invention can also be used as reagents to produce "knockout" human cells and their progeny. Likewise, the nucleic acids of the invention can also be used as reagents to produce "knock-ins" in mice. The human or 25 rat OR gene sequences can replace the orthologous ORs in the mouse genome. In this way, a mouse expressing a human or rat OR can be produced. This mouse can then be used to analyze the function of human or rat ORs, and to identify ligands for such ORs.

F. Modulators

30 The compounds tested as modulators of an OR family member can be any small chemical compound, or a biological entity, such as a protein, sugar, nucleic acid or lipid. Alternatively, modulators can be genetically altered versions of an OR gene.

Typically, test compounds will be small chemical molecules and peptides. Essentially any chemical compound can be used as a potential modulator or ligand in the assays of the invention, although most often compounds can be dissolved in aqueous or organic (especially DMSO-based) solutions are used. The assays are designed to

5 screen large chemical libraries by automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (e.g., in microtiter formats on microtiter plates in robotic assays). It will be appreciated that there are many suppliers of chemical compounds, including Sigma (St. Louis, MO), Aldrich (St. Louis, MO), Sigma-Aldrich (St. Louis, MO), Fluka

10 Chemika-Biochemica Analytika (Buchs, Switzerland) and the like.

The OR modulating compounds can be used in any number of consumer products, including, but not limited to, perfumes, fragrance compositions, deodorants, air fresheners, foods, drugs, *etc.*, or ingredients thereof, to thereby modulate the odor of the product, composition, or ingredient in a desired manner. As

15 one of skill in the art will recognize, OR modulating compounds can be used to enhance desirable odors, to block malodors, or a combination thereof.

In one preferred embodiment, high throughput screening methods involve providing a combinatorial chemical or peptide library containing a large number of potential therapeutic compounds (potential modulator or ligand compounds). Such

20 "combinatorial chemical libraries" or "ligand libraries" are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual odorant compositions.

25 A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis, by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (amino acids) in every possible way for a

30 given compound length (*i.e.*, the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks.

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent 5,010,175, Furka, *Int. J. Pept. Prot. Res.*, 37:487-93 (1991) and Houghton *et al.*, *Nature*, 354:84-88 (1991)). Other 5 chemistries for generating chemical diversity libraries can also be used. Such chemistries include, but are not limited to: peptoids (e.g., PCT Publication No. WO 91/19735), encoded peptides (e.g., PCT Publication WO 93/20242), random bio-oligomers (e.g., PCT Publication No. WO 92/00091), benzodiazepines (e.g., U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides 10 (Hobbs *et al.*, *PNAS*, 90:6909-13 (1993)), vinylogous polypeptides (Hagihara *et al.*, *J. Amer. Chem. Soc.*, 114:6568 (1992)), nonpeptidal peptidomimetics with glucose scaffolding (Hirschmann *et al.*, *J. Amer. Chem. Soc.*, 114:9217-18 (1992)), analogous 15 organic syntheses of small compound libraries (Chen *et al.*, *J. Amer. Chem. Soc.*, 116:2661 (1994)), oligocarbamates (Cho *et al.*, *Science*, 261:1303 (1993)), peptidyl phosphonates (Campbell *et al.*, *J. Org. Chem.*, 59:658 (1994)), nucleic acid libraries 20 (Ausubel, Berger and Sambrook, all *supra*), peptide nucleic acid libraries (U.S. Patent 5,539,083), antibody libraries (Vaughn *et al.*, *Nature Biotechnology*, 14(3):309-14 (1996) and PCT/US96/10287), carbohydrate libraries (Liang *et al.*, *Science*, 274:1520-22 (1996) and U.S. Patent 5,593,853), small organic molecule libraries 25 (benzodiazepines, Baum, *C&EN*, Jan 18, page 33 (1993); thiazolidinones and metathiazanones, U.S. Patent 5,549,974; pynrolidines, U.S. Patents 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent 5,506,337; benzodiazepines, 30 5,288,514, and the like).

Devices for the preparation of combinatorial libraries are commercially 25 available (see, e.g., 357 MPS, 390 MPS (Advanced Chem Tech, Louisville KY), Symphony (Rainin, Woburn, MA), 433A (Applied Biosystems, Foster City, CA), 9050 Plus (Millipore, Bedford, MA)). In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, NJ; Tripos, Inc., St. Louis, MO; 3D Pharmaceuticals, Exton, PA; Martek Biosciences; Columbia, 30 MD; etc.).

G. Methods for Representing and Predicting the Perception of Odor

The invention also preferably provides methods for representing the perception of odor (or taste) and/or for predicting the perception of odor (or taste) in a mammal, including in a human. Preferably, such methods may be performed by using the 5. receptors and genes encoding said olfactory receptors disclosed herein.

Also contemplated as within the invention, is a method of screening one or more compounds for the presence of an odor detectable by a mammal, comprising: contacting said one or more compounds with the disclosed receptors, preferably wherein the mammal is a human. Also contemplated as within the invention is a 10 method for representing olfactory perception of a particular smell in a mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n olfactory receptors of said vertebrate, where n is greater than or equal to 4; and generating from said values a quantitative representation of olfactory perception. The olfactory receptors may be an olfactory receptor disclosed herein, the 15 representation may constitutes a point or a volume in n -dimensional space, may constitutes a graph or a spectrum, and may constitutes a matrix of quantitative representations. Also, the providing step may comprise contacting a plurality of recombinantly-produced olfactory receptors with a test composition and quantitatively measuring the interaction of said composition with said receptors.

20 Also contemplated as within the invention, is a method for predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n olfactory receptors of said vertebrate, where n is greater than or equal to 4, 25 for one or more molecules or combinations of molecules yielding known olfactory perception in a mammal; and generating from said values a quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known olfactory perception in a mammal, providing values X_1 to X_n representative of the quantitative stimulation of each of n olfactory receptors of 30 said vertebrate, where n is greater than or equal to 4, for one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal; and generating from said values a quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding

unknown olfactory perception in a mammal, and predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal by comparing the quantitative representation of olfactory perception in a mammal for the one or more molecules or

5 combinations of molecules yielding unknown olfactory perception in a mammal to the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known olfactory perception in a mammal. The olfactory receptors used in this method may include an olfactory receptor disclosed herein.

10 In another embodiment, novel molecules or combinations of molecules are generated which elicit a predetermined olfactory perception in a mammal by determining a value of olfactory perception in a mammal for a known molecule or combinations of molecules as described above; determining a value of olfactory perception in a mammal for one or more unknown molecules or combinations of molecules as described above; comparing the value of olfactory perception in a mammal for one or more unknown compositions to the value of olfactory perception in a mammal for one or more known compositions; selecting a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal; and combining two or more unknown molecules or combinations of molecules to form a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal. The combining step yields a single molecule or a combination of molecules that elicits a predetermined olfactory perception in a mammal.

In another embodiment of the invention, there is provided a method for simulating a fragrance, comprising: for each of a plurality of cloned olfactory receptors, preferably human receptors, ascertaining the extent to which the receptor interacts with the fragrance; and combining a plurality of compounds, each having a previously-ascertained interaction with one or more of the receptors, in amounts that together provide a receptor-stimulation profile that mimics the profile for the fragrance. Interaction of a fragrance with an olfactory receptor can be determined using any of the binding or reporter assays described herein. The plurality of compounds may then be combined to form a mixture. If desired, one or more of the plurality of the compounds can be combined covalently. The combined compounds

substantially stimulate at least 75%, 80% or 90% of the receptors that are substantially stimulated by the fragrance.

In another preferred embodiment of the invention, a plurality of standard compounds are tested against a plurality of olfactory receptors to ascertain the extent 5 to which the receptors each interact with each standard compound, thereby generating a receptor stimulation profile for each standard compound. These receptor stimulation profiles may then be stored in a relational database on a data storage medium. The method may further comprise providing a desired receptor-stimulation profile for a scent; comparing the desired receptor stimulation profile to the relational database; 10 and ascertaining one or more combinations of standard compounds that most closely match the desired receptor-stimulation profile. The method may further comprise combining standard compounds in one or more of the ascertained combinations to simulate the scent.

H. Kits

15 OR genes and their homologs are useful tools for identifying olfactory receptor cells, for forensics and paternity determinations, and for examining olfactory transduction. OR family member-specific reagents that specifically hybridize to OR nucleic acids, such as AOLFR1 probes and primers, and OR family member-specific reagents that specifically bind to an OR protein, *e.g.*, OR antibodies are used to 20 examine olfactory cell expression and olfactory transduction regulation.

Nucleic acid assays for the presence of DNA and RNA for an OR family member in a sample include numerous techniques known to those skilled in the art, such as southern analysis, northern analysis, dot blots, RNase protection, S1 analysis, amplification techniques such as PCR, and *in situ* hybridization. In *in situ* 25 hybridization, for example, the target nucleic acid is liberated from its cellular surroundings in such a form so as to be available for hybridization within the cell, while preserving the cellular morphology for subsequent interpretation and analysis. The following articles provide an overview of the art of *in situ* hybridization: Singer *et al.*, *Biotechniques*, 4:230-50 (1986); Haase *et al.*, *Methods in Virology*, vol. VII, pp. 30 189-226 (1984); and *Nucleic Acid Hybridization: A Practical Approach* (Names *et al.*, eds. 1987). In addition, an OR protein can be detected with the various immunoassay

techniques described above. The test sample is typically compared to both a positive control (e.g., a sample expressing a recombinant OR protein) and a negative control.

The present invention also provides for kits for screening for modulators of OR family members. Such kits can be prepared from readily available materials and 5 reagents. For example, such kits can comprise any one or more of the following materials: OR nucleic acids or proteins, reaction tubes, and instructions for testing OR activity. Optionally, the kit contains a biologically active OR receptor. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user.

10

EXAMPLES

Genomic, predicted amino acid sequence, and predicted coding sequences (cds), of novel G protein-coupled human odorant receptors, and classes of such receptors, are described. Each example describes a discrete protein and nucleic acid pair. Accordingly, Example 1 describes SEQ. ID. NOS. 1 and 2, for the human 15 olfactory receptor protein designated AOLFR1, and the human DNA encoding AOLFR1, respectively; Example 2 describes SEQ. ID. NOS. 3 and 4, for the human olfactory receptor protein designated AOLFR2, and the human DNA encoding AOLFR2, respectively; and so on in the manner described, through the final Example sequence.

20

In the protein sequences presented herein, the one-letter code X or Xaa refers to any of the twenty common amino acid residues. In the DNA sequences presented herein, the one letter codes N or n refers to any of the of the four common nucleotide bases, A, T, C, or G.

25

EXAMPLES

AOLFR1 sequences:

30 MKTFSSFLQIGRNMHQGNQTTITEFILLGFFKQDEHQNLLFVLFLGMYLTVIGNGLIIVAISLD
TYLHTPMYLFNLANSFADISSISNSVPKMLVNIQTKSQSISYESCITQMFYSIVFVVIDNLLIGTM
AYDHFVAICHPLNYTILMRPRFGILLTVISWFLSNIIALTHTLLIQLLFCNHNTLPHFFCDLAPLL
KLSCSDTLINELVLFIVGLSVIIFPFTLSFFSYVCIIRAVLRSSTQGKWKAFSTCGSHLTVVLLFY
GTIVGVYFFPSSTHPEDTDKIGAVLFTVVTPMINPFIYSLRNKDMKGALRKLINRKISSL (SEQ ID
NO: 1)

35

ATGAAGACTTTAGTTCCTTCTTCAGATCGGCAGAAATATGCATCAAGGAAACCAAACCA
CCATCACTGAATTCAITCTCCTGGGATTITTCAGCAGGATGAGCATCAAAACCTCCTCTT
GTGCTTTCTTGGGTATGTACCTGGTCAGTGTGATTGGGAACGGGCTCATCATTGTGGCTA
TCAGCTTGGATACGTACCTTCATACCCCCATGTATCTCTTCCCTGCCAATCTATCCTTGCT
GATATTCCCTCCATTCCAACTCAGTCCCCAAATGCTGGTGAATATTCAAACCAAGAGTC

AATCCATCTTATGAGAGCTGCATCACACAGATGACTTTCTATTGTGTTGTCGTCATT
 GACAATTGCTCTGGGACCATGGCCTATGACCACTTGTGGCGATCTGCCACCCCTCTGA
 ATTATACAATTCTCATGCGGCCAGGTTGGCATTTGCTCACAGTCATCTCATGGTTCTC
 AGTAATATTATTGCTCTGACACACACCCCTCTGCTCATTCAATTGCTCTCTGTAACCACAA
 5 CACTCTCCCACACTCTCTGTGACTTGGCCCTCTGCTCAAACACTGTCCTGTTAGATAACAT
 TGATCAATGAGCTTGTGTTATTGTGGGTTATCAGTTATCATCTTCCCTTACACTC
 AGCTTCTTCTCATGTCATCAGAGCTGTCCTGAGAGTATCTCCACACAGGGAA
 AGTGGAAAGCCTCTCCACTTGTGGCTCACCTGACAGTTGATTACTGTTACGGAAC
 10 CATTGTAGGCCTGTACTTTTCCCCTCCACTCACCTGAGGACACTGATAAGATTGGT
 GCTGTCCTATTCACTGTGGTACACCCATGATAAACCCTCATCTACAGCTGAGGAATA
 AGGATATGAAAGGTGCCCTGAGAAAGCTCATCAATAGAAAAATTCTCCCTTGA (SEQ
 ID NO: 2)

AOLFR2 sequences:

15 MMMVLRNLSMEPTFALLGFTDYPKLQIPLFLVFLMLYVITVVGNLGMIIKINPKFHTPMYFFL
 SHLSFVDFCYSSIVTPKLLENLVMADKSIFYFSCMMQYFLSCTAVVTESFLLAVMAYDRFVAIC
 NPLLYTVAMSQRLCALLVAGSYLWGMGPLVLLCYALRLNFSGPNVINHFFCEYALISVSGS
 DILIPHLLLFSFATFNEMCTLLIILTSYFIVTFLKIRSVGRHKAFSTWASHLTAITIFHTILFL
 20 YCVPNSKNSRQTVKVASVFYTVNPMLNPPISLRNKDVKDAFWKLIHTQVPFH (SEQ ID NO:
 3)

25 ATGATGATGGTTTAAGGAATCTGAGCATGGAGGCCACCTTGCCTTTAGGTTCACAG
 ATTACCCAAAGCTTCAGATTCCTCTTCTGTGTTCTGCTCATGTATGTTACAGTG
 GTAGGAAACCTTGGGATGATCATAATAATCAAGATTAACCCAAATTTCACACTCCTATGT
 ACTTTCTCCTAGTCACCTCTCTTGTGATTTGTTACTCTCCATTGTCACTCCAAAGC
 TGCTTGAGAACTTGGTAATGGCAGATAAAAGCATCTACTTAGCTGCATGTCAGTA
 30 CTICCTGTCTGCACTGCTGTGGACAGAGTCTTCTGCTGGCAGTGATGGCCTATGAC
 CGCTTGTGCCATCTGCAATCCTCTGCTTATACAGTGGCCATGTCACAGAGGCTCTGTG
 CCCTGCTGGTGGCTGGTCATATCTCTGGGCATGTTGGCCCTGGTACTCCTTGTAT
 GCTCTCCGGTTAAACTCTGACCTAATGTAATCAACCACTCTTGTGAGTAACTGC
 TCTCATCTGTGCTGGCTCTGATATACTCATCCCCCACCTGCTGTTTCAGCTTCGCA
 35 CCTCAATGAGATGTGACTACTGATCATCCTACTTCTATGTTTCATTGTGACT
 GTACTAAAATCCGTTCTGTTAGTGGGCCACAAAGCCTCTCCACCTGGGCCCTCCACC
 TGACTGCTATCACCATCTCATGGGACCATCTTCTACTGTGTAACCAACTCCAAA
 AACTCTGGCAAACAGTCAAAGTGGCTCTGATTTCACACAGTTGTCACCCATGCTGA
 ACCCTCCGATCTACAGCCTAAGGAATAAAGACGTGAAGGATGCTTCTGGAAGTTAAC
 TACACAAGTTCCATTCACTGA (SEQ ID NO: 4)

AOLFR3 sequences:

40 MLLTDRNTSGTTFTLLGFSDYPELQVPLFLVFLAIYNVTVLGNIGLIVI
 KINPKLHTPMYFFLSQ
 LSFVDFCYSSIIAPKMLVNLVVKDRTISFLGCVVQFFFCTVV
 TESFLLAVMAYDRFVAICNPL
 LYTVDMSQKLCVLLVGSYAWGVSCSLE
 LTCALKLCFHGFNTINHFFCEFSLLS
 LSCSDTYI
 NQWLLFFLATFNEISTLLIVLTSYAFIVTILKMR
 SVGRKA
 FSTCASHLTAITIFHTILFLYCV
 PNSKNSRHTVKVASVFYTVNPMLNPLI
 SLRNKDVKDTVTEILD
 TKVFSY (SEQ ID NO: 5)

45 ATGCTGCTGACAGATAGAAATACAAGTGGGACCA
 CGTTACCCCTTGGGCTTCTCAGATT
 ACCCAGAACTGCAAGTCCC
 ACTCTTCCTGGTTTTCTGGCCATCTACA
 ATGTCACTGTC
 GGGAA
 TATTGGGTTGATTGTGATCAT
 CAAAATCAACCCAA
 ACTGCA
 TACCCCCATGTACT
 TTTCTCAGCCA
 ACTCTCC
 TTGTTGGGTTG
 GATCTGCAAAAGACAGAAC
 CATTTCAT
 TTTTAGGATGCGTAGTACA
 ATTCT
 TTTCTCTGTA
 CTTGTTGGTCA
 CTGA
 TACACAGTTGACAT
 GTCCCAGAA
 ACTCTGCGTGC
 TGCTGGTTG
 GGGGACTCT
 ATGCTGCTGGGAGTCT
 CATGTTCC
 TGA
 GACTGCTCTG
 TTTAAAGTTATGTT
 TCTGAT
 ACTTACATCA
 ACCAGTGGCTGCT
 ATTCTTCTG
 GAGTTCTC
 CAC
 TACTCTC
 CC
 TTCTGCT
 GAT
 ACTTACATCA
 ACCAGTGGCTGCT
 ATTCTTCTG
 GAGTTCTC
 CAC
 TTTAATGAA
 ACTCAG
 GAC
 ACT
 TAC
 CGTTCT
 CAC
 AT
 CT
 TAT
 GCG
 TT
 CATT
 GTT
 GTA
 ACC
 CAT

5 CCTCAAGATGCGTTCAGTCAGTGGCGCCGCAAAGCCTCTCCACCTGTGCCCTCCACCTG
 ACTGCCATCACCCTCCTGGCACCATCCTCTTACTGTGTGCCAACTCCAAAAA
 CTCCAGGCACACAGTCAAAGTGGCCTCTGTGTTTACACCGTGGTGTACCCCCATGTGAAT
 CCCCTGATCTACAGTCTGAGAAATAAAGATGTCAAGGATACAGTCACCGAGATACTGGAC
 5 ACCAAAGTCTCTTACTGA (SEQ ID NO: 6)

AOLFR4 sequences:

10 MENQNNVTEFILLGLTENLEWKIFSASFVFLVMYVATVLENLLIVVTIITSQSLRSPMYFFLTFLS
 LLDVMFSSVVAPKVIVDTLSKSTTISLKGCCTQLFVEHFFGGVGIILLTVMAYDRYVAICKPLHY
 TIIMSPRVCCLMVGGAWVGGFMHAMIQLLFMYQIPFCGPNIIDHFICDLFQLLTLACTDTHILGL
 LVTLNSGMMCVAIFLILIASYTIVLCSLKSYSKGRHKALSTCSSHTVVVLFVPCIFLYMRPV
 VTHPIDKAMAIVSDSIIPTMLNPLIYTLRNAEVKSAMKKLWMKWEALAGK (SEQ ID NO: 7)

15 ATGGAAAATCAAAACAATGTGACTGAATTCAATTCTCTGGGTCTCACAGAGAACCTGGAGC
 TGTTGAAAATATTCTGCTGTGTTCTGTATGTATGTAGCCACAGTGTGAAAATCT
 ACTTATTGTGGTAACTATTATCACAAGTCAGAGTCTGAGGTACCTATGTATTCTTCTTA
 CCTCTTGTCCCTTGGATGTCACTGTTCTCATCTGCGTGGCCCAAGGTGATTGTAGAC
 ACCCTCTCCAAGAGCACTACCACATCTCTCAAGGCTGCCTCACCCAGCTGTTGTGGAGC
 20 ATTCTTGGTGGTGGGGATCATCCTCCTACTGTGATGGCTATGACCGCTACGTGGC
 CATCTGTAAGCCCCTGCACTACACGATCATGAGTCCACGGGTGTGCTGCCAATGGTA
 GGAGGGGCTTGGGGGGATTATGCACGCAATGATAACACTCTCTCATGTATCAA
 TACCCCTCTGTGGCTAAATATCATAGATCACTTATATGTGATTGTTCACTGTGACA
 CTGCCCTGCACGGACACCCACATCCTGGGCCTCTAGITACCCCTAACAGTGGATGATGT
 25 GTGTGGCCATCTTCTTATCTTAATTGCGTCCCTACACGGTACATCCTATGCTCCCTGAAGTCT
 TACAGCTCTAAAGGGCGGCACAAAGCCCTCTACCTGCAGCTCCACCCACCTCACGGTGGTTG
 TATTGTTCTTGTCCCCGTATTCTTGTACATGAGGCGTGTGGTCACTCACCCATAGAC
 AAGGCAATGGCTGTCAAGACTCAATCATCACACCCATGTTAAATCCCTGATCTACAC
 TGAGGAATGCAGAGGTGAAAGTGCATGAAGAAACTCTGGATGAAATGGGAGGCTTGG
 30 CTGGGAAATAA (SEQ ID NO: 8)

AOLFR5 sequences:

35 MGKENCTTVAEFLGLSDVPELRVCLFLFLIYGVTLANLGMIALIQVSSRLHTPMYFFLSH
 LSSVDFCYSSIIIVPKMLANIFNPKDKAISFLGCMVQFYLFCTCVTEVFLLAVMAYDRFVAICNPL
 LYTVTMSWKVRVELASCCYFCGTVCVSLIHLCLALRIPFYRSNVINHFFCDLPPVLSACSDITVN
 ETLLFLVATLNESVTIMIILTSYLLILTTILKMGSAEGRHKAFSTCASHLTAITVFHGTVLSIYCRP
 SSGNSGDADKVATVFYTVVIPMLNSVIYSLRNKDVKEARLKVMGSKIHS (SEQ ID NO: 9)

40 ATGGGCAAGGAAAATGCACCAACTGTGGCTGAGTTCAATTCTCCTGGACTATCAGATGTCC
 CTGAGTTGAGAGTCTGCCTCTCCTGCTGTTCTCTCATCTATGGAGTCACGGTGTAGCC
 AACCTGGGCATGATTGCACTGATTCAAGTCAGCTCTGGCTCCACACCCCATGTACTTT
 TCCTCAGCCACTTGTCCCTGTAGATTCTGCTACTCCTCAATAATTGTGCCAAAATGTG
 GCTAATATCTTAAACAGGACAAAGCCATCTCCTCTAGGGTGCATGGTCAATTCTACT
 TGTTTGCACITGTGGTCACTGAGGTCCTCTGCTGGCCGTGATGGCTATGACCGCTT
 45 GTGGCCATCTGTAACCTTGTATACACAGTCACCATGTCCTGGAAAGGTGCGTGTGGAGC
 TGGCTTCTGCTGCTACTTCTGTGGACGGTGTGTTCTCTGATTCAATTGTGCTTAGCTCTT
 AGGATCCCCCTCTATAGATCTAATGTGATTAACCACTTTCTGTGATCTACCTCCTGTCTT
 AAGTCTTGCCTGCTCTGATATCACTGTGAATGAGACACTGCTGTTCCCTGGGCCACTTIG
 AATGAGAGTGTGTTACCATCATGATCATCCTCACCTCCTACCTGCTAATTCTCACCAACCATCCT
 50 GAAGATGGGCTCTGCAGAGGGCAGGCACAAAGCCTCTCCACCTGTGCTTCCCACCTCACA
 GCTATCACTGTCTTCCATGGAACAGTCCITTCCATTATTGAGGCCCCAGTTCAAGGCAATA
 GTGGAGAGTGTGACAAAGTGGCCACCGTGTCTACACAGTCGTGATTCTATGCTGAACCTC
 TGTGATCTACAGCCTGAGAAATAAAGATGTGAAAGAAGCTCTCAGAAAAGTGTGATGGGCTC
 CAAAATTCACTCCTAG (SEQ ID NO: 10)

AOLFR6 sequences:

MMASERNQSSTPTFILLGFSEYPEIQVPLFLVFLFVYTVTVVGNLGMIIIRLNSKLHTIMYFFLS
 HLSLTDFCFSTVTPKLLLENLVVEYRTISFGCIMQFCFACIFGVTFMLAAMAYDRFVAVCK
 5 PLLYTTIMSQKLCALLVAGSYTWGIVCSLILTYFLLDSFCESTFINNFIQDHSVIVSASYSDPYIS
 QRLCFIIAIFNEVSSLIIILTSYMLIFTTIMKMRSAQRQKTFSTCASHLTAITIFHGTILFLYCVPNP
 KTSSLIVTVASVFYTVAPMLNPLIYSLRNKDINNMFEKLVVTKLHY (SEQ ID NO: 11)

10 ATGATGGCATCTGAAAGAAATCAAAGCAGCACACCCACTTTATTCTCTGGGTTTCAG
 AATACCCAGAAATCCAGGTTCCACTCTTCTGGTTTCTGTTCTGCTACACAGTCAGTGA
 GTGGGAAACTGGGCATGATAATAATCATCAGACTCAATTCAAAACTCCATACAATCATGT
 ACTTTTCCTTAGTCATTGTCCTTGACAGACTCTGTTTCCACTGTAGTTACACCTAAA
 CTGTTGGAGAACTTGGTTGTGGAATACAGAACCATCTCTTCTGTTGCTACATGCAAT
 TTTGTTTGTGCTTGCACTTGGAGTGCAGAGAAACTTCATGTTAGCAGCGATGGCTATGAC
 15 CGTTTGTGGCAGTTGTAAACCCCTGCTGTATACCACTATTATGTCAGAACGCTCTGTC
 TCTCTGGTGGCTGGCTTACATGGGGATAGTGTGCTCCCTGATACTCACATATTTC
 CTTCTGACTTATCGTTGTGAATCTACCTTCATAAATAATTATCTGTGACCAACTCTGT
 AATTGTTCTGCCTCCTACTCAGACCCCTATATCAGCCAGAGGCTATGCTTATTATTGCCA
 TATTCAATGAGGTGAGCAGCCTAATTATCATTGACATCATATATGCTTATTTCACTACC
 20 ATTATGAAGATGCGATCTGCAAGTGGCGCCAGAAAACCTTCTCCACCTGTGCCCTCCCACC
 TGACAGCCATCACTATCTCCATGAACTATCCTTACTGTGTTCTAATCCTAAA
 ACTTCTAGCCTCATAGTTACAGTGGCTCTGTGTTTACACAGTGGCGATTCCAATGCTGA
 ACCCATTGATCTACAGCCTAGGAACAAAGATATCAATAACATGTTGAAAAATTAGTTG
 CACCAAATTGATTACCACTGA (SEQ ID NO: 12)

AOLFR7 sequences:

25 MSYFYRLKLMKEAVLVKLPFTSLPLLQLTLSRKSRDMEIKNYSSSTSGFILLGLSSNPQLQPLF
 AIFLIMYLLAIVGNVLIIPAIYSDPRLHTPMYFFLSNLSDMDICFTVIVPKMLVNFLSETKVISY
 VGCLAQMYFFMAFGNTDSYLLASMAIDRLVAICNPLHYDVVMKPRHCLLMLLGSCSISHLHSL
 30 FRVLLMSRLSFCASHIKHFFCDTQPVLKLSCSDTSSSQMVMTETLAVVTPFLCIIFSYLRIMV
 TVLRIPSAAGKWKAFSTCGSHLTAVALFYGSIIYVYRPLSMYSVVRDRVATVMYTVVTPMLN
 PFIYSLRNKDMKRLKQLQDRIYR (SEQ ID NO: 13)

35 ATGAGCTATTTTACAGGCTTAAGCTTATGAAAGAAGCTGCTTGGTCAAACCTGCCCTTA
 CATCTCTCCACTGCTTCTCCAAACCTATCCAGGAAGTCCAGAGACATGGAGATAAAGAA
 CTACAGCAGCAGCACCTCAGGTTCATCCTCTGGCCTCTTCCAACCCCTCAGCTGCAG
 AACCTCTTTGCCATCTCCTCATCATGTACCTGCTCGCTGCGGTGGGAATGTGCTCAT
 CATCCCAGGCCATCTACTCTGACCCCAGGCTCCACACCCCTATGTAATTCTCAGCAACT
 TGTCTTCATGGATATCTGCTTACAACAGTCATAGTGCCTAAGATGCTGGTGAATTCTA
 40 TCAGAGACAAAGGTTATCTCTATGTGGCTGCCTGGCCAGATGTACTTCTTATGGCAT
 TTGGGAACACTGACAGCTACCTGCTGGCCTCATGGCCATCGACCGGCTGGTGGCCATCTG
 CAACCCCTACACTATGATGTGGTTATGAAACCACGGCATTGCTGCTCATGCTATTGGGT
 TCTGCAGCATCTCCACCTACATTCCCTGTCGCGTGTACTTATGTCGCTGTCTT
 CTGTGCTCTCACATCATTAAGCACTTTCTGTGACACCCAGCCTGTGCTAAAGCTCTCCT
 GCTCTGACACATCCTCCAGCCAGATGGGGTGTACTGAGACCTTAGCTGTCTATTGTGAC
 45 CCCCTTCTGTGTATCATCTTCTTACCTGCGAATCATGGTCAGTGTGCTCAGAACCTCC
 CTGCAGCCGGGAAGTGGAAAGGCCCTCTCACCTGTTGGCTCCACCTCACTGCAGTAGCCCT
 TTTCTATGGGAGTATTATTTATGTCTATTAGGCCCTGTCATGTACTCAGTGGTAGGG
 ACCGGGTAGCCACAGTTATGTACACAGTAGTGCACACCCATGCTGAACCCCTCATCACAG
 CCTGAGGAACAAAGATATGAAGAGGGGTTGAAGAAATTACAGGACAGAACCTACCGGTA
 50 A (SEQ ID NO: 14)

AOLFR8 sequences:

55 MATSNHSSGAEFILAGLTQRPELQLPLFLGIYVVTVVGNLGMIFLIALSSQLYPPVYYFLSH
 LSFIDLCYSSVTPKMLVNFPPEENIISFLECITQLYFFLIFVIAEGYLLTAMEYDRYVAICRPLL
 NIVMSHRVCSIMMAVVYSLGFLWATVHTTRMSVLSFCRSHTVSHYFCDILPLLTSCSSTHINEI

LLFIIGGVNTLATTAVLISYAFIFSSILGIHSTEGQSKAFGTCSHLLAVGIFFGSITFMYFKPPSS
TTMEKEKVSSFYITIIPMLNPLIYSLRNKDVKNALKKMTRGRQSS (SEQ ID NO: 15)

5 ATGGCTACTTCAAACCATTCTCAGGGCTGAGTTATCCTGGCAGGCTTGACACAACGCC
CAGAACCTCAACTGCCACTCTCCTCTGGAAATATGTGGTCACAGTGGTGGG
GAACCTGGCATGATCTCTTAATTGCTCTCAGTCTCAACTTACCCCTCAGTGTATTATT
TTCTCAGTCATTGCTTCTGATCTGCTACTCCTCTGTCACTTACCCCTAAGATGCTG
GTGAACCTTGTCCAGAGGAGAACATTATCTCCTCTGGAAATGCATTACTCAACTTTATT
CTTCCTTATTGTAATTGAGAAGGCTACCTCTGACAGCCATGGAATATGACCGTTAT
10 GTTGCTATCTGCGCCACTGCTTACAATATTGTCATGTCATGCCCACAGGGTCTGTTCCATAAT
GATGGCTGTGGTATACTCACTGGGTTCTGTGGGCCACAGTCCATACTACCCGATGTC
GTGTTGTCATTCTGTAGGTCTCATACTGGTCAGTCATTATTGTGATATTCTCCCTTATT
GACTCTGCTTGCTCCAGCACCCACATCAATGAGATTCTGCTGTTCAATTGGAGGAGTT
AATACCTTAGCAACTACACTGGCGGTCTTATCTTATGCTTCTGTTCAATTCTCTAGTATCCT
15 TGGTATTCTTCACTGAGGGCAATCCAAGCCTTGGCACTGTAGCTCCATCTCTG
GCTGTGGCATCTTTGGCTATAACATTGATCTTCAAGCCCCCTCCAGCACTAC
TATGGAAAAAGAGAAGGTGTCTCTGTGTTACATCACAATAATCCCCATGCTGAATCCT
CTAATCTATAGCCTGAGGAACAAGGATGTGAAAAATGCACTGAAGAAGATGACTAGGGGA
AGGCAGTCATCCTGA (SEQ ID NO: 16)

20

AOLFR9 sequences:

MLARNNSLVTEFILAGLTDPEFWQPFFFLFLVIYIVTMVGNLGLIIFGLNSHLHTPMYYFLFN
LSFIDLCYSSVFTPKMLMFVSKKNIISNVGCMTRLFFFVISSECYMLTSMAYDRYVAICNPL
LYKVTMSHQVCMSLTFAAYIMGLAGATAHTGCMRLTFCSANINHYLCDILPLLQLSCTSTYV
25 NEVVVLIVVGTNTIVPSCTILISYVFIVTSILHIKSTQGRSKAFSTCSSHVIALSLFFGSAAFMYIKY
SSGSMEQGVFSVFTYTNVVPMLNPLIYSLRNKDVKVALRKALIKIQRRNIF (SEQ ID NO: 17)

30 ATGCTGGCTAGAAACAACCTCTTAGTGAATTTATTCTTGTGGATTAACAGATCGTC
CAGAGTTCTGGCAACCCCTCTTTCTGTTCTAGTGAATCTACATTGTCACCATGGTAGGC
AACCTTGGCTTGATCACTCTTTCGGTCTAAATTCTCACCTCCACACACCAATGTACTATT
CCTCTCAATCTCTCCTCATTGATCTCTGTTACTCCTCTGTTCACTCCAAAATGCTAAT
GAACTTGTGTCAAAAAGAAATATTATCTCAATGTTGGGTGCATGACTCGGCTGTTTC
TTTCTTTTCGTCATCTGAATGTTACATGTTGACCTCAATGGCATATGATCGCTATGT
GCCATCTGTAATCATTGCTGATAAGGTACCATGTCACCATCAGGTCTGTTATGCTCA
35 CTTTGCTGCTTACATAATGGGATTGGCTGGAGGCCACGGCCCACACCGGGTGCATGTTAG
ACTCACCTCTGCTGAGTCTAATCATTAACCATTACTTGTGACATACTCCCCCTCC
AGCTTCTGCACCAGCACCTATGTCAACGAGGTGGTTGTTCTCATTGTTGTGGTACTAA
TATCACGGTACCCAGTTGTAACCATCCTCATTCTATGTTTCATTGTCACTAGCATTCTC
40 ATATCAAATCCACTCAAGGAAGATCAAAGCCTTCAGTACTTGTAGCTCTCATGTCATTG
TCTGCTCTGTTGGGTGAGCGGCATTCTACATGTTACACTAATGTTGGCCATGCTCAATCCCCTCATC
TACAGTTGAGGAACAAGGATGTCAAAGTTGCACTGAGGAAAGCTCTGATTAAAATTGAG
AGGAGAAATATATTCTAA (SEQ ID NO: 18)

45 **AOLFR10 sequences:**

MLARNNSLVTEFILAGLTDPEFRQPLFFLFLVIYIVTMVGNLGLIIFGLNSHLHTPMYYFLFN
SFIDLCYSSVFTPKMLMFVSKKNIISVGCMTQLFFFVISSECYILTSMAYDRYVAICNPLLY
KVTMSHQVCMSLTFAAYIMGLAGATAHTGCMRLTFCSANINHYLCDILPLLQLSCTSTYVN
EVVVLIVVGINIMVPSCTILISYVFIVTSILHIKSTQGRSKAFSTCSSHVIALSLFFGSAAFMYIKYS
50 SGSMEQGVSSVFTYTNVVPMLNPLIYSLRNKDVKVALRKALIKIQRRNIF (SEQ ID NO: 19)

55 ATGCTGGCTAGAAACAACCTCTTAGTGAATTTATTCTTGTGGATTAACAGATCGTC
CAGAGTTCCGGCAACCCCTCTTTCTGTTCTAGTGAATCTACATTGTCACCATGGTAGGC
AACCTTGGCTTGATCATTCTCTGGTCTAAATTCTCACCTCCACACACCAATGTACTATT
CCTCTCAATCTCTCCTCATGATCTCTGTTACTCCTCTGTTCACTCCAAAATGCTAAT
GAACTTGTATCAAAAAGAAATATTATCTCTATGTTGGGTGCATGACTCAGCTGTTTCT

5 TTCTCTTTTGTCTGATCTCTGAATGCTACATATTGACCTCAATGGCATATGATCGCTATGTG
GCCATCTGTAATCCATTGCTGTATAAGGTACCATGTCCCCTCAGGCTGTTCTATGCTCAC
TTTGCTGCTTACATAATGGGATTGGCTGGAGCCACGGCCCACACGGGTGCATGCTTAGA
CTCACCTCTGAGTCTAATATCATCAACCATTACTTGTGTGACAATCTCCCCCTCTCCA
GCTTTCTGCACCAGCACCTATGTCACGAGGTGGTGTCTCATTGTTGTGGGTATTAAT
ATCATGGTACCCAGTGTACCATCCTCATTCTTATGTTTCATTGTCACTAGCATTCTCA
TATCAAATCCACTCAAGGAAGATCAAAGCCCTCAGTACTTGTAGCTCTATGTCATTGCT
CTGTCCTGTTTGGTCAGCGGCATTATGTATATTAAATATTCTCTGGATCTATGGA
10 GCAGGGAAAAGTTCTCTGTTCTACACTAATGTGGTGCCATGTCATCCTCTCATCT
ACAGTTGAGGAACAAGGATGTCAAAGTTGCACTGAGGAAAGCTCTGATTAAAATTAGA
GAAGAAATATATTCTAA (SEQ ID NO: 20)

AOLFR11 sequences:

15 MTLRNSSS VTEFILVGLSEQPELQLPLFLLGLYVFTVVGNLGLITLIGINPSLHTPMYFFLFNL
FIDLCYSCVFTP KMLNDFVSESIISYVGCM TQLFFFCCFVNSECYVLVSMAYDRYVAICNPLLY
MVTMSPRVCFLLMFGSYVVGFAGAMAHTGSMRLTFCDSNVIDHYLCDVLP LLQLSCTSTHV
SELVFFIVVGVITMLSSISIVISYALILSNILCIPSAEGRSKAFSTWGSHIAVALFFGSGTFTYLTT
FPGSMNHGRFASVFTNVVPMLNPSIYSLRNKDDKLALGKTLKRVLF (SEQ ID NO: 21)

20 ATGACTCTGAGAACAGCTCCTCAGTGA
CTGAGTTATCCTGGGATTATCAGAACAGC
CAGAGCTCCAGCTCCCTCTTCCCTATTCT
AACTTGGGCTTGTACCTTAATTGGGATAA
ACCTAGCCTTCACACCCCCATGTACT
CCTCTCAACTTGTCTTATAGATCTGT
ATGACTTTGTTCAAGAAAGTATCAT
CTCTTATGTGGGATGTATGACTCAGC
TATTTCTTC
25 TGTTCTTGTCAATTGTAGTGCTATGT
GTGGTATCAATGGCCTATGATCGCTATGT
GGC
CATCTGCAACCCCCCTGCTCTACATGG
TCACCATGTCCCCAAGGGTCTGCTTCTG
CTGATGT
TTGGTCTCTATGTGGTAGGGTTGCT
GGGCCATGGCCACACTGGAAGCATGCT
CGACT
GACCTTCTGTGATTCCAACGT
CATTGACCATTATCTGTGT
GACGTTCTCCCCCTTGCAGC
TCTCCTGCACCAGCACC
ATGCTATCCAGCATAAGC
ATCGTCATCTCTTACGCTT
GATACTCTCAACATCCTCTGTAT
TCCTCTGCAGAGGGCAGAT
CCAAGCCATTAGCACAT
GGGGCTCCCACATAATTGCT
GCTCTGTTTTGGTCAGGG
ACATTCACTTAACAA
ACATCTTCTGGCTCTATGAA
CCATGGCAGATTGCTCAGT
CTTACACCAATGTGG
TCCCTGCTTAACCC
CTCGATCT
ACAGTTGAGGAATAAGG
ATGATAAAACTGCC
CTGGGAAAAC
CTGAGAGAGTGC
TCT
35 TCTAA (SEQ ID NO: 22)

AOLFR12 sequences:

40 MERNHNPDCNVLFNFFFADKKKNKRRNFGQIVSDVGRICYSVSLSLGEPTTMGRNNLTRPSEFIL
LGLSSRPEDQKPLFAVFLPIYLITVIGNLILAIRSDTRLQTPMYFFLSILSFVDICYVTVIPLKMLV
NFLSETKTISYGECLTQMYFFLAFLGNTDSYLLAAMAIDRYVAICNPFHYYITIMSHRCCVLLVLS
FCIPHFHSLHILLTNQLIFCASNVIIHFFCDDQPVLKLSSSHVKEITVMTEGLAVIMTPFSCIII
SYLRLILITVLKIPSAGKRKAFTCGSHLTVVTLFYGSISYVFQPLSNYTVDQIATIYTVLTP
MLNPFITSLRNKDMKQGLAKLMHRMKCQ (SEQ ID NO: 23)

45 ATGGAAAGAAACCACAATCCAGATAATTGTAATGTTAAATTCTTCTTGCTGATAAGA
AGAATAAAAGGAGAAATTGACAGATTGATCAGATGTTGAAAGAATCTGTTACAGTG
TTAGTTATCTTAGGTGAACCCACAACATGGGAAGAAATAACCTAACAAAGACCCCTCTGA
ATTCACTCCCTTGGACTCTCCTCTCGACCTGAGGATCAGAAGCCGCTCTTGCTGTGTTCC
50 TCCCCATCTACCTTATCACAGTGTAGGAAACCTGCTTATCATCTGGCCATCCGCTCAGA
CACTCGTCTCCAGACGCCATGTACTCTTCTAAGCATCCTGCTTGTGACATTGCT
ATGTGACAGTCATTATCCCTAACAGATGCTGGTGAACCTCTATCAGAGACAAAGACCATCTC
TTACGGTGAGTGTCTGACCCAGATGTACTTTCTAGCCTTGGAAACACAGACAGTTAC
CTGCTAGCAGCCATGCCATTGACCGCTATGTGCCATATGTAATCCCTCCACTACATCA
55 CCATTATGAGTCACAGATGCTGTCTGCTTCTGGTTCTCCCTCTGCATTCCACATT
CACTCCCTCTGCACATTCTGACTAATCAGCTCATCTCTGTCGCTCCAATGTCATCCA
TCACCTTTCTGCGATGATCAACCAGTGTCTTAAATTGTCCTGTTCCCATTTGTCAGAAG

AAATCACAGTAATGACAGAAGGCTTGGCTGTATAATGACCCCGTTTCATGCATCATCAT
 5 CTCTTATTAAGAACCTCATCACTGTTCTGAAGATTCTCAGCTGCTGGAAAGCGTAAAGCATTAGCTA
 TGTCTATTTCAGCCCTGTCACACTATACTGTCAAGGATCAAATAGCAACAAATTATCTAC
 ACCGTACTGACTCCATGCTAAATCCATTATCTATAGTCTGAGGAACAAAGACATGAAGC
 AGGGTTGGCAAAGTTGATGCACAGGATGAAATGTCAGTAA (SEQ ID NO: 24)

AOLFR13 sequences:

10 MDQKNGSSFTGFILLGFSDRPQLELVLFVVLIFYIFTLLGNKTIIVLSHLDPHLHNPMYFFFSNL
 SFLDLCYTTGIVPQLLVNLRGADKSISYGGCVVQLYISLGLGSTEVCVLLGVMAFDRAAVCRPL
 HYTVMHPCLYVLMASTSWVIGFANSLLQTVLILLTLCGRNLEHFLEVPPLKLACVDTT
 MNESELFVSVIILVPVALIFSYSQIVRAVVRKSATGQRKVFGTCGSHLTVVSLFYGTAIYAY
 LQPGNNYSQDQGXISLFYTIITPMINPLIYTLRNKDVKGALKVLWKNYDSR (SEQ ID NO:
 25)

15 ATGGATCAGAAAAATGGAAGTTCTTCACTGGATTATCCTACTGGGTTCTGACAGGC
 CTCAGCTGGAGCTAGCCTCTTGTGGTCTTTGATCTTCACTTGACCCACATCTCACAACTCTATGTATT
 20 AACAAAACCATCATTGATTATCTCACTTGACCCACATCTCACAACTCTATGTATT
 CTTCTCCAACCTAACGTTTTGGATCTGTGTTACACAACGGCATTGTTCCACAGCTCCGG
 TTAATCTCAGGGAGCAGACAAATCAATCTCCTATGGTGGTTGTGAGTTCACTGCTGTACAT
 25 CTCTCTAGGCTTGGATCTACAGAACGGTCTCTAGGAGTGATGGCATTGACCGCTAT
 GCAGCTGTTGCAGGCCCTCCACTACACAGTAGTCATGCACCCCTGTCTGTATGTGCTGA
 TGGCTCTACTTCATGGGTATTGGTTGCAACTCCCTATTGCAAGACGGTGTCTCATCTG
 CTTTAACACTTTGTGGAAGAAAATTAGAACACTTCTTGTGAGGGTCCCTCATTGCT
 30 CAAGCTTGCCGTGTTGACACTACTATGAATGAACTGAACACTCTTCTTGTCACTGCTATT
 TTCTCTTGACCTGTTGCAATTATCATATTCTCTATAGTCAGATTGTCAGGGCAGTCGTG
 AGGATAAAAGTCAGAACAGGGCAGAGAAAAGTGTGAGCATGTGGCTCCACCTCACA
 GTGGTTCCCTGTTACGGCACAGCTATCTATGCTACCTCCAGCCGGCAACAACTACTC
 TCAGGATCAGGGCAAGKTCATCTCTCTACACCATTACACCCATGATCAACCC
 CTCATATATACACTGAGGAACAAGGATGTGAAAGGAGCACTTAAGAAGGTGCTCTGGAAG
 AACTACGACTCCAGATGA (SEQ ID NO: 26)

AOLFR14 sequences:

35 MALPLLLSPSCFASSQSLSSRMNSENLTRAAVAPAEVLLGITNRWDLRVALFLTCPVYLVSL
 LGNMGMAILRMDARLHTPMYFFLANLSSLDACYSSAIGPKMLVDLLPRATIPYACALQMF
 VFAGLADTECCLLAAMAYDRYVAIRNPLLYTTAMSQRCLCLLGAAGLGGAVSAFVHTLTF
 RLSFCRSRKINSFFCDIPPLLAISCSDTSLNELLFAICGFIQTAATVLAITSYGFAGAVIHMRSVE
 GSRRRAASTGGSHLTAVAMMYGTLJFMYLRPSSYALDTDKMASVFYTLVIPSNPLIYSLRNKE
 VKEALRQTWSRFHCPGQGSQ (SEQ ID NO: 27)

40 ATGGCCTTGCATTGCTCTATCTCCCTCTGCTTGCCTCTCAGTCCTGTCCAGTAG
 GATGAACCTAGAGAACCTACCCGGGCCGGTTGCCCTGCTGAATTGCTCCTGGC
 ATCACAAATCGCTGGACCTGGCTGCTGCTGGCCCTCTTCCCTGACCTGCCTGCTACCTGG
 45 TGAGCCTGCTGGAAACATGGCATGGCGCTGCTGATCCGCATGGATGCCGGCTCCACA
 CACCTATGTAATTCTCTGGCCAACCTCTCCCTGCTGGATGCCCTGCTATTCTCCGCCATC
 GGCCCCAAGATGCTAGTGGACTGCTGCTGCCCGAGCCACCATCCCTACACAGCCTGTG
 CCCTCCAGATGTTGCTTGCAGGTCTGGCTGATACTGAGTGTGCTGCTGGCAGCCAT
 GGCTATGACCGCTACGTGGCCATCAGAAACCCACTTCTCTATACACAGCTATGCGCAG
 CGTCTATGCCTGGCCTTGTGGAGCATCAGGCCCTGGGGAGTCAGTGTGCTTGTGTC
 50 ACACAAACCTCACCTCCGCCTGAGCTCTGCCGCTCCCGGAAGATCAATAGCTTCTCTG
 CGATATCCCTCACTGCTGGCCATCTCGTGCAGTGACACCAAGTCTCAATGAACCTCTCT
 TCGCCATCTGTGGCTTACCCAGACAGCCACGGTGTAGCTATCACGGTGTCTATGGCTT
 CATCGCTGGGGCTGTGATCCACATGCGCTCGGTGAGGGCAGTCGGCGAGCAGCCTCCAC
 CGGTGGTTCCCACCTCACAGCCGTGGCATGATGTACGGGACACTCATTTCATGTACCTG
 55 CGCCCCAGCTCCAGCTATGCCCTGGACACTGACAAGATGCCCTGTGTTCTATACCCTGG

TCATCCCGTCTCTCAACCCACTCATCTACAGCCTCCGCAATAAGGAGGTCAAGGAGGCCCT
CAGGCAGACCTGGAGGCCATTCCACTGTCCAGGGCAGGGTCCCAGTGA (SEQ ID NO: 28)

AOLFR15 sequences:

5 MRENNQSSTLEFILLGVTQQEQEDFFYILFLFIYPITLIGNLLIVLAICSDVRLHNPMYFLLANLS
LVDIFFSSVTIPKMLANHLLGSKSISFGGCLTQMYFMIALGNTDSYILAAMA YDRAVAISHPLH
YTTIMSPRSCIWLIAGSWVIGNANALPHTLLTASLSFCGNQE VANFYCDITPLLKLSCSDIHFHV
KMMYLGVGIFSVPLLCIIVSYIRVFSTVFQVPSTKGVLKAFSTCGSHLTVVSLYYGTVVMGTYFR
PLTNYSLKDAVITVMYTA VTPMLNPFISLRNRMKAALRKLFNKRSS (SEQ ID NO: 29)

10 ATGAGGGAAAATAACCACTCCTCTACACTGGAA TTCACTCCCTGGGAGTTACTGGTCAGC
AGGAACAGGAAGATTCTTCTACATCCTCTTCTGTTCATTTACCCATCACATTGATTGGA
AACCTGCTCATTGCTCTAGCCATTGCTCTGATGTTGCCCTCACAAACCCATGTATTCT
CCTGCCAACCTCTCCTGGTGCACATCTCTCATCGGTAAACCATCCCTAACAGATGCTGG
15 CCAACCATCTCTGGCAGCAAATCCATCTCTTGGGGATGCCAACCGCAGATGTATT
CATGATAGCCTTGGGTAAACACAGACAGCTATATTGCTGCAATGCCATATGATCGAGCT
GTGGCCATCAGCCACCCACTTCACTACACAACAATTATGAGTCCACGGTCTGTATCTGGC
TTATTGCTGGTCTTGGGTGATTGGAAATGCCATGCCCTCCCCAACACTCTGCTCACAGC
TAGTCTGCTCTCTGTCACCAGGAAGTGGCCAACCTCTACTGTGACATTACCCCTG
20 CTGAAGTTATCCTGTTCTGACATCCACTTCTATGTGAAGATGATGTACCTAGGGTTGGCA
TTTCCTCTGTGCCATTACTATGCATCATTGCTCCTATATTGAGTCTTCTCCACAGTCTCC
AGGTTCCCTCCACCAAGGGCGTCAAGGCCTCTCCACCTGTGGTCCACCTCACGGT
TGTCTCTTGTTATTATGGTACAGTCATGGCACGTATTCCGCCCTTGACCAATTATAGCC
25 TAAAAGACCGAGTGTACACTGTAATGTACACGGCAGTGACCCCAATGTTAAATCCTTCAT
CTACAGTCTGAGAAATCGGGACATGAAGGCTGCCCTGCGGAAACTCTCAACAAAGAGAAT
CTCCTCGTAA (SEQ ID NO: 30)

AOLFR16 sequences:

30 MRRNCTLVTEFILLGLTSRRELQILLFTLFLAIYMVTVAGNLGMIVLIQANAWLHMPMYFFLSH
LSFVDFLCSSNVTPKMLEIFLSEKKISYPACLVQCYLFIALVHVEIYILAVMAFDRYMAICNPLL
YGSRMSKSVCSFLITVPVYVGALTGLMETMWTYNLAFCGPNEINHFYCADPPLIKLACSDTYN
KELSMFIVAGWNLSFLIICISYLYTFPAILKIRSTEGRQKAFSTCGSHLTAVTIFYATLFFMYLR
PPSKESVEQGKMOVAVFYTTVPMNLIIYSLRNKNVKEALIKELSMKIYFS (SEQ ID NO: 31)

35 ATGAGAAGAAACTGCACGTTGGTACTGAGTTCA TTCTCTGGGACTGACCAGTCGCCGG
GAATTACAATTCTCCTCTCACGCTGTTCTGGCCATTACATGGTCACGGTGGCAGGG
ACCTTGGCATGATTGCTCTCATCCAGGCCAACGCCCTGGCTCCACATGCCCATGTACTTTTC
CTGAGCCACTTATCCTCGTGGATCTGTGCTCTCTCCAATGTGACTCCAAGATGCTGG
AGATTTCCTTCAGAGAAGAAAAGCATTCCTATCCTGCCGTCTGTGAGTGTACCT
40 TTTATCGCCTTGGTCCATGTTGAGATCTACATCCTGGCTGTGATGCCCTTGACCGGTACAT
GGCCATCTGCAACCCCTCGCTTTATGGCAGCAGAATGTCCAAGAGTGTGCTCCTTCCTC
ATCACGGTGCCTTATGTGTATGGAGCGCTCACTGGCCTGATGGAGACCATGTGGACCTACA
ACCTAGCCTCTGTGGCCCAATGAAATTAACTACCTCTACTGTGCGGACCCACCTGAT
TAAGCTGGCTTGTGACACCTACAACAAGGAGTTGTCATGTTATTGTGGCTGGCTGG
45 AACCTTCTTTCTCTCATCATATGTA TTCCCTACCTTACATTCCCTGCTATT
AAGATTGCTCTACAGAGGGCAGGCAAAAAGCTTTCTACCTGTGCGCTCCCATCTGACAG
CTGTCACTATATTCTATGCAACCCCTTCTCATGTATCTCAGACCCCCCTCAAAGGAATCT
GTTGAACAGGGTAAATGGTAGCTGTATTATACACAGTAATCCCTATGCTGAACCTTA
50 TAATTATAGCCITAGAAATAAAATGTAAGAAGCATTAACTCAAAGAGCTGTCAATGA
AGATATACTTTCTTAA (SEQ ID NO: 32)

AOLFR17 sequences:

55 MLNFTDVTTEFILLGLTSRREWQVLFFIFLVVIITMVGNIGMMVLK VSPQLNNPMYFFLSHLS
FVDVWFSSNVTPKMLENLFSDKTITYAGCLVQCFFFIALVHVEIFILAAMAFDRYMAIGNPLL
YGSKMSRVVCIRLITFPYIYGFLSLAATLWTYGLYFCGKIEINHFYCADPPLIKMACAGTFVKE

YTMILAGINFTYSLTVIISYLFILIAILRMRSAEGRQKAFSTCGSHLTAVIIFYGTLIFMYLRRPTE
ESVEQGKVMAVFYTTVIPMLNPMIYSLRNKDVKKAMMKVISRSC (SEQ ID NO: 33)

5 ATGCTCAA TTTCACCGATGTGACAGAGTTCATTCTTGGGGCTAACGAGCCGTCGAGAAT
GGCAAGTTCTCTTCTCATCTTCTGTGGTCTACATCACCATGGTGGCAATATC
GGCATGATGGTGTAAATCAAGGTCAAGGTCAGTCTCAGCTTAACAACCCCCATGTACTTTCTCA
GTCACTTGTCAATTGTTGATGTGGTTTCTTCCAATGTCAACCCCTAAATGTTGGAAAAC
CTGTTTCAGATAAAAAACAAATTACTTATGCTGGTTGTACTACAGTGTCTTCTTCA
TGCTCTGTCCATGTGGAAATTATTCTTGTGCTCGATGCCCTTGATAGATACTATGGCAA
10 TTGGGAATCCTCTGTTATGGCAGTAAAATGTCAGGGTGTCTGATTGACTGATTAC
TTTCCCTACATTATGGTTCTGACGAGTCTGGCAGCAACATTATGGACTTACGGCTTGT
ACTCTGTGGAAAATTGAGATCAACCATTTCTACTGTGAGATCCACCTCTCATCAAAT
GGCCTGTGCCGGGACCTTGTAAAAGAATATAACATGATCATACTTGCCGGCATTAACCTC
ACATATTCCCTGACTGTAATTATCATCTTACTTATTCATCCTCATGCCATTCTGCGAAT
15 GCGCTCAGCAGAAGGAAGGCAGAAGGCCCTTCACATGTGGTCCCCTGACAGCTGT
CATTATATTCTATGGTACTCTGATCTCATGTATCTCAGACGTCCCACAGAGGAGTCTGTG
GAGCAGGGGAAGATGGTGGCTGTCTATACCACAGTGTACCCCCATGTTGAATCCCATGA
TCTACAGTCTGAGGAACAAGGATGTAAAAAGGCCATGATGAAAGTGTACAGCAGATCAT
GTAA (SEQ ID NO: 34)

20

AOLFR18 sequences:

MSNTNGSAITEFILLGLTDCPELQSLLFVLFLVVYLVTLGNLGMIMLMRLDSRLHTPMYFFLT
NLAFVDLCYTSNATPQMSTNIVSEKTISFAGCFTQCYIFIALLTEFYMLAAMAYDRYVAIYDP
25 LRYSVKTSRRVCICLATFPYVYGFSDGLFQAILTFRLTFCRSNVINHFYCADCPLIKLSCSDTYVK
EHAMFISAGFNLSSSLTIVLVSYAFILAIIRIKSAEGRHKAFSTCGSHMMAVTLFYGTLFCMYI
RPPTDKTVEESKIIAVFYTFVSPVNLPIYSLRNKDVKQALKNVLR (SEQ ID NO: 35)

30 ATGTCCAACACAAATGGCAGTGCAATCACAGAATTCACTTACTTGGGCTCACAGATTGCC
CGGAACCTCCAGTCTGCTTGTGCTTCTGGTTTACCTCGTCACCCCTGCTAGGC
AACCTGGGCACTGATAATGTTAATGAGACTGGACTCTGCCCTCACACGCCCATGTACTTCT
TCCTCACTAACTTAGCCTTGTGGATTGTGCTATACATCAAATGCAACCCCGAGATGTC
GACTAATACTGTATCTGAGAAAGACCATTCCTTGTGGCTTACACAGTGTACATT
TCATTGCCCTCTACTCACTGAGTTTACATGCTGGCAGCAATGGCCTATGACCGCTATGT
GCCATATATGACCCCTGCGCTACAGTGTAAAACGTCCAGGAGAGTTGCACTCTGCTTG
35 GCCACATTCCCTATGTCTATGGCTCTCAGATGGACTCTTCCAGGCCATCTGACCTTCCG
CCTGACCTTCTGTAGATCCAATGTCTACCAACACTTCTACTGTGCTGACCCGCCCTCATTA
AGCTTCTGTCTGATACTTATGTCAAAGAGCATGCCATGTTCATATCTGCTGGCTTCAAC
CTCTCCAGCTCCCTCACCATCGTCTGGTCTATGCCCTCATCTGCTGCCATCCCTCG
GATCAAATCAGCAGAGGAAGGCACAAGGCATTCTCCACCTGTGGTCCCATATGATGGC
40 TGTCAACCTGTTATGGACTCTCTTGTATATAAGACCAACAGATAAGACT
GTTGAGGAATCTAAAATAATAGCTGTCTTACACCTTGTGAGTCCGGTACTTAATCCAT
TGATCTACAGTCTGAGGAATAAAGATGTGAAGCAGGCCCTGAAGAAATGTCCTGAGATGA
(SEQ ID NO: 36)

45

AOLFR19 sequences:

METKNYSSSTSGFILLGLSSNPKLQKPLFAIFLIMYLTAVGVLNLAIYSDPRLHTPMYFFLSNL
SFMDICFTTVIPKMLVNFLSETKIISYVGCLIQMYFFMAFGNTDSYLLASMAIDRLVAICNPLH
YDVMVKPWHLMLLGSISHLHSLFRVLLMSRLSFCASHIHKFFCDTQPVLKLSCSDTSSQ
50 MVVMTETLAIVTPFLCTIFSYLQIIVTVLRIPSAAGKWKAFSTCGSHLTVVVLFYGSVIYVFR
PLSMYSVMKGRVATVMYTVVTPMLNPFYSLRNKDMKRGGLKLRHRIYS (SEQ ID NO: 37)

55 ATGGAGACAAAGAATTATAGCAGCAGCACCTCAGGCTTCATCCTCCTGGGCCTCTTCCA
ACCCCTAACGCTGCAGAAACCTCTTGGCATCTCCTCATCATGTACCTACTCACTGCGGTG
GGGAATGTGCTCATCATCCTGGCATCTACTCTGACCCCAAGGCTCCACACCCCTATGTACT
TTTTCTCAGCAACTGTCTTCATGGATATCTGCTTCACAACAGTCATAGTGCCTAACAGATG
CTGGTGAATTCTATCAGAGACAAAGATTATCTCTTATGTGGCTGCCATCCAGATGT

5 ACTTCTTCATGGCATTTGGGAACACTGACAGCTACCTGCTGGCCTATGGCCATCGACCG
GCTGGTGGCCATCTGCAACCCCTTACACTATGATGTGGTTATGAAACCATGGCATTGCCTA
CTCATGCTATTGGGTTCTGCAGCATCTCCCACCTACATTCCCTGTCGCGTGCTACTTAT
GTCTCGCTTGTCTTCTGTGCCTCTCACATCATTAAGCACTTTCTGTGACACCCAGCCTG
10 TGCTAAAGCTCCCTGCTGACACATCCTCCAGCCAGATGGTGGTATGACTGAGACCTT
AGCTGTCATTGTGACCCCTTCTGTGTACCATCTTCTCCTACCTGCAAATCATCGTCACTG
TGCTCAGAATCCCCTCTGCAGCCGGAAAGTGAAGGCCTCTACCTGTGGCTCCACCT
CACTGTAGTGGTCTGTCTATGGGAGTGTATGTCTATGCTATTAGGCCTCTGTCCATGT
ACTCAGTGTGAAGGGCCGGTAGCCACAGTTATGTACACAGTAGTGACACCCATGCTGA
ACCTTTCATCTACAGCCTGAGGAACAAAGATATGAAAAGGGTTGAAGAAATTAAGAC
ACAGAATTACTCATAG (SEQ ID NO: 38)

AOLFR20 sequences:

15 MVEENHTMKNEFILTGFDTDHPPELKTLFVVFFAIYLITVVGNIQLVALIFTHCRLHTPMYIFLGN
LALVDSCCACAITPKMLENFFSEGKRISLYECAVQFYFLCTVETADCFLLAAVAYDRYVAICNP
LQYHIMMSKKLCIQMTTGAIFIAGNLHSMIHVGLVFRLVFCGLNHINHFYCDTLPLYRLSCVDPF
INELVLFIFSGSVQVFITGSVLISLYILLTIFRMKSKEGRAKAFSTCASHFSSVSLFYGSIFFLYIRP
NLLEGGNDIPAAILFTIVVPLNPFIYSLRNKEVISVLRKILLKIKSQGSVNK (SEQ ID NO: 39)

20 ATGGTTGAAGAAAATCATACCATGAAAAATGAGTTATCCTCACAGGATTACAGATCACC
CTGAGCTGAAGACTCTGCTGTTGTGGTCTTGCATCTATCTGATCACCGTGGTGG
GAATATTAGTTGGTGGCACTGATATTACACACTGTCGGCTCACACACCAATGTACATC
TTCTGGAAATCTGGCTTGTGGATTCTGCTGTCGCTGTGCTATTACCCCCAAATGTT
AGAGAACTTCTTCTGAGGGAAAAGGATTCCCTCTATGAATGTGCACTGAGTTTAT
25 TTCTTGCAGTGGAAAATGCACTGCAACTGCTGTTCTGCACTGAGTCCAGTGGCTATGACCGCT
ATGTGGCCATCTGCAACCCACTGCACTGAGTACCATCATGATGTCAAGAAACTCTGCATTCA
GATGACCAACAGGCCCTCATAGCTGGAAATCTGCATTCCATGATTGATGTAGGGCTTGT
TTAGGTTAGTTCTGTGGATTGAATCACATCAACCCTTACTGTGATACTCTTCCCT
30 GTATAGACTCTCCTGTGTTGACCTTTCATCAATGAACTGGTTCTATTCACTCTCAGGT
CAGTTCAAGTCTTACCATAGGTAGTGTCTTAATATCTTATCTATATTCTTCTACTATT
TTCAGAATGAAATCCAAGGAGGGAAAGGGCAAAGCCTTTACTGTGATCCCACCTT
CATCAGTTCAATTATTCTATGGATCTATTCTTCTACATAGACCAATTGCTTGA
GAAGGAGGTAATGATATACCAGCTGCTATTATACAATAGTAGTTCCCTACTAAATC
CTTCATTATAGTCTGAGAAACAAGGAAGTAATAAGTGTCTAAGAAAATTCTGCTGAA
35 AATAAAATCTCAAGGAAGTGTGAACAAATGA (SEQ ID NO: 40)

AOLFR21 sequences:

40 MEPRKNVTDFVLLGFTQNPKEQKVLFVMFLFYILTIVGNLLIVVTVTVSETLGSPMSFFLAGL
TFIDITYSSSISPRLLISDLFFGNNSISFQSFMAQLFIEHLFGGSEVFLLVMAYDRYVAICKPLHYLV
IMRQWVCVLLLVSVWVGGFLQSVFQLSIIYGLPFCGPVIDHFFCDMYPLLKACTDTHVIGLL
VVANGGLSCTIAFLLLISYGVILHSLKLSQKGRQKAHSTCSSHTVVVFFFVPCIFMCARPAR
TFSIDKSVSVFYTIVTPMLNPLIYTLRNSEMTSAMKLL (SEQ ID NO: 41)

45 ATGGAGCCAAGGAAAATGTGACTGACTTTGCTCTTGGGCTTCACACAGAACTCAAAG
GAGCAGAAAGTACTTTGTTATGTTCTGCTCTTACATTTGACCATGGTGGCAACCT
GCTCATTGTAGTGACCGTAACTGTCAGTGAGACCTGGCTCACCAATGTCTTCTTCTT
GCTGGCTTAACATTAGATATCATTTATTCTTCATCCATTCCCCAGATTGATTTCAGA
CTTGTCTTGGATAATTCCATATCCTCAATCTTCATGGCCAGCTTTATCGAGC
ACCTTTTGGTGGTCAGAGGTCTTCTCTGTGATGCCATGACCGCTATGTGGC
50 CATCTGTAAGCCCTTGCAATTATTGGTTATCATGAGACAATGGGTGTGTTTGCTGCTG
GTAGTGTCTGGTGGAGGATTCTGCAATCAGTATTCAACTTAGCATTATTATGGGC
TCCCATTCGTGGCCCCATGTCAATTGATCATTCTGTGACATGTATCCCTATTGAAA
CTGGCCTGCACTGACACCCATGTTATTGGCCTCTAGTGGTGGCCAATGGAGGACTGTCTT
GCACTATTGCGTTCTGCTCTACTCATCTTATGGTGTACCTGCACACTCTAAAGAAA
55 CTTAGTCAGAAAGGGAGGCAAAAAGCCCACTCAACCTGCAGTTCCCACATCACTGTGGTTG
TCTCTTCTTGTCTTGTATTGTGCTAGACCTGCTAGGACCTTCTCATTGAC

AAATCAGTGAGTGTGTTTATACAGTCATAACCCCAATGCTGAACCCCTTAATCTACACTC
TGAGAAATTCTGAGATGACAAGTGCTATGAAGAAGCTTAG (SEQ ID NO: 42)

AOLFR22 sequences:

5 MRXXNNXTEFVLLGFSQDPGVXKALFVFMLLTYXXTVVGNLLIVVDIILASPXLGSPMYFFLAC
LSFIDAAYSTTISPPLIVGLFCDKKTISFQGCMGQLFIDHFFGAEVFLLVVMACDRYVAICKPL
HYLTIMNRQVCFLLVXXMIGGFVHSASFQIVVYSLPFCGPXIVHFSCDMHPLLEACTDTYFI
GLTVVVVNSGAICMVIFNLLISYGVILSSLKTYSQEKRKGKALSTCSSGTVVVLFFVPCIFIYVRP
VSNFPTDKFMTVFTYIITHMLSPLIYTLRNSEMRNAIEKLLGKKLTIFIIGGVSVLM (SEQ ID NO:
10 43)

ATGAGACANNNNAACAATATNACAGAATTGTCCTCCTGGGCTTTCTCAGGATCCTGGTG
TGNNAAGCATTATTGTCATGTTTACTCACATACNNNNNAAGTGGTGGGAACCT
15 GCTCATTGNGATATTATTGCCAGCCCTNNNTGGGTTCCCAATGTATTCTCCTTG
CCTGCCTGTCATTATAGATGTCATATTCCACTACCATTTCTCCCAAGTTAATTGTAAGGC
TTATTCTGTGATAAAAAGACTATTCTTCAAGGGTGCATGGGCCAGCTATTATAGACC
ATTCTTGGTGGGCTGAGGTCTCCTCTGGTGTGATGGCCTGTGATCGCTATGTGGC
CATCTGTAAGCCACTGCACTATTGACCATCATGAATCGACAGGTTGCTTCTGTGTTGG
TNNTNNCCATGATTGGAGGTTTGTACATTCTGGTTCAATTGTTGTACAGTCTCCT
20 TTCTGTGGTCCCAGTCATTGTCATTCACTGTCAGTTGACATGCACCCATTACTGGAACTGGC
ATGCACTGACACCTACTTATAGGCCTCACTGTTGTCAATAGTGGAGCAATCTGTATG
GTCATTTCACCTCTGTTAATCTCTATGGAGTCATCCTAACGCTCCCTAAACACTACAG
TCAGGAAAAGAGGGGTAAGGCCTTGCTACCTGCAGCTCCGGCAGTACCGTTGTCTC
25 TTTTTGTACCCCTGTATTTCATATATGTTAGACCTGTTCAAACCTTCCACTGATAAGTT
CATGACTGTGTTTATACCATTATCACACACATGTCAGTCCTTAATATACGTTGAGA
AATTCAAGAGATGAGAAATGCTATAGAAAACCTTGGTAAAAGTTAACTATATTATTA
TAGGAGGAGTGTCCGTCATGTAG (SEQ ID NO: 44)

AOLFR23 sequences:

30 MAKNNLTRVTEFILMFMDHPKLEIPLFLVFLSFYLVTLLGNVGMIMLIQVDVKLYTPMYFFLS
HLSLLDACYTSVTPQILATLATGKTVISYGHCAAQFFLFTICAGTECFLAVMAYDRYAAIRNP
LLYTVAMNPRLCWSLVVGAYVCGVSGAILRTCTFLSFCKDNQINFHCDLPLKLACSDTA
NIEIVIIFGNFVILANASVILISYLLIKTILVKSSGGRAKTFSTCASHITAVALFFGALIFMYLQS
GSGKSLEEDKVSVFYTVVIPMLNPLIYSLRNKDVKDAFRKVARRLQVSLSM (SEQ ID NO: 45)

35 ATGGCCAAGAATAATCTCACCAAGAGTAACCGAACATTCTCATGGGCTTATGGACCACC
CCAAATTGGAGATTCCCTCTTCTGGTGTCTGAGTTCTACCTAGTCACCCCTTGGG
AATGTGGGGATGATTATGTTAATCCAAGTAGATGTCAAACTCTACACCCCAATGTAATTCT
TCTTGAGCCACCTCTCCCTGCTGGATGCCATGTTACACCTCAGTCATACCCCTCAGATCTA
40 GCCACATTGGCCACAGGAAAACGGTCATCTCTACGGCCACTGTGCTGCCAGTTCTT
TATTCAACCATCTGTGCAAGGACAGAGTGTCTCTGCTGGCAGTGATGCCATGATCGCTA
TGCTGCCATTGCAACCCACTGCTCTATACCGTGGCCATGAATCCCAGGCTTGCTGGAGC
CTGGTGGTAGGAGCTATGTCTGTGGGTTGTCAGGAGCCATCCTGCGTACCACTTGCACCT
TCACCCCTCTCTGTAAAGGACAATCAAATAAACCTTCTCTGTGACCTCCCACCCCTG
45 CTGAAGCTTGCCTGCAGTGACACAGCAAACATCGAGATTGTCATCATCTTGGCAATT
TTGTGATTTGCCAATGCCCTCGTCATCTGATTTCTATCTGCTCATCAAGACCAATT
TTGAAAGTGAAGTCTTCAGGTGGCAGGGCCAAGACTTCTCCACATGTGCTCTCACATCA
CTGCTGTGCCCTTTCTTGAGGCCCTATCTCATGTATCTGCAAAGTGGCTCAGGAAA
50 TCTCTGGAGGAAGACAAAGTCGTGTCITCTATACAGTGGTCATCCCCATGCTGAACC
CTCTGATCTACAGCTTAAGAAACAAAGATGTAAGACGCCCTCAGAAAGGTCGCTAGGA
GACTCCAGGTGTCCCTGAGCATGTAG (SEQ ID NO: 46)

AOLFR25 sequences:

55 METGNLTWVSDVFLGLSQTRELQRFLFLMFLFVYITTVVMGNILIIITVTSDSLQLHTPMYFLRN
LAVIDLCFSVTAPKMLVDLLSEKKTISYQGCMQIFFFHFLGGAMVFLSVMAFDRLIAISRPL
RYVTVMNTQLWVGLVVATWVGGFVHSIVQLALMLPLPFCGPNIIDNFYCDVPQVRLACTDT

SLLEFLKISNSGLDVVWFULLMSYLFILVMLRSHPGEARRKAASTCTTHIIVVSMIFVPSIYL
ARPFTPFMDKLVSIHTVMTPMLNPMIYTLRNQDMQAAVRRLGRHRLV (SEQ ID NO: 47)

5 ATGGAAACAGGGAACCTCACGTGGGTATCAGACTTGTCTTCCTGGGGCTCTCGCAGACTC
GGGAGCTCCAGCGTTCTGTTCTAATGTTCTGTTGTCATCACACTGTTATGGGA
AACATCCTTATCATCACAGTGACCTCTGATTCCCAGCTCCACACACCCATGTACITCT
GCTCCGAAACCTGGCTGCTTAGACCTCTGTTCTCTCAGTCAGTCTGCTCCAAAATGCTAG
TGGACCTCCTCTGAGAAGAAAACCATCTTACCAAGGGCTGCATGGGTCAAGATCTTCTT
CTTCACTTTGGGAGGTGCCATGGTCTCTCAGTGATGGCCTTGACCGCCTCA
10 TTGCCATCTCCCAGGCCCCCTCCGCTATGTCACCGTCATGAACACTCAGCTGGGTGGGGCT
GGTGGTAGCCACCTGGGTGGGAGGCTTGTCACCTCTATTGTCAGCTGGCTGATGCTC
CCACTGCCCCCTCTGTCGCCCCAACATTGGATAACTCTACTGTGATGTTCCCCAAGTACT
GAGACTTGCCCTGACTGACACCTCACTGCTGGAGTCCCTCAAGATCTCAACAGTGGGCTG
CTGGATGTCGTCGGTCTTCCCTCTGATGTCCTACTTATTCATCCTGGTGATGCTGAG
15 GTCACATCCAGGGAGGCAAGAAGGAAGGCAGCTCCACCTGCACCAACCCACATCATCGT
GGTTCCATGATCTCGTCCAAGCATTACCTCTATGCCCGCCCTCACTCCATTCCCTA
TGGACAAGCTTGTGTCATCGGCCACACAGTCATGACCCCCATGCTCAACCCATGATCTA
TACCTGAGGAACCAGGACATGCAGGCAGCAGTGAGAAGATTAGGGAGACACCGGCTGGT
TTGA (SEQ ID NO: 48)

20

AOLFR26 sequences:

MAAKNSSVTEFILEGLTHQPGLRIPLFLFLGFYTVTVVGNLGLITLIGLNSHLHTPMYFFLFNLS
LIDFCFSTTITPKMLMSFVSRKNIISFTGCMQLFFFCCFVVSESFILSAMAYDRYVAICNPLLYT
25 VTMSCQVCLLLLLGAYGMGFAGAMAHTGSIMNLTCFCADNLVNHFMCDILPYLELSCNNSYMN
ELVVFIVVAVDVGMPIVTFVIFSYALILSSILHNSSTEGRSKAFSTCSSHIIVVSLFFGSGAFMYLKP
LSILPLEQGKVSSLFYTIIVPVLNLIYSLRNKDVKVALRRTLGRKIFS (SEQ ID NO: 49)

30 ATGGCAGCCAAAACCTCTGTGACAGAGTTATCCTCGAAGGCTTAACCCACCAGCCGG
GAATCGGGATCCCCCTCTTCTGTTCTGGGTTCTACACGGTCACCGTGGTGGGGAA
CCTGGGCTTGATAACCTGATTGGGCTGAACCTCACTGCACACTCCCATGTACTTCTTCC
TTTTAACCTCTTTAATAGATTCTGTTCTCCACTACCATCACTCCAAAATGCTGATG
AGTTTGTCTCAAGGAAGAACATCATTCTTCACAGGGTGTATGACTCAGCTCTTCTTCT
CTGCTTCTTGTGCTCTGAGCTTCACTGTCAGCGATGGCGTATGACCGCTACGTGG
CCATCTGTAACCCACTGTTGACACAGTCACCATGTCCTGCCAGGTGTGTTGCTCCCTTG
35 TTGGGTGCCTATGGGATGGGGTTGCTGGGCCATGGCCACACAGGAAGCATAATGAAC
CTGACCTTCTGTGCTGACAACCTTGTCAATCATTCTCATGTGTCACATCTTCTCCCTGA
GCTCTCTGCAACAGCTTACATGAATGAGCTGGTCTTATTGTTGGCTGTTGAC
GTGGAATGCCCATGGTCACTGTCAGTCTTATTCTTATGCCCTCATCTCCAGCATCTACA
40 CAACAGTTCTACAGAAGGCAGGTCAAAGCCTTAGTACTGCACTCCACACATAATTGTA
GTTCTCTTTCTTGGTCTGGTCTTCTGTTCTACCTAAATAGCTCCCGTGTAAACCCATTAA
GAGCAAGGGAAAGTGTCTCCCTGTTCTACCTAAATAGCTCCCGTGTAAACCCATTAA
TCTATAGCTGAGGAACAAGGATGTCAAAGTGCCTGAGGAGAACTTGGCAGAAAAA
TCTTTCTTAA (SEQ ID NO: 50)

45

AOLFR27 sequences:

MPSQNSIISEFNLFGFSAFPQHLLPILFLYLLMFLFTLLGNLLIMATIWIIEHRLHTPMYFLFLCTL
SVSEILFTVAITPRMLADLLSTHHSITFVACANQMFFSFMFVHSFLVMGYDRYVAICHPLR
YNVLMSPRDCAHLVACTWAGGSVMGMMVTIVFHLTFCGSNVIIHFFCHVLSLLKACENKT
50 SSVIMGVMLVCVTALIGCLFLIILSYFIVAAIRIPSAEGRHKTSTCVSHLTVVVTHYSFASFIY
LKPGLHSMYSDALMATTYTVFTPFLSPIFLRNKELNAINKNFYRKFCPPSS (SEQ ID NO:
51)

55

ATGCCTAGTCAGAACTATAGCATATCTGAATTAAACCTCTTGGCTCTCAGCCCTCCC
CCAGCACCTCTGCCATCTTGTCTGCTGACCTCCTGATGTTCTGTTCACATTGCTGG
GCAACCTTCTCATCATGGCCACAATCTGGATTGAACACAGACTCCACACACCCATGTACCT
CTTCTTGTGACCCCTCCGCTCTGAGATTCTGTTCACTGTCAGTGCCATCACCCCTCGCATGC

5 TGGCTGATCTGCTTCCACCCATCATTCCATCACCTTGTGGCITGTGCCAACAGATGTT
 TTCTCCTTCATGTTGGCTTCACTCACTCCTTCCTCTGGTATGGCTATGATCGCTA
 TGTGGCCATCTGCCACCCACTCGCTAACATGTGCTCATGAGCCCCGTGACTGTGCCAT
 CTTGTGGCTGTACCTGGCTGGCTCAGTCATGGGGATGATGGTACAACGATAGTT
 10 TCCACCTCACTTCTGTGGGCTAAATGTGATCCACCATTITCTGTATGTGCTTCCCT
 TGAAGTTGGCCTGTGAAAACAAGACATCATCTGTCATCATGGGTGTGATGCTGGTGTG
 CACAGCCCTGATAGGCTGTTATTCTCATCATCCTCTCCATGTCTTATTGTGGCTGCCA
 TCTTGAGGATTCCCTCTGCCGAAGGCCGGCACAAGACATTCTACGTGTATCCCACCT
 CACTGTGGTGGTCACGCACATAGTTGCCTCTTACCTCAAGGCCAAGGGCCTCC
 15 ATTCTATGTACAGTGACGCCTGATGGCACCACCTACTGTCTTCAGCCCTTCCTAGC
 CCAATCATTTCAGCCTAAGGAACAAGGAGCTGAAGAATGCCATAAATAAAACTTTACA
 GAAAATTCTGTCCTCCAAGTTCCTGA (SEQ ID NO: 52)

AOLFR28 sequences:

15 MPNFTDVTEFTLLGLTCRQELQVLFFVVFLAVYMITLLGNIGMIIISIQLQSPMYFFLSHLSF
 ADVCFSSNVTPKMLENLLSETKTISYVGCLVQCYFIAVVHVEVYILAVMAFDRYMAGCXPL
 YGSKMSRTVCVRЛИSXYXYGSVSLICLWTYGLYFCGNFEINHFYCADPPLIQACGRVHIKE
 ITMIVIAGINFTYSLSVLISYTLIVVAVLRMRSADGRRKAFSTCGSHLTAVSMFYGTPIFMYLR
 RPTEESVEQGKVMAVFYTTVIPMLNPMIYSLRNKDVKЕAVNKAITKTVRQ (SEQ ID NO: 53)
 20 ATGCCTAATTTCACGGATGTGACAGAATTACTCTCCTGGGGCTGACCTGTCGTCAGGAGC
 TACAGGTTCTCTTTTGTGGTCTAGCGTTTACATGATCACTCTGTTGGAAATATT
 GGTATGATCATTTGATTAGCATCAGTCCTCAGCTTCAGAGTCCCAGTACTTTCTGAG
 25 TCATCTGCTTTGCGGACGTGCTCTCCACGTTACCTGGAAATGCTGGAAACT
 TATTATCAGAGACAAAAACATTCTATGTGGATGCTTGGTGCAGTGCTACTTTCT
 TGCGTTGTCCACGTGGAGGTCTATATCCTGGCTGTGATGCCCTTGACAGGTACATGCC
 GGCCTGCAANCCCTGCTTATGGAGTAAATGTCAGGACTGTGTTGTCAGGCTCATCT
 CTGTGNNNTATGNNTATGGATTCTGTCAGCTAATATGCACACTATGGACTTATGGCTT
 30 ATACTCTGTTGGAAACTTGAAATCAATCACTTCTATTGTGCAGATCCCCCTCATCCAGA
 TTGCGCTGTGGGAGAGTGCACATCAAAGAAATCACAATGATTGTTATTGCTGGAATTAACTT
 CACATACTCCTCTGGTCTCATCTCCTACACTCTCATTGTAGTAGCTGTGCTACGCA
 TGCCTCTGCCGATGGCAGGAGGAAGGCGTCTCCACCTGTGGTCCCACGTGACGGCTGT
 TTCTATGTTTATGGGACCCCCATCTCATGTATCTCAGGAGACCCACTGAGGAATCCGTA
 35 GAGCAGGGAAAATGGTGGCTGTGTTTACACCACAGTAATTCTATGTTGAATCCCAGTA
 TCTACAGTCTGAGAAATAAGGATGTAAGAAGCAGTCAACAAAGCAATACCAAGACAT
 ATGTGAGGCAGTAA (SEQ ID NO: 54)

AOLFR29 sequences:

40 MMSFAPNASHSPVFLLGFSRANISYTLFLFLAIYLTTILGNVTLVLLISWDSRLHSPMYYLLR
 GLSVIDMGLSTVLPQLLAHLVSHYPTIPAARCLAQFFFFYAFGVTDTLVIAMALDRYVAICD
 PLHYALVMNHQRCACLLALSWVSVSILHTMLRVGLVPLCWTGDAGGNVNLPHFFCDHRPLR
 ASCSDIHSNELAIFFEGGFLMLGPCALIVLSYVRIGAAILRLPSAAGRRRAVSTCGSHLTMVGL
 YGTIICVYFQPPFQNSQYQDMVASVMYTAITPLANPFVYSLHNKDVKGALCRLLEWKVDP
 (SEQ ID NO: 55)
 45 ATGATGAGCTTGCCTTAATGCTTACACTCTCCGGTTTTGCTCCTGGGTTCTGAG
 AGCTAACATCTCCTACACTCTCCTCTCTGGTCTGGTATTTACCTGACCAACATAC
 TGGGGAAATGTGACACTGGTCTGCTCATCTCTGGACTCCAGACTGCACTCACCCATGTA
 TTATCTGCTCGTGGCCTCTCTGTGATAGACATGGGCTATCCACAGTTACACTGCCAG
 50 TTGCTGGCCCATTGGTCTCTATTACCAACATTCTGCTGCCGCTGCTGGCTCAGTT
 CTTTTCTCTATGCAATTGGGTTACAGATAACACTGTGCTATTGCTGTCATGGCTCTGGATC
 GCTATGTGGCCATCTGTGACCCCTGCACTATGCTTGGTAATGAATCACCAACGGTGTG
 CTGCTTACTAGCCTGAGCTGGGTGCTCCACTGCACACCAATGTTGGGTGTTGGACTC
 GTCCTGCCTCTTGCTGGACTGGGATGCTGGGGCAACGTTAACCTCCTCACITCTT
 55 TGACCAACGGCCACTCTGCGAGCCTCTGTTCTGACATACATTCTAATGAGCTGGCCATA
 TTCTTGAGGGTGGCTCCTATGCTGGCCCTGTGCCCTATTGTACTCTCTATGTCCG

5 AATTGGGGCCGCTATTCTACGTTGCCCTCAGCTGCTGGTCGCCGCCAGCAGTCTCCACC
 TGTGGATCCCACCTCACCATGTTGGTTCTACGGCACCATCATTGTGTACTTCCA
 GCCTCCCTCCAGAACTCTCAGTATCAGGACATGGTGGCTCAGTAATGTATACTGCCATT
 ACACCTTGGCCAACCCATTGTGTATAGCCTCCACAATAAGGATGTCAAGGGTGCACTCT
 GCAGGCTGCTGAATGGGTGAAGGTAGACCCCTGA (SEQ ID NO: 56)

AOLFR30 sequences:

10 MGFLSPMHPCRPPTQRRMAAGNHSTVTEFLKGLTKRADLQLPLFLLFLGIYLVTIVGNLGMIT
 LICLNSQLHTPMYYFLNSLNSMDLCYSSVTPKMLVNFVSEKNIISYAGCMYSQLYFFLVFVIAEC
 YMLTVMAYDRYVXXCHPLLYNIIMSHHTCLLLVAVVYAIIGLIGSTIETGLMLKLPYCEHLISHY
 FCDILPLMKLSCSSTYDVEMTVFFSAGFNIVTSLTVLSYTFILSSILGISTTEGRSKAFSTCSSHL
 AAVGMFYGSTAFMYLPSTISSLTQENVASVFYTTVIPMLNPLIYSLRNKEVKAAVQKTLRGK
 LF (SEQ ID NO: 57)

15 ATGGGGTTCTGTCTCCCATGCATCCCTGCAGGCCCTCCCACCCAGAGGAGAATGGCTGCAG
 GAAAATCACTCTACAGTACAGAGTTCATCTCAAGGGTTAACGAAGAGAGCAGACCTCC
 AGCTCCCCCTCTTCTCCTCTTGGATCTACTTGGTACCATCGTGGGGAACCTGGGC
 ATGATCACTCTAATTGTCTGAACTCTCAGCTGCACACCCCATGTACTACTTTCTCAGCAA
 TCTGTCACTCATGGATCTCTGCTACTCCTCCGTATTACCCCTAACAGATGCTGGTGAACCTTG
 20 TGTCAGAGAAAAACATCATCTCCTACGCAGGGTGCATGTACAGCTACTTCTTCTCCTTGT
 TTTTGTCACTGCTGAGTGTACATGCTGACAGTGATGGCCTACGACCCTATGTTGNCNTC
 TGCCACCCTTGCTTACAACATCATTATGTCATCACACCTGCCTGCTGCTGGTGGCTGT
 GGTCTACGCCATGGACTCATGGCTCCACAATAGAAACTGGCCTATGTTAAAAGTGC
 25 TATTGTGAGCACCTCATCAGTCACTACTCTGTGACATCCTCCCTCATGAAGCTGTCCTG
 CTCTAGCACCTATGATGTTGAGATGACAGTCTTCTTACACCTCATTCTCTCCAGCATCTCGGCATCAGCAC
 ACAGAGGGAGATCCAAAGCCTCAGCACCTGCAGCTCCACCTGCAGCCGTGGAAAT
 GTTCTATGGATCAACTGCATTATGTAACCTCCACAATCAGTTCTGACCCAG
 30 GAGAATGTGGCCTCTGTGTTACACCAACGGTAATCCCCATGTTGAATCCCCAACTACA
 GCCTGAGGAACAAGGAAGTAAAGGCTGCCGTGCAGAAAACGCTGAGGGGTAACGTGTTT
 GA (SEQ ID NO: 58)

AOLFR31 sequences:

35 MGTGNDTTVVEFTLLGLSEDTTVCAILFLVFLGIYVVTLMGNISITVLIRRSHHLHTPMYIFLCHL
 AFVDIGYSSSVPVMLMSFLRKETSLPVAGCVAQLCSVTFGTAECAFLLAAMAYDRYVAICSP
 LLYSTCMSPGVCILVGMSYLGCGVNAWTFIGCLLRLSFCGPNKVNHFFCDYSPLLKLA
 SHDFTFEIIPAISSGSIIVATVCVIAISYIYILITLKMHSTKGRHKA
 FSTCTSHLTAVTLYGTITFIYVMP
 KSSYSTDQNKVVSVFYTIVIPMLNPLIYSLRNKEIKGALKRELRIKIFS (SEQ ID NO: 59)

40 ATGGGGACTGGAAATGACACCACTGTGGTAGAGTTACTCTTTGGGGTTATCTGAGGATA
 CTACAGTTGTGCTATTCTTATGTTCTAGGAATTATGTTGTCACCTTAATGGGT
 AATATCAGCATAATTGTATTGATCAGAAGAAAGTCATCATCTCATACACCCATGTACATT
 45 TCCTCTGCCATTGGCCTTGTAGACATTGGTACTCCTCATCAGTCACACCTGTCATGCTC
 ATGAGCTTCTAACGGAAAGAAACCTCTCCCTGTTGCTGGTTGTGTCAGCTCTGTT
 CTGTAGTACGTTGGTACGGCCAGTGCTTCTGCTGGCTGCCATGGCTATGATGCTA
 TGTGCCATCTGCTACCCCTGCTACTCATCTGCATGTCCTGGAGTCTGCATCATCT
 TAGTGGGCATGTCCTACCTGGGTGGATGTTGAATGCTTGACATTCAATTGGCTGCTTATT
 50 AAGACTGTCTTCTGTGGGCCAAATAAAAGTCATCACTTTCTGTGACTATTCAACCACTTT
 TGAAGCTTGTGTTGTCCTGATGATTACTTTGAATAATTCCAGCTATCTCTTCTGGATCT
 ATCATTGTGCCACTGTGTCATAGCCATATCCTACATCTATATCCTCATCACCACCTCT
 GAAGATGCACCTCACCACAGGGCCGCCAACAGGCCCTCTCCACCTGCACCTCCACCTCACT
 GCAGTCACCTGTCTATGGGACCATTAACCTCATTATGATGCTGCTGTTCTACACCGTGGTGA
 AACTGACCAAGAACAAGGTGGTGTCTGTTCTACACCGTGGTGAATTCCCATGTTGAACCCC
 CTGATCTACAGCCTCAGGAACAAGGAGATTAAGGGGGCTCTGAAGAGAGAGCTTAGAATA
 55 AAAATATTCTTCTGA (SEQ ID NO: 60)

AOLFR32 sequences:

MNSLKDGNHTALTGFILLGLTDDPILRVILFMIILSGNLSIIILIRISSQLHHPMYFFLSHLAFADM
 AYSSSVPNMLVNFLVERNTSYLGCAIQLGSAAFFATVECVLLAAMAYDRFVAICSPLLYSTK
 MSTQSVQLLLVYIAGFLIAVSYTTSFYFLLFCGPNVNHFCDFAPILELSCSDISVSTVVLSF
 5 SSGSIIVVTCVIAVCYIYLITILKMRSTEHHKAFSTCTSHLTVVTLFYGTITFIYVMPNFSYST
 DQNKKVSVLYTVVIPMLNPLIYSLRNKEIKGALKRELVRKILSHDACYFSRTSNNDIT (SEQ ID
 NO: 61)

10 ATGAATTCCCTGAAGGACGGGAATCACACCGCTCTGACGGGTTCATCCTATTGGGTTAA
 CAGATGATCCAATCCTCGAGTCATCCTCTCATGATCATCCTATCTGGAATCTCAGCATA
 ATTATTCTTATCAGAATTCTCTCAGCTCATCCTATGTATTTCTTGAGCCACTT
 GGCTTTGCTGACATGGCCTATTCATCTCTGTACACCCAACATGCTGTAAACTCCCTGG
 TGGAGAGAAAATACAGTCTCCTACCTTGGATGTGCCATCCAGCTTGGTTAGCGGGCTTCTT
 TGCAACAGTCGAATGCGTCCTCTGGCTGCCATGGCCTATGACCGCTTGTGGCAATTGC
 15 AGTCCACTGCTTATTCAACCAAAATGCCACACAAGTCAGTGTCCAGCTACTCTTAGTAG
 TTTACATAGCTGGTTCTCATTGCTGCTCCTATACTACTCTCTATTTTACTCTCT
 GTGGACCAAATCAAGTCATCATTTCTGTGATTGCTCCCTACTTGAACCTCCTGT
 TCTGATATCAGTGTCTCCACAGTTGTTCTCATTTCTGGATCCATATTGTGGTCAC
 TGTGTGTGTCATAGCCGCTGCTACATCTATATCCTCATCACCACCTGAAGATGCGCTCCA
 20 CTGAGGGGCCACCAAGGCCCTCTCCACCTGCACTTCCCACCTCACTGTGGTACCCCTGTT
 CTATGGGACCATTACCTTCATTATGTGATGCCAATTAGCTACTCAACTGACCAGAAC
 AAGGTGGTGTCTGTGTTGACACAGTGGTGAATCCATGTGAACCCCCGATCTACAGCC
 TCAGGAACAAGGAGATTAAGGGGCTCTGAAGAGAGAGCTGTTAGAAAAATACTTCTC
 ATGATGCTTGTATTTAGTAGAACTTCAAATAATGATATTACATAG (SEQ ID NO: 62)

25

AOLFR34 sequences:

MLEGVHLLLLLTDVNSKEIQLSGNQTSVSHFILVGLHHPPQLGAPLFLAFLVIYLLTVSGNG
 LIITVLVDIRLHRPMCLFLCHLSFLDMTISCAIPKMLAGFLLGSRIISFGGCVIQLFSFHFLGCT
 ECFLYTLMAYDRFLAICKPLHYATIMTHRVCNSLALGTWLGGTIHSLFQTSFVRLPFCGPNRV
 30 DYIFCDIPAMLRLACADTAINELVTFADIGFLALTFCMILTSYGYIVAILRIPSADGRRNAFST
 CAAHLTVVVYYYVPCFTIYLRPCSQEPLDGVAVFYTIVTPLLNSIIYTLCNKEMKAALQRLGG
 HKEVQPH (SEQ ID NO: 63)

35

ATGTTAGAGGGTGTGAGCATCTCCCTCTGCTACITCTTTGACAGATGTGAACAGCAAGG
 AACTGCAAAGTGGAAACCAGACTTCTGTGTCACCTCATTTGGTGGCCTGCACCACCC
 ACCACAGCTGGGAGCGCCACTCTCTTAGCTTCCCTGTACATCTATCTCCTCACTGTTCTG
 GAAATGGGCTCATCATCCTCACTGTCTTAGTGGACATCCGGCTCCATCGTCCCATGTGCTT
 GTTCCCTGTGTCACCTCTCCCTGGACATGACCATTTCTGTGCTATTGTCCCCAAGATGC
 TGGCTGGCTTCTCTGGTAGTAGGATTATCTCCTTGGGGCTGTGTAATCCAACATATT
 40 TCTTCCATTCCCTGGCTGTACTGAGTGCTCCTTACACACTCATGGCTTATGACCGTT
 CCTTGCCATTGTAAAGCCCTAACATATGCTACCATCATGACCCACAGAGTGTGAACTCCC
 TGGCTTAGGCACCTGGCTGGAGGGACTATCCATTCACTTCCAAACAAGTTTGATT
 CCGGCTGCCCTCTGTGGCCCAATCGGGTCGACTACATCTCTGTGACATTCCCTGCCATGC
 TCGCTCTAGCCTGCGCCATACGGCCATCAACGAGCTGGTACCTTGCAGACATTGGCTT
 45 CCTGGCCCTCACCTGCTCATGCTCATCCTCACTTCCATGGCTATTGTAGCTGCCATCC
 TCGAATTCCGTAGCAGATGGCGCCGAATGCCCTCTCCACTTGTGCTGCCACCTCAC
 TGGTGTCTTACTATGTGCCCTGCACCTTCAATTACCTGCGGCCCTGTTACAGGGAGC
 CCCTGGATGGGGTGGTAGCTGTCTTACACTGTGTCATACCCCTGCTTAACCTCATCATC
 TACACACTGTGCAACAAAGAAATGAAGGCAGCATTACAGAGGCTAGGGGCCACAAGGAA
 50 GTGCAGCCTCACTGA (SEQ ID NO: 64)

AOLFR35 sequences:

MEPLNRTEVSEFFLKGSGYPALEHLLFPLCSAMYLVTLLGNTAIMAVSVLDIHLHPTVYFFLG
 NLSTLDICYTPTFVPLMLVHLLSSRKTISFAVCAIQMCLSLSTGSTECLLLAITAYDRYLAICQPL
 55 RYHVLMSHRLCVLLMGAAWVLCLLKSVTMVISMRPLFCGHHVVSHFTCKILAVLKLACGNT
 SVSEDFLLAGSILLPVPLAFICLISYLLILATILRVPSAARCKAFSTCLAHIAVVLIFYGTIIFMY

LKPKSKEAHISDEVFTVLYAMVTTMLNPTIYSLRNKEAARKVWGRSRASR (SEQ ID NO: 65)

5 ATGGAGCCGCTAACAGAACAGAGGTGTCGGAGTTCTGAAAGGATTTCTGGCTACC
 CAGCCCTGGAGCATCTGCTCTCCCTCTGTGCTCAGCCATGTACCTGGTACCCCTCCTGGG
 GAACACAGCCATCATGGCGGTGAGCGTGTAGATATCCACCTGCACACGCCCGTGTACTTC
 TTCCGGCAACCTCTAACCTGGACATCTGCTACAGCCCACCTTGTGCCCTGTGATGCT
 GGTCCACCTCTGTACCCGGAAAGACCATCTCCCTTGCTGTCTGCCATCCAGATGTGTC
 TGAGCCTGTCACGGGCTCCACGGAGTGCCTGCTACTGGCCATACGGCCTATGACCGCTA
 10 CCTGGCATCTGCCAGCCACTCAGGTACCACGTGCTCATGAGCCACCGGCTCTGCGTCTG
 CTGATGGGAGCTGCCCTGGCTCTGCCCTCAAGTCGGTACTGAGATGGTCATCTCCA
 TGAGGCTGCCCTCTGTGGCCACCGTGGTCAGTCACCTCACCTGCAAGATCCTGGCAGT
 GCTGAAGCTGGCATCGGCAACACGTCGGTCAGCGAAGACTCCTGCTGGCAGGCTCCAT
 CCTGCTGCTGCCGTACCCCTGGCATTCTGCTCTGCTACTTGCTCATCCTGGCACCCA
 15 TCC TGAGGGTGCCCTGGCCGCCAGGTGCTGCAAAGCCTCTCCACCTGCTGGCACACCT
 GGCTGTAGTGCTGCTTTCTACGGCACCACATCTCATGTACTTGAAAGCCAAGAGTAAG
 GAAGCCCACATCTGTGATGAGGTCTTCACAGTCCTATGCCATGGTCACGACCATGCTGA
 ACCCCACCATCTACAGCCTGAGGAACAAGGAGGTGAAGGAGGCCAGGAAGGTGTGGG
 GCAGGAGTCGGCCTCCAGGTGA (SEQ ID NO: 66)

20

AOLFR36 sequences:

MYLVTVRNLLSILA VSSDSHPHTPMYFFLSNLWADIGFTLATVPKMTVDMGSHSKVISYGG
 CLTQMSFLVLFACIVDMFLTVMA YDCFVAICRPLHYPVIVNPFLCVFFVLVSFFLSLLDSQLHS
 25 WIVLQFTFFKNVEISNFVCEPSQLLKLASYDSVINSIFIYFDNTMFGFLPISGILLSYYKIVPSILRIS
 SSDGKYKAFSACGCHLA VVCLFYGTIGVYLTSAVAPPLRNGMVASVMYAVVTPMLNPFIYS
 LRNRDIQSALWRVCNKTVESHLFHPFSCVVEKGQPHSIPTSANPAP (SEQ ID NO: 67)

30 ATGTATCTGGTCACGGTGCTGAGGAACCTGTCAGCATCCTGGCTGTCAGCTGACTCCC
 ACCCCCCACACACCCATGTACTTCTTCTCCACCTGTGCTGGGCTGACATCGGTTTCACC
 TTGGCCACGGTTCCCCAAATGATTGTGGACATGGGGTCGACATAGCAAAGTCATCTCTATG
 GGGGCTGCCCTGACACAGATGTCTTCTTGTGACTTTTGATGACATGAAAGTCATCTCTATG
 GACTGTGATGGCTTATGACTGCTTGTAGCCATCTGTCGCCCTCTGCACTACCCAGTCATC
 GTGAATCCTCACCTCTGTGCTTCTCGTTGGTGTCCCTTTCTCTAGCCTGTTGGATTCC
 CAGCTGCACAGTTGGATTGTGTTACAATTCAACCTCTTCAAGAAATGTGAAATCTCTAAATT
 35 TTGTCTGTGAGCCATCTCAACTCTCAAGCTTGCCTCTATGACAGCGTCATCAATAGCATA
 TTCATATATTTGATAAAACTATGTTGGTTCTTCCCATTCAGGGATCCCTTTGTCTTAC
 TATAAAATTGTCCTCCATTCTAAGGATTTCATCATCAGATGGGAAGTACAAGCCTTCT
 CAGCCTGTGGCTGTCACCTGGCAGTTGTTGCTATTGGAACAGGCATTGGCGTGT
 40 CCTGACTTCAGCTGGCACCAACCCCTCAGGAATGGTATGGTGGCGTCAGTGATGTACGCT
 GTGGTACCCCCCATGCTGAACCCCTTCATCTACAGCCTGAGAACACAGGGACATTCAAAGTG
 CCCGTGGAGGGTGTGCAACAAAACAGTCGAATCTCATGATCTGTTCCATCCTTTCTTG
 TGTGGTTGAGAAAGGGCAACCACATTCAATCCCTACATCTGCAAATCCTGCCCTAG
 (SEQ ID NO: 68)

45

AOLFR37 sequences:

MEKANETSPVMGFVLLRLSAHPELEKTFVLLMYL VILLNGNGVLILV TILDRLHTPMYFFLG
 NLSFLDICFTSSVPLVLDLSFLTPQETISFACAVQMA SFAMAGTECLLSMMAFDRYVAICNP
 LRYSVIMS KAA YMPMAASSWAIGGAASV VHTSLAIQLPFCGDNVINHFTCEILAVLKLACADIS
 50 INVISMEVTNVIFLGVPVLFISFSYVFIITIIRIPSAEGRKKVFSTCSAHLTVVIVFYGTLFFMYG
 KPKSKDSMGADKEDLSDKLIPLFYGVVTPMLNPIYSLRNKDVKAAVRRLRPKGFTQ (SEQ ID
 NO: 69)

55 ATGGAAAAAGCCAATGAGACCTCCCTGTGATGGGGTTCTGTTCTCCTGAGGCTCTGCC
 ACCCAGAGCTGGAAAAGACATTCTCGTGTCTCATCCTGCTGATGTACCTCGTGTACCTGCT
 GGGCAATGGGGTCCTCATCCTGGTACCCATCCTGACTCCCGCTGCACACGCCCATGTAC
 TTCTCCTAGGGAACCTCTCCTCTGGACATCTGCTTCACTACCTCCTCAGTCCACTGGT

CCTGGACAGCTTTGACTCCCCAGGAAACCATCTCCTCTCAGCCTGTGCTGTGCAGATG
 GCACTCTCCTTGCCATGGCAGGAACAGACTGCTGCTGAGCATGATGGCATTGATC
 GCTATGTGGCCATCTGCAACCCCTTAGGTAACCTCGTGATCATGAGCAAGGCTGCCTACAT
 GCCCATGGCTGCCAGCTCTGGCTATTGGTGGTGTGCTTCCGTGGTACACACATCCTG
 5 GCAATTCACTGCCCCCTGTGGAGACAATGTCATCAACCACITCACCTGTGAGATTCTGG
 CTGTTCTAAAGTTGGCCTGTGCTGACATTCCATCAATGTGATCAGCATGGAGGTGAGGAA
 TGTGATCTCCTAGGAGTCCCCTGCTGTCATCTTCTCCTATGTCTTATCATCACCA
 CCATCCTGAGGATCCCCTGAGCTGAGGGGAGGAAAAGGTCTTCTCACCTGCTCTGCCA
 CCTCACCGTGGTGTGCTTACGGGACCTTATTCTCATGTATGGGAAGCCTAAGTCT
 10 AAGGACTCCATGGGAGCAGACAAAGAGGATTTCAAGACAAACTCATCCCCCTTCTATG
 GGGTGGTACCCCGATGCTCAACCCCATCATCTATAGCCTGAGGAACAAGGATGTGAAGG
 CTGCTGTGAGGAGACTGCTGAGACCAAAAGGCTCACTCAGTGA (SEQ ID NO: 70)

AOLFR38 sequences:

15 MYLVTVLRNLLIILAVSSDSHLHTPMCFLSNLWADIGFTSAMVPKMIVDMQSHSRVISYAGC
 LTQMSFFVLFACIEDMLLTVMAYDRFVAICHPLHYPVIMNPFLGVFLVLSFFLSLLDSQLHSHW
 IVLQFTFFKNVEISNFVCDPSQLLNACSDSVINSIFYLDSIMFGFLPISGILLSYANNVPSILRISS
 SDRSKAFSTCGSHLAVVCLFYGTGIGVYLTSAVSPPPRNGVVASVMYAVVTPMLNPFIYSLR
 NRDIQSALWRLRSRTVESHDLLSVDLHFPSCVGEKGQPH (SEQ ID NO: 71)

20 ATGTACCTGGTCACGGTGTGAGGAACCTGCTCATCATCTGGCTGTCAGCTCTGACTCCC
 ACCTCCACACCCCCATGTGCTTCTCCTCCAACCTGTGCTGGGCTGACATCGGTTCAACC
 TCGGCCATGGTCCCAAGATGATTGTGGACATGCAGTCGATAGCAGAGTCATCTCTTATG
 25 CGGGCTGCCATGACACAGATGTCTTCTTGTGCTTGTGATGATAGAAGACATGCTCTG
 ACAGTGATGGCTATGACCGATTGTGGCCATCTGTCACCCCTGCACTACCCAGTCATCA
 TGAATCCTCACCTGGTGTCTCTAGTTGGTCTTCTCAGCTGCTTCTCAGCTGTTGGATTCC
 CAGCTGCACAGTTGGATTGTGTTACAATTCACTTCTCAAGAATGTGGAAATCTCCAATT
 TTGTCGTGACCCATCTCAACTCTCAACCTTGCCTGTTCTGACAGTGTGTCATCAATAGCATA
 30 TTCAATATTAGATAGTATTATGTTGGTTTCTTCTCCATTCAGGGATCTTGTCTTAC
 GCTAACAAATGCCCCCTCATTCTAACAGATAGGAAGTCTAACGCTTCT
 CCACCTGGCTCTCACCTGGCAGTTGTTGCTTATTTATGGAACAGGCATTGGCGTGTA
 CCTGACTTCAGCTGTGTCACCACCCCCCAGGAATGGTGTGGCATCAGTGATGTACGCT
 GTGGTCACCCCATGCTGAACCTTCTACAGCCTGAGAAATAGGGACATTCAAAGTG
 35 CCCTGTGGAGGCTGCGCAGCAGAACAGTCGAATCTCATGATCTGTTATCTCAAGATCTGCT
 CCATCCCTTCTGTGGTGGGTGAGAAAGGTCAACCACATTAA (SEQ ID NO: 72)

AOLFR39 sequences:

40 MGVKNHSTVTEFLSGLTEQAEQLQPLFCLFLGIYTVVVGNLMSIIRLNRLQHPTMYYFLSS
 LSFLDFCYSSVTPKMLSGFLCRDRSISYSGCMIQLFFCVCVISECYMLAAMACDRYVAICSP
 LYRViMSPRVCSSLVAAVFSVGFTDAVIHGGCILRLSFCGSNIKHYFCDIVPLIKLSCSSTYIDEL
 LIVVIGGFNMVATSLTIIISYAFILTSILRHSKKGRCKAFSTCSSHLTAVLMFYGSMSMYLK
 SSSLTQEKVSSVFYTTVILMLNPLIYSLRNNEVRNALMKLLRKISLSPG (SEQ ID NO: 73)

45 ATGGGTGTAAAAAACATTCCACAGTGACTGAGTTCTTCTCAGGATTAACGAACAAAG
 CAGAGCTTCAGCTGCCCTCTCTGCCTCTTAGGAATTACACAGTTACTGTGGTGGG
 AAACCTCAGCATGATCTCAATTATTAGGCTGAATCGTCAACTTCATACCCCATGTACTAT
 TTCTGAGTAGTTGTCTTTAGATTCTGCTATTCTCTGTCATTACCCCTAAATGCT
 ATCAGGGTTTATGCAGAGATAGATCCATCTCTTCTGGATGCTGATGATTCACTGCTT
 TTTCTGTGTTGTATTCTGAATGCTACATGCTGGCAGCCAATGGCTCGATCGCTAC
 50 GTGGCCATCTGCAGCCCCACTGCTCACAGGGTCATCATGTCCTCTAGGGTCTGTTCTGC
 TGGTGGCTGCTGTCTCAGTAGGTTCACTGATGCTGATCCATGGAGGTTGTATAACT
 CAGGGTTGCTTCTGTGGATCAAACATCATTAAACATTATTCTGTGACATTGTCCTCTTA
 TAAACTCTCCTGCTCCAGCACTTATATTGATGAGCTTTGATTTGTGATTGGGATTT
 AACATGGTGGCCACAAGCCTAACATCATTATTCTCATATGCTTTATCCTCACCAAGCATCCT
 55 GCGCATCCACTCTAAAAAGGGCAGGTGCAAAGCGTTAGCACCTGAGCTCCACCTGACA
 GCTGTTCTATGTTATGGGTCTGATGTCCATGTATCTCAAACCTGCTTAGCAGTTC

ACTCACCCAGGAGAAAGTATCCTCAGTATTTATACCACTGTGATTCTCATGTTGAATCCC
TTGATATATAGTCTGAGGAACAATGAAGTAAGAAATGCTCTGATGAAACTTTAAGAAGA
AAAATATCTTATCTCCAGGATAA (SEQ ID NO: 74)

5 **AOLFR40 sequences:**

MSNATLLTAFILETGLPHAPGLDAPLFGIFLVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNLS
FIDMWFSTVTPKMLMTLVSPSGRTISFHSCVAQLYFFFHFLGSTECKFLYTVMSYDRYLAISYPL
RYTNMMTGRSCALLATGTWLGSLSLHSAVQTILTFHLPYCGPNQIQHYFCDAAPILKLACADTS
10 ANEMVIFVNIGLVASGCFVLIVLSYVSIVCSILRIRTSEGRHRAFQTCASHCIVVLCFFGPGLFIYL
RPGSRDALHGVVAVFYTTLPLFNPVVYTLRNKEVKALLKLKNGSVFAQGE (SEQ ID NO:
75)

15 ATGTCCAACGCCACCCACTGACAGCGTTCATCCTCACGGGCCTTCCCCATGCCCGAGGGC
TGGACGCCCCCTCTTGGAAATCTTCTGGTGGTTACGTGCTACTGTGCTGGGAACCT
CCTCATCCTGCTGGTGTACAGGGTGGATTCTCACCTCCACACCCCCATGTACTACTTCTCA
CCAACCTGTCCTCATTGACATGTGGTCTCCACTGTCACGGTGCCAAAATGCTGATGAC
CTTGGTGTCCCAAGCGGCAGGACTATCTCCTCACAGCTGCGTGGCTCAGCTCTATT
TCCACTTCTGGGAGCACCAGTGTGTTCTACACAGTCATGTCCTATGATCGCTACCT
20 GCCCATCAGTACCCGCTCAGGTACACCAACATGATGACTGGCGCTCGTGTGCCCTCTG
GCCACCGGCACTGGCTCAGTGGCTCTGCACTGCTGTCAGCCACCATATTGACTTTCC
ATTGCCCCTACTGTGGACCCAACCAGATCCAGCAGACTACTCTGTGACGCACCGCCCATCCT
GAAACTGGCCTGTGCAAGACACCTCAGCCAACAGAGATGGTCATCTTGTGAATATTGGGCTA
25 GTGGCCTCGGGCTGCTTGTCTGATAGTGTGCTCCTATGTGTCCATCGTCTGTCCATCCT
GCGGATCCGCACCTCAGAGGGGAGGCACAGAGCCTTCAGACCTGTGCGCTCCACTGTATC
GTGGTCCTTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT
CTTGCACTGGGTTGTGGCCGTTTCTACACCACGCTGACTCCTCTTCAACCCCTGTTGT
ACACCCCTGAGAAACAAGGAGGTAAAGAAAGCTCTGTTGAAGCTGAAAAATGGGTCACTGAT
TTGCTCAGGGTGAATAG (SEQ ID NO: 76)

30 **AOLFR41 sequences:**

MNPENWTQVTSFVLLGFPSSHILQFLVFLGLMVTYIVTATGKLLIIVLSWIDQRLHIQMYFFLRN
FSFLELLLVTVVVPKMLVVILTGDHTSFVSCIIQSYLYFFLGTTDFLLAVMSLDRYLAICRPLR
YETLMNGHVCSQLVLASWLAGFLWVLCPTVLMASLPFCGPNGIDHFFRDSWPLRLSCGDT
35 LLKLVAFMLSTLVLLGSLALTSVSYACILATVLRAPTAERRKAFSTCASHLTVVVITYGSSIFLY
IRMSEAQSQKLLNKGASVLSCLTPLLNPFIITRNDKVQQALREALGWPRLTAVMKLRTVSQRK
(SEQ ID NO: 77)

40 ATGAACCTGAAAACGGACTCAGGTAACAAGCTTGTCTGGGTTCCCCAGTAGCC
ACCTCATACAGTTCTGGTGTCTGGGTTAATGGTACCTACATTGTAACAGCCACAGG
CAAGCTGCTAATTATTGTGCTCAGCTGGATAGACCAACGCCCTGCACATACAGATGTACTTC
TTCTGCGGAATTCTCCTCCTGGAGCTGTTGCTGGTAACTGTTGTGGTCTCCAAAGATGCT
TGTCGTCTCCTCACGGGGATCACACCATCTCATTGTCAGCTGCATCATCCAGTCCTACC
TCTACTTCTTCTAGGCACCACTGACTCTTCTCTGGCCGTATGTCCTCTGGATCGTTAC
CTGGCAATCTGCCGACCACTCCGCTATGAGACCCGTATGAATGGCATGTCCTGTTCTCCAAAC
45 TAGTGCTGGCCTCCTGGTAGCTGGATTCTCTGGCTTGGCCCATGTCCTCATGGCC
AGCCTGCCTTCTGTGGCCCAATGGTATTGACCATCTTCTGTCAGCTGGCCCTTGCT
CAGGCTTCTGTGGGACACCCACCTGCTGAAACTGGTGGCTTCAATGCTCTACGTTG
GTGTTACTGGGCTCACTGGCTCTGACCTCAGTTCTATGCCCTGCATTCTGCCACTGTTCT
CAGGGCCCCCTACAGCTGCTGAGCGAAGGAAAGCGTTTCACTTGCCCTCGCATCTAC
50 GTGGTGGTCACTCATCTATGGCAGTTCCATCTTCTACATTGCTATGTCAGAGGCTCAGTC
CAAACGTCTAACAAAGGTGCCCTCGTCTGAGCTGCATCATCACACCCCTCTTGAACCCA
TTCATCTTCACTCTCCGCAATGACAAGGTGCAGCAAGCACTGAGAGAAGCCTGGGTGGC
CCAGGCTCACTGCTGTGATGAAACTGAGGGTCACAAGTCAAAGGAAATGA (SEQ ID NO:
78)

AOLFR42 sequences:

MNPANHSQVAGFVLLGLSQVWELRFVFFTVPFAVYFMTVVGNLIVVIVTSDPHLHTTMYFL
 5 GNLSFLDFCYSSITAPRMLVDLNSGNPTISFGGCLTQLFFFHFIGGIKIFLLTVMAHYDRYIAISQL
 HYTLIMNQTVCALLMAASWVGGFIHSIVQIALTIQLPFCGPDKLDNFYCDVPQLIKLACTDFV
 10 LELLMVSNNGLVTLMCFVLLLGSYTALLVMLRSHSREGRSKALSTCASHIAVVTLIFVPCIVYV
 TRPFRTFPMMDKAVSVLYTIVTPMLNPAIYTLRNKEVIMAMKKLWRRKKDPIGPLEHRPLH
 (SEQ ID NO: 79)

15 ATGAATCCAGCAAATCATTCCAGGTGGCAGGATTGTTACTGGGGCTCTCTCAGGTTT
 GGGAGCTTCGGTTGTTCTCACTGTTTCTGCTGTGTTATTTATGACTGTAGTGGGA
 AACCTTCTTATTGTGGTCATAGTGACCTCCGACCCACACCTGCACACAACCAGTGTATTTCT
 CTTGGGCAATCTTCTTCTGGACTTTGCTACTCTCCATCACAGCACCTAGGATGCTGG
 TTGACTTGCTCTCAGGCAACCCCTACCATTTCTTGGATGCTGACTCAACTCTTCTC
 TTCCACTTCATTGGAGGCATCAAGATCTCCTGCTGACTGTCACTGGGTATGACCGCTACA
 20 TTGCCATTCCCAGCCCCCTGCACTACACGCTCATTATGAATCAGACTGTCTGCACTCCTT
 ATGGCAGCCTCCTGGGTGGGGGCTTCATCCACTCCATAGTACAGATTGATTGACTATCC
 AGCTGCCATTCTGTGGGCCTGACAAGCTGGACAACCTTTATGTGATGTGCCTCAGCTGAT
 CAAATTGGCCTGCACAGACCTTGTCTAGAGCTTTAATGGGTGCTAACATGGCCTG
 GTGACCCCTGATGTGTTCTGGTCTCTGGATCGTACACAGCACTGCTAGTCATGCTCC
 25 GAAGCCACTCACGGGAGGGCCGCAGCAAGGCCCTGTCTACCTGTGCCTCTCACATTGCTGT
 GGTGACCTTAATCTTGTGCCTGCATCTACGTCTACACAAGGCCTTTCGGACATTCCCCA
 TGGACAAGGCCGTCTGTGCTACACAATTGTCACCCCCATGCTGAATCCTGCCATCTA
 TACCCCTGAGAAACAAGGAAGTGTACATGCCATGAAGAAGCTGTGGAGGAGGAAAAAGG
 ACCCTATTGGTCCCCCTGGAGCACAGACCCCTACATTAG (SEQ ID NO: 80)

AOLFR43 sequences:

30 MQKPQLLVPILATSNGNLVHAAYFLLVGIPGLGPTIHFWLAFFLCMYALATLGNLTIVLII
 RRLHEPMYFLFLAMLSTIDLVLSSITMPKMASLFLMGIQEIEFNICLAQMFLIHALS
 MAFDRFVAICHPLRHASVLTGCTVAKIGLSALTRGFVFFFPLPFIKLWLSYQTHVTHSFCLHQ
 DIMKLSCTDTRVNVVYGLFIILSVMGVDSLFIGFSYIILWAVLELSSRRAALKAFNTCISHLC
 LVFVPLIGLSVVHRLGGPTSLHVVMANTYLLLPPVNPLVYGAKTKEICSRVLCMFSQGGK
 (SEQ ID NO: 81)

35 ATGCAGAACCCCCAGCTCTGGTCCCTATCATAGCCACTTCAAATGGAAATCTGGTCCACG
 CAGCATACTTCCTTTGGTGGGTATCCCTGGCTGGGCCTACCATACACTTTGGCTGGCT
 TTCCCACTGTGTTTATGTATGCCCTGGCCACCCCTGGTAACCTGACCATGTCCTCATCAT
 TCGTGTGGAGAGGCAGCTGCATGAGCCATGTACCTCTGGCCATGCTTCCACTATT
 GACCTAGTCCTCTCCCTATCACCATGCCAAGATGGCAGTCTTCTGATGGCATCCA
 GGAGATCGAGTTCAACATTGCTGCCAGATGTTCCCTATCCATGCTCTGTCAGCCGTG
 40 GAGTCAGCTGCTCTGGCCATGGCTTTGACCGCTTTGTCGGCCATTGCCACCCATTGC
 GCCATGCTTCTGTGCTGACAGGGGTGTACTGTGGCCAAGATGGACTATCTGCCCTGACCA
 GGGGTGTTGTTCTCTTCTCCCACCTGCCCTCATCCTCAAGTGGTTGTCTACTGCCAAACAC
 ATACTGTCACACACTCCCTCTGTCTGCACCAAGATATTATGAAGCTGTCTGTACTGACAC
 CAGGGTCAATGTGGTTATGGACTCTTCATCATCCTCTCAGTCATGGGTGTTGACTCTCT
 45 TCATTGGCTCTCATATATCCTCATCCTGTGGCTGTTTGAGGCTGTCTCTGGAGGGCA
 GCACTCAAGGCTTCAACACCTGCATCTCCACCTCTGTGCTGTTCTGGTCTATGTACC
 CCTCATTGGGCTCTGGTGCATAGGCTGGTGGTCCACCTCCCTCTCCATGTGGTT
 ATGGCTAACCTACTTGTCTGCTACCACCTGTAGTCACCCCCCTGTCTATGGAGCCAAGA
 CCAAAGAGATCTGTCAGGGCTCTGTATGTTCTCACAAGGTGGCAAGTGA (SEQ ID
 50 NO: 82)

AOLFR44 sequences:

55 MSSCNFTHATFVLIGGLEKAHFVVGPLLSSMYVAMFGNCIVVIVRTERSLHAPMYLFLC
 MLAIDLALSTSTMPKILALFWFDSREISFEACLTQMFFIHALSAIESTILLAMA
 FDRYVAICHPLRHAALNNTVTAQIGIVAVVRRGSLFFFPLPLLKRLAFCHSNVLSHS
 YCVHQDVMKLAYADTLPNVVYGLTAIILVMGVDMFISLSYFLIRTVLQLPSK
 SERAKAFTGTCVSHIGVVLAFYVPLIGL

VVHRFGNSLHPIVRVVMGDIYLLPPVINPIYGA GTKQIRTRVLAMFKISCDKDLQAVGGK
(SEQ ID NO: 83)

5 ATGAGTTCTGCAACTCACACATGCCACCTTGTGCTTATTGGTATCCCAGGATTAGAGA
AAGCCCATTTCTGGGTTGGCTTCCCCCTCCTTCATGTATGTAGTGGCAATGTTGGAAAC
TGCATCGTGGTCTTCATCGTAAGGACGGAACGCAGCCTGCACGCTCGATGTACCTCTTC
TCTGCATGCTGCAGCATTGACCTGGCTTATCCACATCCACCATGCCTAAGATCCCTGCC
CTTCTGGTTGATCCCAGAGATTAGCTTGTAGGCTGTCTACCCAGATGTTCTTAT
TCATGCCCTCTCAGCCATTGAATCCACCATCCTGCTGGCATGGCCTTGACCGTTATGTGG
10 CCATCTGCCACCCACTCGGCCATGCTGCAGTGCCTAACAAACAGTAACAGCCCAGATTGG
CATCGTGGCTGTGGTCCGGATCCCTCTTCCACTGCCTCTGCTGATCAAGCGGC
TGGCCTCTGCCACTCCAATGCTCTCGCACTCTATTGTGTCACCAGGATGTAATGAA
GTGGCCTATGCAGACACTTGCCTAATGTGGTATATGGTCTTACTGCCATTGCTGGTC
ATGGGCGTGGACGTAATGTTATCTCCTGCTCTATTCTGATAATACGAACGGTCTG
15 AACTGCCTTCCAAGTCAGAGCGGGCAAGGCCTTGGAACCTGTGTGTCACACATTGGTGT
GGTACTCGCCCTATGTGCCACTTATTGGCCTCTCAGTGGTACACCCTGGAAACAGC
CTTCATCCCATTGTGCGTGTGTGACATCTACCTGCTGCTGCCTCTGTCATCAA
TCCCACATCTATGGGCCAAACCAAACAGATCAGAACACGGGTGCTGGCTATGTTCAAG
ATCAGCTGTGACAAGGACTTGCAGGCTGTGGGAGGCAAGTGA (SEQ ID NO: 84)

20

AOLFR45 sequences:

MLPSNITSTHPAVFLLVGIPGLEHLHAWISIPFCFAYTLALLGNCTLLFIQADAALHEPMYLFLA
MLATIDLVLSSTTLPKMLAIFWFRDQEINFFACLVQMFFLHSFSIMESA VLLAMAFDRYVAICKP
25 LHYTTVLTGSLITKIGMAAVARAVTLMTPFLRRHYCRGPVIAHCYCEHMA VVRLACGDT
SFNNIYGIAVAMFSVVL DLLFVILSYVFIQAVLQLASQEARYKAFTCVSHIGAILSTYTPVVIS
SVMHRVARHAAPRVHILLAIFYLLFPPMVNPITYGVTKQIREYVLSLFQRKNM (SEQ ID NO:
85)

30 TGGAAACAAGAGGTAATCTTGCAGGTGGATAGCACAGGTTGAACCTCAATCATATATA
CTGTAGAAGGTATATAGAAGGTGAAGAAGCCCTGTAACAAACATCCAGCTGTCTTTGTTGGTAGGAAT
GGAGCCATGCTTCCCTCTAATATCACCTAACACATCCAGCTGTCTTGTGTTGTTGCTTATACTCTGG
35 CCCTGCTAGGCAACTGTACCCCTCTTCATTATCCAGGCTGATGCAGCCCTCATGAACCC
ATGTACCTCTTCTGCCATGTTGGCAACCATTGACTTGGTCTTCTCTACAACCGCTGCC
CAAATGCTTGCCTATTCTGGTTCAAGGGATCAGGAGATCAACTCTTGCCTGTCTGGTC
CAGATGTTCTCCTTCACTCCTCTCCATCATGGAGTCAGCAGTGCCTGGCATGGCCT
TGACCGCTATGTGGCCATCTGCAAGCCATTGCACTACACGACGGTCTGACTGGTCCCTC
ATCACCAAGATTGGCATGGCTGCTGTGGCCGGGCTGTGACACTAATGACTCCACTCCCT
40 TCCCTGCTCAGCGCTTCAACTACTGCCAGGCCAGTGATTGCCATTGCTACTGTGAACA
CATGGCTGTGGTAAGGCTGGCGTGTGGGACACTAGCTTCAACAATATCTATGGCATTGCT
GTGGCCATGTTAGTGTGGTGTGGACCTGCTCTTGTATCTGTCTTATGTCTTCTCATCT
TCAGGCAGTTCTCCAGCTTGCCTCTCAGGAGGCCGCTACAAAGCATITGGGACATGTGTG
TCTCACATAGGTGCCATCTGCCCCCTGTGTCACACTCCAGTAGTCATCTCAGTCATGCACCG
45 TGTAGCCGCCATGCTGCCCTCGTGTCCACATACTCCTGCTATTCTATCTCCTTTCC
CACCCATGGCAATCTATCATATATGGAGTCAGACCAAGCAGATTGAGTATGTGCT
CAGTCTATCCAGAGAAAGAACATGTAGATGGATAGTCTCTTCTTATCCACTTGCCA
AGTAATGAGAAATGCTGGATTGGGGTTGAGGGAAAAATCTAAATAGGAAATTCAGAGT
ATCTTGACAATTCTCTAGTATGATAAGGAAATGAGGTTCTTCACTCAGATCTACGA
50 GTCAAGGTCAAACCAGGAGTGCACCTATAGTCTGGTCTGATAGTAGAGGTTGACCTTCCA
TTGTCAAGACTCATCACATGGCTAAGGAAGACAAACCTCTCAAAGTGGTATTGTAATCTG
GGTGAAGACAGTAGGACCTTATTGGCTGAGATTGCCAAACAGCTGAGTC (SEQ ID
NO: 86)

AOLFR46 sequences:

55 MNIKHCGWMIHTWLNI REDDSDFKNFIGQIQLSGNPHSTTSRMYFLCFCTSLLGFKVHWV
SRLIXKLYMASPNNDSTAPVSEFLICFPNFQSWQHWLSLPLSLLFLLAMGANTLLITIQL
LEAS

5 LHQPLYYLLSLLSLLDIVLCLTVIPKVLAIWFDLRSISFPACFLQMFIMNSFLTMESCTFMVMA
 YDRYVAICHPLRYPsiITDQFVARAVVFIARNAFSLPVPMLSARLRYCAGNIKNCICSNLSVS
 KLSCDDITFNQLYQFVAGWTLLGSIDLILIVISYSILKVLRIKAEGA VAKALSTCGSHFILILFFS
 TVLLVLVITNLARKRIPPDVPIIILNILHHLIPPAALNPIVYGVRTKEIKQGIQNLLKRL (SEQ ID NO:
 87)

10 ATGAATATAAAACATTGTGGCTGGCATATGATACATACTGGTTAAATATAAGGGAGGAT
 GATGACAGTGATTTAAAAACTTTATTGGACAGATACAGGGCCTCAGTGGAAACCCACACT
 CTACTACGTCTAGAATGTACTTTATGTTCTGACTTCTACTAGGTTAAGGTACAC
 15 TGGGTCTCCAGATTGATCANGAAACTTACATGGCATCTCCAACAATGACTCCACTGCC
 CAGTCTCTGAATTCTCCTCATCTGCTTCCCACACTCCAGAGCTGGCAGCAGCTGGTTGTCT
 CTGCCCCCTCAGCCTCTCTGCAACCAGCCCCGTACTACCTGCTCAGCCTCCCTCCCTGCTGG
 20 ACATCGTGCTCTGCTCACCAGTCATCCCCAAGGCTCTGGCATCTCTGGTTGACCTCAGG
 TCGATCAGCTTCCCAGCCTGCTCCTCCAGATGTTCATCATGAACAGTTTTGACCATGGA
 GTCCTGCACGTTATGGTCATGGCTATGACCGTTATGTGGCATCTGCCATCCATTGAGA
 TACCCGTCTATCATCACTGACCACTGGCTAGGGCCGGTCTTGTATAGCCCGGA
 25 ATGCCCTTGTCTCTCTGCTTCCATGCTTCTGCCAGGCTCAGATACTGTGCAAGGAAAC
 ATAATCAAGAACTGATCTGCACTGAGTAACCTGTCTGTGTCACACTCTCTGTGATGACATCA
 CTTCATCAGCTCACCAGTTGTGGCAGGCTGGACTCTGTTGGCTCTGATCTTATCCTT
 ATTGTTATCTCCTATTCTTTATATTGAAAGTTGTGCTTAGGATCAAGGCCAGGGTGCTGT
 30 GCCAAGGCCTTGAGCACGTGTTCCACTTCATCCTCATCCTCTTCTCAGCACAGTC
 TGCTGGTTCTGGTCATCACTAACCTGGCCAGGAAGAGAATTCTCCAGATGTCCCCATCCT
 GCTCAACATCCTGCACCACCTCATTCCCCCAGCTCTGAACCCATTGTTATGGTGTGAGA
 ACCAAGGAGATCAAGCAGGAAATCCAAAACCTGCTGAAGAGGTTGTAA (SEQ ID NO: 88)

AOLFR47 sequences:

35 MSASNITLTHPTAFLVGIPGLEHLHIWISIPFCLAYTLALLGNCTLLIIQADAALHEPMYLFLA
 MLAAILVLSSSALPKMLAIFWFRDREINFFACLAQMFFLHSFSIMESA VLLAMA FDRYVAICK
 40 PLHYTKVLTGSLITKIGMAAVARAVTLMPLPFLRCFHYCRGPVIAHCYCEHMAVVRLACGD
 TSFNNIYGLAVAMFTVVL DLLVILSYIFILQAVLLASQEARYKAFTGTCVSHIGAILAFYTTVVIS
 SVMHRVARHAAPHVHILLANFYLLFPPMVNPITYGVKTKQIRESILGVFPRKDM (SEQ ID NO:
 89)

45 ATGTCAGCCTCCAATATCACCTTAACACATCCAACCTGGCTCTTGTGGTGGGGATTCCAG
 GCCTGGAAACACCTGCACATCTGGATCTCCATCCCCCTCTGTTAGCATATACACTGGCCCTG
 CTTGGAAACTGCACTCTCCTCTCATCATCCAGGCTGATGCAGCCCTCCATGAACCCATGT
 ACCTCTTCTGCCATATTCTGGTCAGGGATCGGGAGATAAACTCTTGCCTGTCTGGCCCAA
 ATGCTTGCCATATTCTGGTCAGGGATCGGGAGATAAACTCTTGCCTGTCTGGCCCAA
 50 TGGTCTCCTTCACTCCTCTCCATCATGGAGTCAGCAGTCTGCTGGCATGGCCTTGTAC
 CGCTATGTGGCTATCTGCAAGCCACTGCACTACACCAAGGCTCTGACTGGGTCCCTCATCA
 CCAAGATTGGCATGGCTGCTGTCGGCCGGCTGTGACACTAATGACTCCACTCCCCCTCCT
 GCTGAGATGTTCCACTACTGCCAGGGCCAGTGTGACTGCTCACTGCTACTGTGAACACATG
 GCTGTGGTGGGCTGGCTGTGGGACACTAGCTCAACAATATCTATGGCATCGCTGTGG
 CCATGTTATTGTGGTGTGGACCTGCTCCTGTATCCTGCTTATATCTTATTCTCAG
 GCAGTTCTACTGCTTGCCTCTCAGGAGGCCGCTACAAGGCATTGGGACATGTGTCTCTC
 ATATAGGTGCCATCTAGCCTCTACACAACCTGTGGTCATCTCTCAGTCATGCACCGTGTA
 GCCCGCCATGCTGCCCTCATGTCCACATCCTCCTGCCAATTCTATCTGCTCTCCCACC
 CATGGTCATCCATAATCTATGGTGTCAAGACCAAGCAAATCCGTGAGAGCATCTTGGGA
 GTATTCCAAAGAAAGGATATGTAG (SEQ ID NO: 90)

AOLFR48 sequences:

55 MMVDPNGNESSATYFILIGLPGLEEAQFWLAFLCSLYLIAVLGNLTIIYTVRTEHSLHEPMYIFL
 CMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFIAHSLSGMESTVLLAMA FDRYVAICH
 PLRHA TVLTLPRVTKIGVAAVVRAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDDI
 RVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGLTREAQAKAFGTCVSHVCAVFIFYVFIGLSM

VHRFSKRRDSPLPVILANIYLLVPPVLPNPIVYGVKTKEIRQRJRLFHVATHASEP (SEQ ID NO: 91)

5 ATGATGGTGGATCCCAATGGCAATGAATCCAGTGCTACATACTTCATCCTAATAGGCCTCC
 CTGGTTAGAAGAGGCTCAGTTCTGGTGGCTTCCCATTGTGCTCCCTACCTTATTGCT
 GTGCTAGGTAACTTGACAATCATCTACATTGTGCGGACTGAGCACAGCCTGCATGAGCCA
 TGATATATTTCTTGATGCTTCAGGCATTGACATCCTCATCTCCACCTCATCCATGCC
 AAAATGCTGGCCATCTCTGGTTCAATTCCACTACCAATCCAGTTGATGCTTGCTACA
 GATGTTTGGCATCCACTCCTATCTGGCATGGAATCCACAGTGCTGCTGGCATGGCTTT
 10 GACCGCTATGTGGCATCTGTCACCCACTGCCCATGCCACAGTACTTACGTTGCCTCGTG
 TCACCAAAATTGGTGTGGCTGTGGTGGGGGCTGCACTGATGGCACCCCTTCCTGT
 CTTCATCAAGCAGCTGCCCTTGCGCTCCAATATCCTTCCCATTCCACTGCCTACACC
 AAGATGTATGAGCTGGCTGTGATGATATCCGGGCAATGTCGCTATGGCCTATCGT
 CATCATCTCGCCATTGGCCTGGACTCACITCTCATCTCCTCTCATATCTGCTTATTCTA
 15 AGACTGTGTGGCTGACACGTGAAGGCCAGGCCAAGGCATTGGCACTTGCCTCTCA
 TGTGTGTGTGTTATCTATGTACCTTCATTGGATTGTCCATGGCATCGCTTTA
 GCAAGCGCGTGACTCTCCGCTGCCGTATCTGGCCAATATCTATCTGCTGTTCCCTCCT
 GTGCTCAACCCAATTGTCTATGGAGTGAAGACAAAGGAGATTGACAGCGATCCCTCGA
 CTTTCCATGTGGCCACACACGCTTCAGAGCCCTAG (SEQ ID NO: 92)

20

AOLFR49 sequences:

MLTFHNVCVPSSFWLTGIPGLESILHVWLSIPFGSMYLVAVVGNVILAVVKIERSLHQPMYFF
 LCMLAAIDLVLSTSTIPKLLGIFWFGACDIGLDACLGQMFLIHCFAVESGIFLAMAFDRYVAIC
 25 NPLRHSVMVLTYTUVVGRGLVSLLRGVLYIGPLPLMRLRLPLYKTHVISHSYCEHMAVVALTC
 GDSRVNNVYGLSIGFLVLILDSVIAAASYVMIFRAVMGLATPEARLKTLCASHLCAILIFYVP
 IAVSSLIHRFGQCVPPPVTLLANFYLLIPILNPIVYAVRTKQIRESLLQIPRIEMKIR (SEQ ID
 NO: 93)

30 ATGCTCACTTTCATATAATGTCTGCTCAGTACCCAGCTCCTCTGGCTCACTGGCATCCCAGG
 GCTGGAGTCCTACACGTCTGGCTCTCCATCCCCTTGGCTCCATGTACCTGGTGGCTGTG
 GTGGGAATGTGACCATCCTGGCTGTGGTAAAGATAGAACGCAGCCTGCACCAGCCCAG
 TACTTTTCTGTGATGTTGGCTGCCATTGACCTGGTCTGTACTTCCACTATACCCAA
 ACTTCTGGGAATCTCTGGTCTGGTCTGTGACATTGGCCTGGACGCGCTGTTGGGCCAA
 ATGTCCTTATCCACTGCTTGCCACTGTTGAGTCAGGCATCTCCTGCCATGGCTTTGA
 35 TCGCTACGTGGCCATCTGCAACCCACTACGTATAGCATGGTGCCTACATTACAGTGGTG
 GGTGTTGGGCTTGTCTCCTCCGGGTTCTACATTGGACCTGCTGCTGAT
 GATCCGGCTGCGCTGCCCTTATAAAACCCATGTTATCTCCACTCCTACTGTGAGCAC
 ATGGCTGTAGTTCGCTTGACATGTCAGCAGCAGGGTCAATAATGTCTATGGGCTGAGC
 ATCGGCTTCTGGTGTGATGGGACTCAGTGGTATTGCTGACCTATGTGATGATT
 40 CAGGGCGTGTGATGGGTTAGCCACTCCTGAGGCTAGGTTAAACCCCTGGGACATGCGC
 TTCTCACCTCTGTGCCATCCTGATCTTATGTTCCATTGCTGTTCTCCCTGATTACCG
 ATTGGTCAGTGTGTGCCCTCCAGTCACACTCTGCTGGCCAATTCTATCTCCTCATTC
 CTCCAATCTCAATCCATTGCTATGCTGTTCGCACCAAGCAGATCCGAGAGAGCCTCT
 CCAAATACCAAGGATAGAAATGAAGATTAGATGA (SEQ ID NO: 94)

45

AOLFR50 sequences:

MNLDSFFSFLKSLIMALSNSSWRLPQPSFLVGIPGLEESQHWIALPLGILYLLALVGNVILFII
 WMDPSLHQSMYLFLSMLAAIDLVVASSTAPKALAVLLVRAQEIGYTVCLIQMFFTHAFSSMES
 50 GVLVAMALDRYVAICHPLHHSTILHPGVIGHIGMVVLVRGLLLIPFLILLRKLIFCQATIIGHAY
 CEHMAVVVKLACSETTVNRAYGLTVALLVVGLDVLAIGVSYAHILQAVLKVPNEARLKAFST
 CGSHVCVILVFYIPGMFSFLTHRFGHHVPHVHLLAILYRLVPPALNPVYRVKTQKIHQ
 (SEQ ID NO: 95)

55 ATGAATTGGATTCTTTCTCTTCCCTCAAGTCATTGATAATGGCACTTAGCAATT
 CAGCTGGAGGCTACCCAGCCTCTTTTCCCTGGTAGGAATTCCGGTTAGAGGAAAGC
 CAGCACTGGATCGCACTGCCCTGGCATCCTTACCTCCTGCTAGTGGCAATGTTA

5 CCATTCTCTCATCATGGATGGACCCATCCTGCACCAATCTATGTACCTCTTCTGTCC
 ATGCTAGCTGCCATCGACCTGGTTGGCCTCCACTGCACCCAAAGCCCTGCAGTGC
 TCCTGGTCTGCCCCAAGAGAGATTGGTTACACTGTCTGCCTGATCCAGATGTTCTCACCCAT
 GCATTCTCTCCATGGAGTCAGGGGTACTTGTGGCCATGGCTCTGGATCGCTATGTAGCCA
 10 5 TTTGTCACTTGCACCATTCACAATCCTGCATCCAGGGTCATAGGGCACATCGGAAT
 GGTGGTCTGGTGGGGATTACTACTCCTCATCCCCTCCTCATTCTGTGCGAAAACCTT
 ATCTTCTGCCAAGCACCACATAGGCCATGCCATTGTGAACATATGGCTGTTGTGAAAC
 TTGCTGCTCAGAAACCACAGTCATCGAGCTTATGGGCTGACTGTGGCCTTGTGTTGGT
 TGGGCTGGATGTCCCTGGCATGGTGTTCATGCCACATTCTCCAGGCAGTGCTGAAG
 15 10 GTACCAGGAAATGAGGGCCGACTTAAGGCCTTACGACATGTGGCTCATGTTGTGTC
 TCCTGGTCTTCTATATCCCGGAATGTTCTCCTTCCTCACTCACCGCTTGGTCATCATGTA
 CCCCATCACGTCCATGTTCTGGCCATACTGTATGCCCTGTGCCACCTGCACTCAATCC
 TCTGTCTATAGGGTGAAGACCCAGAAGATCCACCACTGA (SEQ ID NO: 96)

15 **AOLFR51 sequences:**

MCQQILRDCILLIHHLCINRKVSLVMLGPAYNHTMETPASFLVGIPGLQSSHWLAIISAM
 YIALLGNTLIVTAIWMDSTRHEPMYCFCLCVLAADVMASSVVPKMSIFCSGDSSISFSACFTQ
 MFFVHLATAVETGLLTMAFDRYVAICKPLHYKRILTPQVMLGMSMAJITRAIIAIPLSWMVS
 20 20 HLPFCGSNVVVSYCEHIALARLACADPVPSSLYSLIGSSLMVGSDVAFIAASYILILKAVFGLSS
 KTAQLKALSTCGSHVGVMALYYLPGMASIYAAWLQDVLPLHTQVLLADLYVIIPATLNPIY
 GMRTKQLRERIWSYLMHVLFDHSNLGS (SEQ ID NO: 97)

25 ATGTGTCAACAAATCTTACGGGATTGCACTTCTCTCATACATCATTGTGCATTAACAGGA
 AAAAGTCTCACTTGTGATGCTGGTCCAGCTTATAACCACACAATGAAACCCCTGCCTC
 CTTCCCTCTGTGGTATCCCAGGACTGCAATCTCACATCITTGGCTGGCTATCTCACTGA
 GTGCCATGTACATCATAGCCCTGTTAGGAAACACCATCATCGTACTGCAATCTGGATGGA
 TTCCACTCGGCATGAGCCCAGTGTATTGTTCTGTGTTCTGGCTGCTGTGGACATTGTTA
 TGGCCTCTCGGTGGTACCCAAGATGGTGGACATCTCTGCTCAGGAGACAGCTCAATCAG
 CTTTAGTGTGTTTCACTCAGATGTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGA
 30 30 GAATTCTCACGCCCTCAAGTGAATGCTGGGAATGAGTATGGCATCACCATCAGAGCTATCAT
 AGCCATAACTCCACTGAGTGGATGGTGGACATCTACCTTCTGTGCTGCTCCAATGTGGTT
 GTCCACTCTACTGTGAGCACATAGCTTGGCCAGGTAGCATGTGCTGACCCCGTGCCA
 GCAGTCTCTACAGTGTGATTGGTCTCTCTTATGGGGCTCTGATGTGGCCTTCATTGCT
 35 35 GCCTCTATATCTAATTCTCAAGGCACTTGGCTCTCTCAAAGACTGCTCAGTGAA
 AGCATTAAAGCACATGTGGCTCCATGTGGGGTTATGGCTTGTACTATCTACCTGGATG
 GCATCCATCTATGCCGCTGGTGGGCAGGATGTAGTGGCCCTGCACACCCAAAGTCTGC
 TAGCTGACCTGTACGTGATCATCCCAGCCACCTAAATCCCATCATCTATGGCATGAGGAC
 CAAACAACTGCGGGAGAGAATATGGAGTTATCTGATGCATGTCCTTTGACCATTCCAAC
 40 40 CTGGGTTCATGA (SEQ ID NO: 98)

AOLFR52 sequences:

MLGPAYNHTMETPASFLVGIPGLQSSHWLAIISAMYIALLGNTLIVTAIWMDSTRHEPMY
 CFCLCVLAADVMASSVVPKMSIFCSGDSSISFSACFTQMFVHLATAVETGLLTMAFDRYV
 45 45 AICKPLHYKRILTPQVMLGMSMAVTIRAVTFMPLSWMNNHLPFCGSNVVVSYCKHIALAR
 LACADPVPSSLYSLIGSSLMVGSDVAFIAASYILILRAVFDLSSKTAQLKALSTCGSHVGVMALY
 YLPGMASIYAAWLQDVLPLHTQVLLADLYVIIPATLNPIYGMRTKQLLEGIWSYLMHFLFDH
 SNLGS (SEQ ID NO: 99)

50 50 ATGCTGGTCCAGCTTACAACCAACACAATGAAACCCCTGCCTCCTCCTGTGGGTA
 TCCCAGGACTGCAATCTCACATCTTGGCTGGCTATCTCACTGAGTGCCTGACATCAC
 AGCCCTGTTAGGAAACACCCCTCATCGTACTGCAATCTGGATGGATTCCACTCGGCATGAG
 CCCATGTTAGCTGTGTTCTGTGCTGGCTGTGGACATTGTTATGGCTCCTCCGTGGT
 ACCCAAGATGGTGGACATCTCTGCTCGGGAGACAGCTCCATCAGCTTATGTGCTTGTTC
 55 55 ACTCAGATGTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGGCTGCTGCTGACCATGG
 CTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGAGAATTCTCACGCCCTCA

AGTGATGCTGGGAATGAGTAAGGCCGTACCATCAGAGCTGTCACATTGACTCCACTG
 AGTTGGATGATGAATCATCTACCTTCTGGCTCCAATGTGGTGTCCACTCCTACTGTAA
 GCACATAGCTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCAGCAGTCTACAGTCTG
 ATTGGTCTCTCTTATGGTGGCTCTGATGTGGCCTCATTGCTGCCTCCTATATCTTAAT
 5 TCTCAGGGCAGTATTGATCTCCCAAAGACTGCTCAGTGAAAGCATTAGCACATGT
 GGCTCCCAGTGTGGGGTATGGCTTGACTATCTACCTGGATGGCATCCATCTATGCGG
 CCTGGTGGGCAGGATATAGTGCCTTGACACCCAAGTGCTGCTAGCTGACCTGTACGT
 GATCATCCCAGCCACTTAAATCCCACATCTATGGCATGAGGACCAAACAATTGCTGGAG
 10 GGAATATGGAGTTATCTGATGCACTCCTCTTGACCACTCCAACCTGGGTCATGA (SEQ
 ID NO: 100)

AOLFR54 sequences:

MSDSNLSDNHLPDFLTGIPGLEAAHFWIAIPFCAMYLVALVGNAALILVIAMDNALHAPMY
 LFLCLLSLTDLALSSTTVPKMLAILWLHAGEISFGGCLAQMFCVHSIYALESSILLAMA
 15 ICNPLRYTTILNHAIGRIGFVGLFRSVAIVSPFIFLRLPYCGHVRMHTYCEHMGIA
 RLACA NITVNIVYGLTVALLAMGLDSILIAISYGFILHAVFHLPShDAQHKALSTCGSHIGILVFYIPAFF
 SFLTHRFGHHEVPKHVHIFLANLYVLVPPVLPILYGARTKEIRSRLKLLHLGKTSI (SEQ ID
 NO: 101)

20 ATGTCAGATTCCAACCTCAGTGATAACCACCTTCCAGACACCCCTCTTAACAGGGATCC
 CAGGGCTGGAGGCTGCCACTTCTGGATTGCCATCCCTTCTGTGCCATGTATCTGTAGC
 ACTGGTGGAAATGCTGCCCTCATCCTGGTCAATTGCCATGGACAATGCTCTCATGCACCT
 ATGTACCTCTCCTCTGCCCTCTCACTCACAGACCTGGCTCAGTTCTACCACGTGCC
 25 CAAGATGCTGCCATTGTGGCTCATGCTCTGGAGATTCCCTTGGTGGATGCCCTGGCC
 CAGATGTTGTGTCATTCTATCTATGCTCTGGAGTCCTCGATTCTACTTGCCATGGCCTT
 TGATAGGTATGTGGCTATCTGTAACCCATTAAGGTATACAACCATTCTCAACCAGTGTGTC
 ATAGGCAGAAATGGCTTGTGGCTATTCCGTAGTGTGGTATTGTCTCCCCCTCATCTT
 CTTGCTGAGGCGACTCCCTACTGTGGTCAACGTGTCATGACACACACATACTGTGAGCAT
 30 ATGGGCATCGCCCGACTGGCCTGTGCCAACATCACTGTCAATATTGTCTATGGCTAACTG
 TGGCTCTGCTGCCATGGGACTGGATTCCATTCTCATGCCATTCCATTGGCTTATCCTC
 CATGCAGTCTTCACCTCCATCTCATGATGCCAGCACAAAGCTCTGAGTACCTGTGGCT
 CCCACATTGGCATCATCCTGGTTCTACATCCCTGCCCTCTCCTCACCACCGC
 TTTGGTCAACCACGAAGTCCCAAGCATGTGCACATCTTCTGGCTAATCTCTATGTGCTGG
 TGCCCTGTACTCAATCCTATTCTATGGAGCTAGAACCAAGGAGATTGGAGTCGACT
 35 TCTAAAATGCTCACCTGGGAAGACTCAATATGA (SEQ ID NO: 102)

AOLFR57 sequences:

MSFQVTYMFYLHWTMEKSNNSTLFILLGFSQNKNIEVLCVFLFCYIAIWGNLLIMISITCTQ
 LIHQPMYFFLNYLSLSDLCYTSTVTPKLMVDLLAERKTISYNNCMIQLFTTHFFGGIEIFILTGM
 40 AYDRYVAICKPLHYTIMSRQKCNTIIVCCTGGFIHSASQFLLTIFVPFCGPNEIDHYFCDVYPLL
 KLAESNIHMIGLLVIANSGLIALVTFVVLSSYVFLYTIRAYSAERRSKALATSSHVIVVVLLF
 APALFIYIRPVTTFSEDKVFAFLFYTIAPMFNPLIYTLRNTTEMKNAMRKVWCCQILKRNQLF
 (SEQ ID NO: 103)

45 ATGTCATTCAGGTGACTTATATGTTCTATCTACACTGGACCATGGAAAAAAAGCAATAA
 TA GCACTTTGTTATTCTCTTGGGTTTCCAAAATAAGAACATTGAAGTCCTCTGTTGTA
 TTATTTTGTGCTACATTGCTATTGGATGGGAAACTTACTCATATGATTCTATCAC
 GTGCACCCAGCTCATTACCAACCCATGTATTCTCTCAATTACCTCTCACTCTCGACC
 TTTGCTACACATCCACAGTGACCCCAAATTATGGTGTACTTACTGGCAGAAAGAAAGAC
 50 CATTCTCTATAATAACTGTATGATACAACCTTACCAACCCATTGGAGGCATAGAGA
 TCTTCATTCTCACAGGGATGGCTATGACCGCTATGTGGCATTGCAAGCCCTGCACTA
 CACCATTATTATGAGCAGGCAAAGTGTAAACACAATCATCATAGTTGTGTACTGGGGA
 TTTATACATTCTGCCAGTCAGTTCTCTCACCATTTGTACCATTTGTGGCCCAAATGA
 GATAGATCACTACTCTGTGATGTATCCATTGCTGAAATTGGCCTGTTCTAATATACACA
 55 TGATAGGTCTCTAGTCATTGCTAATTCAAGGCTTAATTGCTTGGTGCACATTGTTGTCTTG
 TTGTTGTCTATGTTTATATTGTATACCATCAGAGCATACTGCAAGAGAGACGCAGCA

5 AAGCTCTGCCACTTGTAGTCTCATGTAATTGTTGGCTCTGTTTGCTCCTGCATTG
 TTCATTTACATTAGACCGGTACAACATTCTCAGAAGATAAAAGTGTGTCGCCCTTTTATAC
 CATCATTGCTCCCATGTTCAACCCCTCTCATATACACGCTGAGAAACACAGAGATGAAGAAC
 GCCATGAGGAAAGTGTGGTGTCAAATACTCCTGAAAAGAAATCAACTTTCTGA (SEQ
 ID NO: 104)

AOLFR58 sequences:

10 MFSMTTEALNNFALGCTNLLMTMIPQIDLKQIFLCPNCRLYMIPVGAFIFSLGNMQNQSFVTEF
 VLLGLSQNPNVQEIVFVFLFYIATVGGNMLIVVTTILSSPALLVSPMYFFLGFLSFLDACPSSVI
 TPKMICDSDLVTKTISFEGCMMQLFAEHFFAGVEVILTAMAYDRYVAICKPLHYSSIMNRL
 CGILMGVAWTGGLLHSMIQILFTFQLPFCGPNVINHFMCDLYPLLEACTDTHIFGLMVINS
 FICIINFSLLLVSYAVILLSLRTHSSEGRWKALSTCGSHIAVVILFFVPCIFVYTRPPSAFSLDKMA
 AIFYIILNPLLNPLIYTFRNKEVKQAMRRIWNRLMVSDEKENIKL (SEQ ID NO: 105)

15 15 ATGTTCTCAATGACAACAGAACACTCAATAATTTCACGGATGTACCAACTTGTAA
 TGACTATGATACCACAAATTGATCTGAAGCAAATTTCCTTGTCTTAATTGCAGACTATA
 CATGATCCCTGTTGGAGCTTCATCTTCCCTGGAAACATGCAAAACCAAAGCTTGTAA
 ACTGAGTTGTCCTCCTGGACTTTACAGAACTTCAAGAGAAATGTTAGGAAATAGTATTGTTG
 TATTTTGTGTTGTCTACATTGCAACTGTTGGGGCAACATGCTAATTGTTAGTAACCATTCTC
 20 AGCAGCCCTGCTCTCTGGTCTCTATGTTACTCTTCTTGGGCTTCTGTCTTCTGGAA
 TCGGTGCTTCTCATCTGTATCACCACAAAGATGATTGTAAGACTCCCTATGTGACAAAA
 ACCATCTCTTGTGAAGGCTGCATGATGCACTCTTGTGACAAACTCTTGTCTGGGGTGG
 AGGTGATTGTCTCACAGCCATGGCTATGATCGTTATGTGGCCATTGCAAGCCCTTGCA
 25 TTACTCTCTATCATGAACAGGAGGCTGTGGCATTCTGATGGGGTAGCCTGGACAGGG
 GGCCTCTTGCTATTCCATGATAACAAATTCTTACTTCCAGCTTCCCTTTGTGGCCCCAA
 TGTCTCATCAATCACTTATGTGACTTGTACCCGTTACTGGAGCTGCTGCACGTGATAACTC
 ACATCTTGGCCTCATGGTGGCATCAACAGTGGGTTATCTGCATCATAAACCTCTCCTTG
 30 TTGCTTGTCTCTCATGTGTCATCTGCTCTCTGAGAACACACAGTTCTGAAGGGCGCTG
 GAAAGCTCTCTCCACCTGTGGATCTCACATTGCTGTTGTGATTGTCTTGTCCCCTGCA
 TATTGTTATATACACGACCTCCATCTGCTTTTCCCTGACAAAATGGCGGCAATATTAT
 ATCATCTTAAATCCCTGCTCAATCCTTGTGATTACACTTCAGGAATAAGGAAGTAAAC
 AGGCCATGAGGAGAATATGGAACAGACTGATGGTGGTTCTGATGAGAAAGAAAATATTA
 AACTTAA (SEQ ID NO: 106)

35 **AOLFR59 sequences:**

40 MGDWNNSDAVEPIFILRGFPGLEVHSWLSILFCLAYLVAFMGNVTILSVIWISSLHQPMYYFI
 SILAVNDLGMISLSTLPTMLAVLWLDAPEIQASACYAQLFFIHTFTFLESSVLLAMAFDRFVAICH
 PLHYPTILTNSVIGKIGLAICLRLSLGVVLPPLLRLHYHYCHGNALSHAFCLHQDVRLSCTDA
 RTNSIYGLCVVIATLGVDISIILSYVLLNTVLDIASREEQLKALNTCVSHICVVLIFFVPVIGVS
 MVHRFGKHLSPIVHILMADIYLLLPPVLPNPIVYSVRTKQIRLGILHKFVLRRRF (SEQ ID NO:
 107)

45 45 ATGGGAGACTGGAATAACAGTGATGCTGTGGAGCCCATAATTCTGAGGGGTTTCTG
 GACTGGAGATGTTCATCTTGGCTCTCCATCCTCTGTCATTTGGTAGAATCCTCTCCATCAGCCCAGTAA
 ATGGGTAATGTTACCATCCTGTCTGTCATTGGTAGAATGACCTGGGATGCTCTGTCACACTCCCACCA
 TTACTTTATTCATCTTAGCAGTGAATGACCTGGGATGCTCCAGAGATCCAGGCAAGTGCTGCTATGCTCAGCT
 TGCTTGTGTTATGGTGGATGCTCCAGAGATCCAGGCAAGTGCTGCTATGCTCAGCT
 50 GTTCTTGTGCTATCTGCCATCCACTGCACTACCCACCATCTCACCAACAGTGTAATTGGC
 AAAATTGGTTGGCTGTTGCTACGAAGCTGGAGTTGACTTCCCACACCTTGTACT
 GAGACACTATCACTACTGCCATGGCAATGCCCTCTCTCACGCCCTCTGTTGACCCAGGAT
 GTTCTAAGATTATCCTGTACAGATGCCAGGACCAACAGTATTGTTGCTGATTCTTAATACT
 TTGCCACACTAGGTGGATTCAATCTCTACTTCTTGTGTCAGTAAAGGACTCAACACATGTGTATCCCATA
 55 GTGCTGGATATTGCATCTGTGAAGAGCAGCTAAAGGACTCAACACATGTGTATCCCATA
 TCTGTGTGGTGTATCTCTTGTGCCAGTTATTGGGGTGTCAATGGCCATCGCTTGGG
 AAGCATCTGTCTCCATAGTCCACATCCTCATGGCAGACATCTACCTCTTCTTCCCCAGT

CCTTAACCTATTGCTATAGTGTAGAACAAAGCAGATTGTCTAGGAATTCTCCACAAG
TTTGTCTAAGGAGGAGGTTAA (SEQ ID NO: 108)

AOLFR60 sequences:

5 MFLPNDTQFHPSSFLLGIPGLETLHIGFPFCAVYMIALIGNFTTLLVIKTDSSLHQPMFYFLA
MLATTDVGLSTATIPKMLGIFWINLRGIIFEACLTQMFHNFILMESAVLVAMAYDSYVAICN
PLQYSAILTNKVVSVIGLGVFVRALIFVIPSILLRLPFCGNHVIPHITYCEHMLAHLSCASIKINI
IYGLCAICNLVFDITVIALSYVHILCAVFRLPTHEPRLKSLSCTGSHVCVILAFYTPALFSFMTHC
10 FGRNVPRYIHILLANLYVVVPPMLNPVIYGVRTKQIYKCVKKILLQEQQMEEKEYLIHTRF
(SEQ ID NO: 109)

ATGTTCCCTTCCAATGACACCCAGTTTACCCCTCCTCCCTGTGCTGGGGATCCAGG
ACTAGAAAACACTTCACATCTGGATCGGCTTCCCTCTGTGCTGTACATGATCGCACTC
15 ATAGGGAACTTCACTATTCTACTTGTGATCAAGACTGACAGCAGCCTACACCAGCCATGT
TCTACTTCCGGCCATGTTGGCCACCACTGATGTGGGTCTCTAACACAGCTACCATCCCTAA
GATGCTTGGAAATCTCTGGATCAACCTCAGAGGGATCATCTTGAAGCCTGCCTCACCCAG
ATGTTTTATCCACAACTTCAACTTATGGAGTCAGCAGTCCTGTGGCAATGGCTATG
ACAGCTATGTGGCCATCTGCAATCCACTCCAATATAGGCCATCCTCACCAACAAGGTTGT
20 TTCTGTGATTGGCTTGGTGTGTTGTGAGGGCTTAATTTCGTCACTCCCTATACATTC
TTATATTGCGGTTGCCCTCTGGGAATCATGTAATTCCCCACACACTGTGAGCACAT
GGGTCTTGCATCTATCTGTGCCAGCATCAAAATCAATATTATTTATGGTTATGTGCCA
TTTGTAAATCTGGTGTGACATCACAGTCATTGCCCTCTTATGTGCATATTCTTGTGCT
25 GTTTCCGTCTCCTACTCATGAGCCCCGACTCAAGTCCCTCAGCACATGTGGTCACATGT
GTGTGTAATCCTTGCCTCTATACACCAGCCCTTTTCTTATGACTCATTGCTTGGCCACCAAT
GCTCAATCCTGTCAATATGGAGTCAGAACCAAGCAGATCTATAAATGTGAAAGAAAAAT
ATTATTGCAGGAACAAGGAATGGAAAAGGAAGAGTACCTAATACATACGAGGTTCTGA
(SEQ ID NO: 110)

AOLFR61 sequences:

MSIINTSYVEITFFLVMPGLEYAHIWISIPICSMYLLIAILGNGTILFIKTEPSLHGPMPYYFLSML
AMSDLGLSLSLPLTVLSIFLNAPETSSSACFAQEFFFHGFVLESSVLLIMSFDRFLAIHNPLRYT
35 SILTTVRVAQIGIVFSFKSMLLVLPPFTLRSRLRYCKKNQLSHSYCLHQDVMKLACSDNRIDVIY
GFFGALCLMVDFILIAVSYTLLKTVPGIASKEELKALNTCVSHICAVIIFYLPIINLAVVHRFAG
HVSPLINVLMANVLLVPPLMKPIVYCVTKQIRVRRVVAKLCQWKI (SEQ ID NO: 111)

ATGCCATTATCAACACATCATATGTTGAAATCACCACTTCTTGGTTGGGATGCCAG
GGCTAGAATATGCACACATCTGGATCTCTATCCCCATCTGCAGCATGTATCTTATTGCTATT
40 CTAGGAAATGGCACCATTCTTTATCATCAAGACAGAGGCCCTCCTGCATGGGCCATGT
ACTATTTCTTCCATGTTGGCTATGTCAGACTTGGGTTGTCTTATCATCTGCCACT
GTGTTAAGCATCTCTGTTCAATGCCCTGAAACTTCTTAGTGCCTGCTTGGCCAGGA
ATTCTTCATGATTCTCAGTACTGGAGTCCTCAGTCCTGATCATGTCTTGTGATA
GATTCTAGCCATCCACAATCCTCTGAGATAACACCTCAATCCTGACAACACTGTCAAGAGTTGC
45 CCAAATAGGGATAGTATTCTCTTAAAGAGCATGCTCCTGGTTCTTCCCTTCCCTTCACTT
TAAGAAGCTGAGATATTGCAAGAAAAACCAATTATCCCATTCTACTGTCTCCACCAAGGA
TGTCTGAGTTGGCCTGTTGACAAACAGAATTGATGTTATCTATGGCTTTGGAGCA
CTCTGCCCTATGGTAGACTTATTCTCATTGCTGTCTTACACCCTGATCCTCAAGACTGT
50 ACCGGGAATTGCATCCAAAAGGAGGAGCTTAAGGCTCTCAATAACTTGTGTTTACACATC
TGTGAGTGCATCTACCTGCCATCATCAACCTGGCCGTTGTCCACCGCTTGGCCGG
GCATGTCCTCTCCCTCATTAATGTTCTCATGGCAAATGTTCTACTTGTACCTCCGCTGA
TGAAACCAATTGTTATTGTGAAAAACTAAACAGATTAGAGTGAGAGTTGTAGCAAAATT
GTGCAATGGAAGATTAA (SEQ ID NO: 112)

AOLFR62 sequences:

55 MFYHNKSIFHPVTFFLIGIPGLEDFHMWISGPFCVYLVALLGNATILLVIKVEQTLREPMFYFL
AILSTIDLALSATSVPRMLGIFWFDAHEINYGACVAQMFLIHAFTGMEAEVLLAMAFLDRYVAIC

APLHYATILTSVLVGISMCIIRPVLLTLPMVYLYRLPFCQAHIAHSYCEHMGIAKLSCGNIRI
NGIYGLFVVSFFVNLVLIGISYVYILRAVFRLPSHDAQLKALSTCGAHGVVICVFYIPSVFSLT
HRFGHQIPGYIHLVANLYLIIPPSLNPIIYGVRTKQIRERVLYVFTKK (SEQ ID NO: 113)

5 ATGTTTATCACAAACAAGAGCATATTCACCCAGTCACATTTCCTCATTGGAATCCAGG
TCTGGAAAGACTTCCACATGTGGATCTCCGGCCTTCTGCTCTGTTACCTGTGGCTTGC
TGGCAATGCCACCATTCTGCTAGTCAGGATAGAACAGACTCTCCGGAGCCATGTT
CTACTTCCTGGCCATTCTTCACATTGATTGGCCCTTCTGCAACCTCTGCTCGCA
TGCTGGGTATCTTCTGGTTGATGCTCACGAGATTAACTATGGAGCTTGTGGCCAGAT
10 GTTTCTGATCCATGCCTTCACTGGCATGGAGGCTGAGGTCTACTGGCTATGGCTTTGAC
CGTTATGTGCCACTGTGCTCCACTACATTACGCAACCCTTGACATCCCTAGTGTGGT
GGGCATTAGCATGTGCAATTGTAATTGCTCCGTTTACTTACACTTCCATGGCTATCTTA
TCTACCGCCTACCCCTTGTCAAGGCTCACATAATAGCCCATTCTACTGTGAGCACATGGG
15 CATTGCAAAATTGCTCTGTGGAAACATTGTATCAATGGTATCTATGGCTTTGTAGTTT
CTTCTTGTCTGAACCTGGTCTATTGGCATCTCGATGTTACATTCTCCGTGCTGTC
TTCCGCCTCCCATCACATGATGCTCAGTAAAGCCCTAACGACGTGTGGCGCTCATGTTG
GAGTCATCTGTGTTCTATATCCCTCAGTCCTCTTACTCATCGATTGGACAC
CAAATACCAGGTTACATTCAATTCTGTTGCCAATCTCTATTGATTATCCCACCCCTCT
20 CAACCCCATCATTATGGGGTGAAGGACCAACAGATTGAGAGCGAGTGCTATGTTT
ACTAAAAAATAA (SEQ ID NO: 114)

AOLFR63 sequences:

MSIINTSYVEITTFVLGMPGLEYAHWISIPCSMYLIAILGNGTILFIKTEPSLHEPMYYFLSML
25 AMSDLGLSLLPTVLSIFLNAPEISSNACFAQEFFFHGSVLESSVLLIMSFDRFLAIHNPLRYTS
ILTVRVAQIGIVFSFKSMLLVLPFPFTLRNLRYCKKNQLSHSYCLHQDMVKLACSDNRIDVIY
GFFGALCLMVDFLIAVSYTLILKTVLGIASKKEQLKALNTCVSHICAVIIFYLPIINLA
HVSPLINVLMANVLLVPPLTNPIVYCVKTKQIRVRVVAKLCQRKI (SEQ ID NO: 115)

30 ATGTCCATTATCACACACATCATGTTGAAATCACCCACCTCTTCTGGTTGGGATGCCAG
GGCTAGAATATGCACACATCTGGATCTCTATCCCCATCTGCAGCATGTATCTTATTGCTATT
CTAGGAAATGGCACCATCTTTTATCATCAAGACAGAGCCCTCTGCTGAGGCCATGT
ACTATTTCTTCCATGTTGGCTATGTCAGACTGGGTTGTCTTATCATCTGCCACT
GTGTTAACATCTCCTGTTCAATGCTCCTGAAATTTCATCCAATGCCCTGCTTGGCCAGGA
ATTCTTCATTATGGATTCTCAGTACTGGAGTCCTCAGTCCTCTGATCATGTCATTGATA
35 GATTCCCTAGCCATCCACAACCCCTCTGAGATAACACCTCAATCTGACAACACTGTCAAGAGTGC
CCAAATAGGGATAGTATTCTCTTAAGAGCATGCTCCTGGTCTTCCCTCCCTTCACCT
TAAGAAACTTGAGATATTGCAAGAAAAACCAATTATCCCTACTGTCTCCACCAGGA
TGTATGAAAGTTGGCCTGTTCTGACAACAGAATTGATGTTATCTATGGCTTTGGAGCA
CTCTGCCTTATGGTAGACTTTATTCTCATGCTGTCCTACACCTGATCCTCAAGACTGT
40 ACTGGGAATTGCATCCAAAAGGAGCAGCTTAAGGCTCTCAATACTTGTTTCACACATC
TGTGCAGTGATCATCTCACCTGCCATCATCAACCTGGCCGTTGTCACCGCTTGGCCG
GCATGTCTCTCCCTCATTAATGTTCTGACAACAGATTAGAGTGAGAGTTGTAGCAAATT
GTGTCAACGGAAGATTAA (SEQ ID NO: 116)

AOLFR64 sequences:

MTILLNSSLQRATFFLTGFQGLEGLHWISIPFCFIYLTVLGNLTILHVICTDATLHGP
MLAVTDLGLCLSTLPTVLGIFWFDTREIGIPACFTQLFFIHTLSSMESSVLLSMSID
50 RSVAVCNPLHDSTVLTACIVKMGLSSVLRSLALLPLPFLKRFQYCHSHVLA
HYGLFVVA
55 ACTVGVDSLLIFLSYALILRTVLSIASHQERLRA
LNTCVSHICAVLLFYIPMIGLSV
HRFGEHLPRVVHLFMSYVYLLVPPLMNPIIYSIKTKQIRQRIKKFQFI
KSLRCFWKD (SEQ ID NO: 117)

ATGACAATTCTCTTAATAGCAGCCTCCAAAGAGGCCACTTCTGACGGGCTCCAAG
55 GTCTAGAAGGTCTCCATGGCTGGATCTATCCCTCTGCTCATCTACCTGACAGTTATC
TTGGGAACCTCACCATCTCACGTCATTGTACTGATGCCACTCTCCATGGACCCATGT

ACTATTTCITGGGCATGCTAGCTGTCACAGACTTAGGCCTTGCCTTCCACACTGCCACT
 GTGCTGGGCATTTCTGGTTGATACCAGAGAGATTGGCATCCCTGCCTGTTCACTCAGC
 TCTTCITCATCCACACCTGTCTCAATGGAGTCATCAGTTCTGTTATCCATGTCCATTGAC
 CGCTCCGTGGCGTCTGCAACCCACTGCATGACTCCACCGCCTGACACCTGCATGTATTG
 5 TCAAGATGGGGCTAACGCTCAGTCTAGAAGTGCCTCCCTCATCCTCCCTTGCCTACCTC
 CTGAAGCGCTCCAATACTGCCACTCCATGTGCTGGCTCATGCTTATTGTCTTCACCTGGA
 GATCATGAAGCTGGCCTGCTAGCATATTGTCAATCACATCTATGGGCTTTGTTGTG
 GCTGACCCGTGGGTGACTCCCTGCTCATCTTCTCATACGCCCTCATCCTTCGCAC
 CGTGCAGCATTGCCCTCCACCAGGAGCAGCTCGAGCCCTCAACACCTGTCTCTCAT
 10 ATCTGTGCTGTACTGCTCTTACATCCCCATGATTGGCTGTCTTGTGCATCGCTTGG
 TGAACATCTGCCCCCGCTGTACACCTCTCATGTCCTATGTGTATCTGCTGGTACCAACCC
 TTATGAACCCATCATACAGCATCAAGACCAAGCAAATCGCCAGCGCATCATTAAGAA
 GTTCAGTTATAAGTCACTTAGGTGTTTGGAAAGGATTAA (SEQ ID NO: 118)

15 **AOLFR65 sequences:**

MAGRMSTSNTQFHPSSFLLGIPGLEDVHIWIGVPFFFVYLVALLGNTALLFVIQSLHEPM
 YYFLAMLDSDLGLSTAIPKMLGIFWFNTKEISFGGLSHMFFIHFHTAMESIVLVAMAFDRYI
 AICKPLRYTMILTSKIISLIAGIAVRLSLYMVVPLVFLRLPFCGHRIIPHTYCEHMGIA
 20 LACASIKVNIRFLGNISLLLDVILIIISYRILYAVFCLPSWEARLKALNTCGSHIGVILA
 THRFGHNPQYIHLANLYVVVPPALNPVITYGVRTKQIRERVLRIFLKTNH (SEQ ID NO: 119)

ATGGCAGGAAGAATGTCTACGTCTAACACACCCAGTTCCATCCTCTTCATTCTACTGCT
 GGGTATCCCAGGGCTAGAACAGATGTGCACATTGGATTGGAGTCCCTTTTCTTGTGTAT
 25 CTTGTTGCACTCCTGGAAACACTGCTCTTGTGATCCAGACTGAGCAGAGTCTCC
 ATGAGCCTATGTACTACTTCCCTGGCCATCTCTGGTTCAATACCAAAGAAATATCTTGGAGGC
 CACCATCCCCAAATGTTGGGCATCTCTGGTTCAATACCAAAGAAATATCTTGGAGGC
 TGCCTTCTCACATGTTCTCATCCATTCTCACTGCTATGGAGAGCATTGTGTTGGTGGC
 30 CATGGCCTTGAACGCTACATTGCCATTGCAAACCTCTCGGTACACCATGATCCTCACCA
 GCAAAATCATCAGCCTCATTGCAAGGCATTGCTGCTGAGGAGCCTGTACATGGTTGTCC
 ACTGGTGTCTCCTCTGAGGCTGCCCTCTGTGGGCATCGTATCATCCCTCATACTTATT
 GTGAGCACATGGGCATTGCCCGTCTGGCCTGTGCCAGCATCAAAGTCAACATTAGGTITGG
 CCTTGGCAACATATCTCTTGTACTGGATGTTATCCTTATTATTCTCTCCTATGTCAGGA
 35 TCCTGTATGCTGTCTGCCTGCCCTCTGGGAAGCTGACTCAAAGCTCTAACACCTGT
 GTTCTCATATTGGTGTATCTAGCTTTACACCAGCATTTCATTCTGACACA
 TCGTTTGGCCATAATATCCCACAGTATATACATATTATAGCCAACCTGTATGTGGTTG
 TCCCACCAAGCCCTCAATCTGTAAATCTATGGAGTCAGGACAAAGCAGATTGAGAGAG
 TGCTGAGGATTTCTCAAGACCAACTCAA (SEQ ID NO: 120)

AOLFR66 sequences:

40 MSFLNGTSLTPASFILNGIPGLEDVHLWISFPLCTMYSIAITGNFGLMYLIYCDEALHRPMYVFL
 ALLSFTDVLMCTSTLPNTLFILWFNLKEIDFKACLAQMFFVHTFTGMESGVLMALDHCVAI
 CFPLRYATILTNSVIAKAGFLTRGVMLVIPSTFLTKRLPYCKGNVIPHTYCDHMSVAKISCGN
 VRVNAIYGLIVALLIGGFIDLCITISYTMILQAVVSLSSADARQAFSTCTAHFC
 45 CAIVLTYVPAFFTFTHFGGHTIPLHIIIMANLYLLMPPTMNPIVYGVKTRQVRES
 VIRFLKGKDNSHF (SEQ ID NO: 121)

ATGTCATTTCTAAATGGCACCGCCCTAACCTCCAGCTTCAATTCACTCTAAATGGCATCCCTG
 GTTGGAAAGATGTGCATTGTTGATCTCCTCCACTGTGTACCATGTACAGCATTGCTATT
 50 ACAGGGAACTTCGGCCTTATGTACCTCATCTACTGTGATGAGGCCTAACAGACCTATGT
 ATGTCTTCTCATATTGTGGTTAATCTCAAGGAGATTGATTAAAGCCTGCCTGCCAGAT
 ACTCTCTCATATTGTGGTTAATCTCAAGGAGATTGATTAAAGCCTGCCTGCCAGAT
 GTCTTGTGCACACCTTCACAGGGATGGAGTCTGGGTGCTCATGCTCATGGCCCTGGAC
 CACTGTGTGCCATCTGCTTCCCTCTGCCATTGCCACCATCTCACTAATTCACTGCTATTG
 55 TAAAGCTGGGTTCTCACTTTCTTAGGGGTGTGATGCTTGTATCCCTCCACTTCTCA
 CCAAGGCCCTCCATACTGCAAGGGCAACGTACACCCACACCTACTGTGACCACATGTC
 TGTGCCAAGATATCTGTGGTAATGTCAAGGGITAACGCCATCTATGGTTGATAGTGCC

5 CTGCTGATTGGGGCTTGATATCCTGTGCATTACAATCTCCTACACTATGATTCTTCAAGC
 AGTTGTGAGTCTATCATCAGCAGATGCTCGACAGAAGGCCCTCAGCACCTGCACTGCCAC
 TTCTGTGCCATAGTCCACCTATGTTCCAGCCTCTTACCTTCTTACACACCATTITGG
 GGGACACACCAATTCTCTACACATACATATTATGGCTAATCTTACCTACTAATGCCTC
 CCACAATGAACCTATTGTGATGGGTGAAAACCAGGCAGGTACGAGAGAAAGTGTCTTA
 GGTTCTTCTTAAGGAAAGGACAATTCTCATAACTTTAA (SEQ ID NO: 122)

AOLFR67 sequences:

10 MSGDNSSSLTPGFFILNGVPGLEATHIWISLPFCFMYIIAVGNCGLICLISHEEALHRPMYYFLA
 LLSFTDVTLCCTMVPNMLCIFWFNLKEIDFNACLAQMFFVHMLTGMESGVLMALDRYVAI
 CYPLRYATILTNPVIAKAGLATFLRNVMILIPFTLLTKRLPYCRGNFIPHTYCDHMSVAKVSCGN
 FKVNAIYGLMVALLIGVFDICCISVSYTMLQAVMSLSSADARHKAFSTCTSHMCSIVITYVAAF
 FTFTHRHFVGHNIPNIIIIIVANLYLLPPTMNPIVYGVTKQIQEGVIKFLLGDKVSFTYDK
 (SEQ ID NO: 123)

15 ATGTCTGGGGACAAACAGCTCCAGCCTGACCCCAGGATTCTTATCTGAATGGCGITCTG
 GGCTGGAAGCCACACACATCTGGATCTCCCTGCCATTCTGCTTTATGTACATCATTGCTGT
 GTGGGAACTGTGGGCTCATCTGCCTCATCAGCCATGAGGAGGCCCTGCACCGGCCATGT
 ACTACTTCTGGCCCTGCTCTCCCTCACTGATGTCACCTGGCACCACATGGTACCTAAT
 20 ATGCTGTGCATATTCTGGTCAACCTCAAGGAGATTGACTTTAACGCCCTGCCTGGCCAGA
 TGTTTTTGTCCATATGCTGACAGGGATGGAGTCTGGGTGCTCATGCTCATGGCCCTGGA
 CCGCTATGTGGCCATCTGCTACCCCTACGCTATGCCACCACCTTACCAACCCGTCACTCG
 CCAAGGCTGGCTTGCACCTCTGAGGAATGTGATGCTCATCTCCATTCACTCTCCTC
 25 ACCAAGCGCCTGCCCTATTGCCGGGGAACTTCATCCCCACACCTACTGTGACCATATGT
 CTGTTGGCCAAGGTATCTGTGGCAATTCAAGGTCATGCTATTATGGCTGATGGTGC
 TCTCCTGATTGGTGTGTTGATATCTGCTGTATCTGTATCTTACACTATGATTGGCAGG
 CTGTTATGAGCTGTATCAGCAGATGCTCGTACAAAGCCTCAGCACCTGACATCTCA
 CATGTGTTCCATTGTGATCACCTATGTTGCTGTTTCACTTTTCACTCATCGTTGTTG
 30 AGGACACAATATCCAAACACATACACATCATCGTGGCCAACCTTATCTGCTACTGCCT
 CCTACCATGAACCCAATTGTTATGGAGTCAGACAGAACGAGATTCAAGGAAAGGTGTAATTA
 AATTTTACTGGAGACAAGGTTAGTTTACCTATGACAATGA (SEQ ID NO: 124)

AOLFR68 sequences:

35 MTTHRNDTSLSTEASDFLLNCFVRSPSWQHWLSPLSLLAVGANTLLMTIWEASLHQPL
 YYLLSLLSLLDIVLCLTVIPKVLTIFWFDLRPISFPACFLQMYIMNCFLAMESCTFMVMAYDRY
 VAICHPLRYPSIITDHFVVKAAMFILTRNVLMLPIPILSAQLRYGRNVIENCICANMSVSRLSC
 DDVTINHLYQFAGGWTLGSDLILIFLSYTFILRAVRLKAEGAVAKALSTCGSHFMLILFFSTIL
 LVFLVLTIVAKKKVSPDVPVLLNVLHHVPAALNPIYGVRTQEIKQGMQRLLKKGC (SEQ ID
 NO: 125)

40 ATGACAACACACCGAAATGACACCCCTCCACTGAAGCTCAGACTCCTCTTGAATTGTT
 TTGTCAGATCCCCCAGCTGGCAGCACTGGCTGTCCTGCCCTCAGCCTCCTTCTG
 GCCGTAGGGGCCAACACCACCCCTCTGATGACCATCTGGCTGGAGGCCCTCTGCACCAGC
 CCCTGTACTACCTGCTCAGCCTCTCCCTGCTGGACATCGTCTGCCTCACTGTCATC
 45 CCCAAGGTCTGACCATCTCTGGTTGACCTCAGGCCATCAGCTCCCTGCCCTGCTTCT
 CCAGATGTACATCATGAATTGTTCTAGCCATGGAGTCTGACATTCATGGTCATGGCC
 TATGATCGTTATGTAGCCATCTGCCACCCACTGAGATATCCATCAATCATGACTGACT
 TGTAGTCAGGCTGCCATGTTATTGACCAAGAAATGTGCTTATGACTCTGCCATCCCC
 ATCCTTCAGCACAACCTCGTTATTGTTGAAGAAATGTCAATTGAGAACTGCACTGTGCCA
 50 ATATGTCGTTCCAGACTCTCTGCGATGATGTCACCATCAATCACCTTACCAATTGCT
 GGAGGCTGGACTCTGCTAGGATCTGACCTCATCCTTATCTCCTCTCCTACACCTTCAATT
 GCGAGCTGTGCTGAGACTCAAGGCAGAGGGTGCCGTGGCAAAGGCCCTAACGACATGTGG
 CTCCCACTTCATGCTCATCCTCTTCAAGCACCACCTCTGCTGGTTTGTCTCACACATGT
 GGCTAAGAAGAAAGTCTCCCTGATGTGCCAGTCTGCTCAATGTTCTCCACCATGTCATT
 55 CCTGCAGCCCTTAACCCCATATTACGGGTGAGAACCCAAGAAATTAAAGCAGGAAATG
 CAGAGGTTGTTGAAGAAAGGGTCTAA (SEQ ID NO: 126)

AOLFR69 sequences:

5 MSYSIYKSTVNIPLSHGVVHSFCHNMNCNFMHIFKFVLDNFNMKNVTEVTLFVLKGFTDNLELQ
 TIFFFLFLAIYLFTLMGNLGLILVVIRDSQLHKPMYYFLSMLSSVDACYSSVITPNMLVDFTTKN
 KVISFLGCVAQVFLACSFGTTECFLLAAMAYDRYVAIYNPLLYSVSMSPRVYMPLINASYVAGI
 LHAТИHTVATFSLSFCGANEIRRVFCDIPLLAISYSHTNQLLLFFYFVGSIELVTILIVLISYGLIL
 LAILKMYSAEGRRKVFSTCGAHLTGVSIYYGTILFMYVRPSSYASDHDMIVSIFYTIVIPLLNPV
 IYSLRNKDVKDSMKKMFGKNQVINKVYFHTKK (SEQ ID NO: 127)

10 ATGTCGTACAGTATATAACAAGAGCACAGTTAACATCCCCTGAGTCATGGTGTGTTCAATT
 CTTTTGTCATAATATGAACGTAACTTTATGCATATCTTCAGTTGTTCTAGATTTCAAC
 ATGAAGAAATGTCAGTGAAGTTACCTTATTGTACTGAAGGGCTCACAGACAATCTGAAC
 TGCAGACTATCTTCTCTTCTGTTCTAGCAATCTACCTCTCACTCTCATGGGAAATTAA
 GGACTGATTTAGTGGTCATTAGGGATCCCAGCTCCACAAACCCATGTACTATTTCTGA
 15 GTATGTTGCTTCTGTGGATGCCGCTATTCCCTCAGTTATTACCCAAATATGTTAGTAGAT
 TTACGACAAAGAATAAAAGTCATTCACTCCTGGATGTTGAGCACAGGTGTTCTGCTT
 GTAGTTTGGAACACACAGAATGCTTCTTGGCTGCAATGGCTTATGATCGCTATGAGC
 CATCTACAAACCTCTCCTGTATTCACTGAGCATGTCACCCAGAGTCTACATGCCACTCATC
 AATGCTTCCATGTTGCTGGCATTTCACATGCTACTATACATACAGTGGCTACATTAGCCT
 20 ATCCTTCTGTGGAGCCAATGAAATTAGGCCTGCTTTGTGATATCCCTCTCCCTGCTA
 TTTCTTATTCTGACACTCACACAAACCAAGCTTCACTCTTCTACTTTGTGGGCTCTATCGAG
 CTGGTCACTATCCTGATTGTTCTGATCTCTATGGTTGATTCTGTTGGCCATTCTGAAGAT
 GTATTCTGCTGAAGGGAGGAGAAAAGTCCTCTCCACATGTGGAGCTCACCTAACGGAGT
 25 GTCAATTATTATGGGACAATCCTCTCATGTATGTGAGACCAAGTCCAGCTATGCTTCG
 GACCATGACATGATAGTGTCAATATTACACCATGTGATTCCCTGCTGAATCCCGTCAT
 CTACAGTTGAGGAACAAAGATGTAAGACTCAATGAAAAAAATGTTGGGAAAAATCA
 GTTATCAATAAAAGTATATTCTACACTAAAAAATAA (SEQ ID NO: 128)

AOLFR70 sequences:

30 MDSTFTGYNLYNLQVKTEMDKLSSGLDIYRNPLKNKTEVTMFILTGFDDFELQVFLLEFAI
 YLFILGNLGLVVLVIEDSWLHNPMYYFLSFLDACYSTVTPKMLVNFLAKNKSISFIGCA
 TQMLLFVTFGTTECFLLAAMAYDHYVAIYNPLLYSVSMSPRVYVPLITASYVAGILHATIHLA
 TFSLSFCGSNEIRHVFCDMPPLLAISCSDHTNQLLLFFYFVGSIEIVTILIVLISCDFILLSILKMHS
 KGRQKAFSTCGSHLTGVTIYHGTILVSYMRPSSYASDHDIIVSIFYTIVIPKLNPIYSLRNKEVK
 35 KAVKKMLKLVYK (SEQ ID NO: 129)

ATGGACTCCACTTACAGGCTATAACCTTATAACCTGCAAGTAAAAACTGAAATGGACA
 AGTTGTCATCAGGTTGGATATACAGGAATCCACTGAAGAACAGACTGAAGTCACCA
 TGTATATTGACAGGCTTCACAGATGATTGAGCTGCAAGTCTTCTATTCTTACTATTT
 40 TTTGCAATCTATCTCTTACCTTGATAGGCAATTAGGGCTGGTTGTGTTGGTATTGAGG
 ATTCTGGCTCCACACCCATGTATTCTTACTGTGTTGTTACTTGGAACTACAGAACGG
 TATTCTACAGTTGTCACTCCAAAATGTTGGCAATTCTGGCAAAAAATAAACCTCATTT
 CATTATCGGATGTGCAACACAGATGCTCTTTGTTACTTGGAACTACAGAACGG
 45 CTCTGGCTGCAATGGTTATGACTATGTAGGCCATCTACACCCCTCTCTGTATTCACT
 GAGCATGTCACCCAGAGTCTATGTGCCACTCATCACTGCTTCCATCGTGCATTTCAC
 ATGCTACTATACATAAGTGGCTACATTAGCCTGCTCTGTGGATCCAATGAAATTAG
 GCATGTCATTGATATGCCCTCTCCCTGCTATTCTGTTCTGACACTCACACAAACC
 AGCTTCACTCTTCACTTTGTTGGCTATTGAGATAGTCACATCCTGATTGCTCATT
 TCCCTGATTCTCATCTGTTGCCATTCTGAAGATGCAATTGCTAAGGGAAAGGCAAAAGG
 50 CCTCTCTACATGTCGGCTCACCTAACCTGAGTGACAATTATCATGGAACAATTCTCGTC
 AGTTATATGAGACCAAGTCCAGCTATGCTTCAGACCATGACATCATAGTGTCAATATT
 ACACAAATTGTGATTCCAAGTTGAATCCCATCATCTATAGTTGAGGAACAAAGAAGTAAA
 AAAGGCAGTGAAGAAAATGTTGAAATTGGTTACAAATGA (SEQ ID NO: 130)

AOLFR71 sequences:

5 MGRRNNTNVPDFILTGLSDSEEVQMALFILFLIIYLITMLGNVGMILIIIRLDLQLHTPMYFFLTH
 LSFIDLSYSTVTPKTLANLLTSNYISFMGCFQMFFFVFLGAAECFLSSMAYDRYVAICSPRLY
 PVIMSKRLCCALVTGPYVISFINSFVNWWMSRLHFCDSNVVRHFFCDTSPILALSCMDTYDIEI
 5 MIHILAGSTLMVSЛИTISASYVSLISTILKINSTSGKQKALSTCASHLLGVTIFYGTMIFTYLKPRK
 SYSLGRDQVASVFYTIVIPMLNPLIYSLRNKEVKNALIRVMQRRQDSR (SEQ ID NO: 131)

10 ATGGGTAGAAGAAATAACACAAATGTGCCTGACTTCATCCITACGGGACTGTCAGATTCTG
 AAGAGGTCCAGATGCCCTCTTATACATTTCTCCTGATATACTAATTACTATGCTGGGC
 10 AATGTGGGGATGATATTGATAATCCGCCTGGACCTCCAGCTTCACACCTCCATGTATT
 TCCCTACTCACTGTCAATTGACCTCAGTTACTCAACTGTCACTCACACCTAAACCTTA
 GCGAACCTACTGACTTCCAACATATTCCCTCATGGGCTGTTGCCAGATGTTCTTT
 TGCTTCTGGGAGCTGCTGAATGTTCTCATCAATGCCATGATCGCTACGTAG
 15 CTATCTGCAGTCCTCACGTTACCCAGTTATTATGTCACATGGCTGTTGCGCTTGTG
 ACTGGGCCATGTGATTAGCTTATCAACTCCTTGTCAATGTGGTTGGATGAGCAGAC
 TGCATTCTGCGACTCAAATGAGTTCGTCACTTTCTGCGACACGTCTCCAATTAGCT
 CTGTCCTGCATGGACACATACGACATTGAAATCATGATAACATTTAGCTGTTCCACCC
 TGATGGGTGCCATTACAAATATCTGCATCCTATGTCATTCTCTCTACCATCCTGAAA
 ATTAATTCCACITCAGGAAAGCAGAAAGCTTGTACTTGTGCCCTCATCTTGGGAG
 20 TCACCATCTTATGGAACATGATTTACTTATTAAAACCAAGAAAAGTCTTATTCTTG
 GGAAGGGATCAAGTGGCTCTGTTTATACTATTGTGATTCCATGCTGAATCCACTCAT
 TTATAGTCTTAGAAACAAAGAAGTTAAAATGCTCTCATTAGAGTCATGCAGAGAAGACA
 GGACTCCAGGTAA (SEQ ID NO: 132)

AOLFR72 sequences:

25 MAPENFTRVTEFILTGVSSCPELQIPLFLVFLVLYGLTMAGNLGIITLTSVDSRLQTPMYFFLQHL
 ALINLGNSTVIAPKMLINFLVKKKTSFYECATQLGGFLFFIVSEVIMLALMACDRYVAICNPLL
 30 YMVVVSRRCLLLVSLTYLYGFSATAIVVSSYVFSVSYCSSNINHFYCDNVPLLALSCSDTYLPE
 TVVFISAATNVVGSILIVLVSYFNTVLSILKICSEGRKKAFSTCASHMMAVTIFYGTLFMYVQP
 RSNHSLDDKMASVFYTLVIPMLNPLIYSLRNKDVKTALQRFMTNLCSFKTM (SEQ ID NO:
 133)

35 ATGGCTCCTGAAAATTCAACCAGGGTCACTGAGTTATTCTTACAGGTGTCTAGCTGTC
 CAGAGCTCCAGATTCCCTCTGGCTTCTGGCTCTATGGCTGACCATGGCAGG
 GAACCTGGCATCATCACCCCTACCACTGGCTCTATTAACTCTGGTAACCTACTGTCATT
 TCCGCAACATCTGGCTCTATTAACTCTGGTAACCTACTGTCATTGCCCCTAAATGCTG
 ATTAACCTTTAGTAAAGAAGAAAACCTACCTCATTCTATGAATGTGCCACCCACTGGGAG
 GGTCTTGTCTTATTGATCGGAGGTAAATCATGCTGGCTTGATGGCTGTGACCGCTAT
 GTGGCTATTGTAACCTCTGCTGTACATGGCTTCTACAGCTATTGTGGTTCATCTTATGTATTCT
 40 GGTCTCCCTCACATAACCTCTATGGCTTCTACAGCTATTGTGGTTATCTGCTCTGCT
 CTGTCCTTATTGCTCTTCTAAATATAATCAATCATTCTACTGTGATAATGTTCTCTGTTA
 GCATTATCTGCTCTGATACTTACTTACAGAAACAGTTGCTTATATCTGAGCAACAA
 ATGTGGTTGGTCCCTGATTATAGTTAGTATCTTATTCAATATTGTTGTCTATT
 45 AAAATATGTCATCAGAAGGAAGGAAAAAGCCTTCTACCTGTGCTTCACATATGATGG
 CAGTCACAATTCTATGGACATTGCTATTGATGTGCAAGCCCCGAAGTAACCATTC
 ATTGGATACTGATGATAAGATGGCTTCTGTTTACACGTTGGAATTCTATGCTGAAT
 CCCTGATCTACAGCTGAGGAATAAGGATGTGAAGACTGCTCTACAGAGATTGACA
 AATCTGTGCTATTCTTAAAACAATGTA (SEQ ID NO: 134)

AOLFR73 sequences:

50 MNHVVKHNTAVTKVTEFILMGITDNPGLQAPLFGFLIIYLVTVIGNLGMVILTYLDSKLHTP
 MYFFLRHLSITDLYSTVIAPKMLVNFIYHKNNTISYNWYATQLAFFEIFISELFILSAMA YDRYV
 AICKPLLYVIIAMAEKVLWVLVIVPYLYSTFVSLFLTIKLFKLSFCGSNIISYFYCDCIPLMSILCSDT
 NELELILIFSGCNLLFSLISIVLISYMFILVAILRMNSRKGRYKAFTCSSHLTVVIMFYGTLFYL
 55 QPKSSHTLAIDKMASVFYTLVIPMLNPLIYSLRNKEVKDALRKLTNRFKIPI (SEQ ID NO: 135)

ATGAATCATGTGGTAAAACACAATCACACGGCAGTGACCAAGGTGACTGAATTATTCTCA
 TGGGGATTACAGACAACCCCTGGCTGCAGGCTCCACTGTTGGACTCTCCTCATCATATA
 TCTGGTCACAGTGATAGGCAATCTGGCATGGTATCTGACCTACTGGACTCCAAGCTA
 CACACCCCCATGTACTTTCTTAGACATTTGTCAACTCACTGATCTGGTACTCCACTGT
 5 CATTGCCCGAAGATGTTAGTAAACTCATAGTCACAAAAACACAATTCTACAATTGG
 TATGCCACTCAGCTAGCATTCTGAGATTTCATCATCTGAGCTCTTATTCTATCAGC
 AATGGCCTATGATCGCTACGTAGCCATCTGTAACCTCTCTGTACGTGATCATGGCA
 GAGAAAGTACTTTGGGTGCTGGTAATTGTTCCCTATCTATAGCACGTTGTGACTATT
 TCTCACAATTAAAGTATTTAAACTGTCCCTCTGTGGCTCAAACACATAATCAGCTATT
 10 GTGACTGTATCCCTCTGATGTCCTACTCTGTTCTGACACAAATGAATTAGAATTAAAT
 TTGATCTCTCAGGCTGTAATTGCTCTCCCTCTCAATTGTTCTCATATCCTACATGTT
 TATTCTAGTGGCCATTCTCAGAATGAACTCAAGGAAAGGGAGGTACAAAGCCTCTCCACC
 TGAGCTCTCATCTGACAGTGGTGATCATGTTCTATGGGACATTGTTATTATTA
 15 ACCAAGTCCAGTCATACTTTGGCTATTGATAAAATGGCCTAGTGTGTTATACCCGTTG
 ATTCCTATGCTGAATCCGTTGATCTACAGCCTAAGGAACAAAGAAGTAAAAGATGCTCTAA
 AGAGAACTTTAACCAATCGATTCAAATTCCCATTAA (SEQ ID NO: 136)

AOLFR74 sequences:

MEQHNLTIVNEFILTGITDIAELQAPLFALFLMIYVISVMGNLGMIVLTKLDSRLQTPMYFFLRH
 20 LAFMDLGYSTTVGPKMLVNFDVKNIISYYFCATQLAFFLFIGSELFILSAMSYDLYVAICNPL
 LYTVIMSRRVCQVLVAIPYLCTFISLLVTIKIFTLSFCGYNVISHFYCDSLPLLPILCSNTHEIELI
 ILIFAAIDLISLLIVLLSYLLILVAILRMNSAGRQKAFSTCGAHLTVVIVFYGTLLFMYVQPKSSH
 SFDTDKVASIFYTLVIPMLNPLIYSLRNKDVKYALRRTWNNLNCNIFV (SEQ ID NO: 137)

25 ATGGAACAAACACAATCTAACAAACGGTGAATGAATTCTTACGGGAATCACAGATATC
 GCTGAGCTGCAGGCACCATTATTGCAATTGCTCATGATCTATGTGATCTCAGTGATGG
 GCAATTGGCATGATTGCTCACCAGTGGACTCCAGGGTGCACAAACCCCTATGTACTT
 TTTCTCAGACATCTGGCTTCTCATGGATCTGGTATTCAACAACTGTGGGACCCAAAATG
 TTAGTAAATTGTTGTGGATAAGAATAATTCTTATTATTGTTGTGCAACACAGCTAGC
 30 TTCTTCTGTGTTCTGGTAGTGAACCTTTATTCTCTCAGCCATGTCCTACGACCTCT
 ATGTGGCCATCTGTAACCCCTCTGCTATACACAGTAATCATGTCACGAAGGGTATGTCAGGT
 GCTGGTAGCAATCCCTACCTCTATTGACACATTCTCTTAGTCACCATAAGATT
 TTACCTTATCCTCTGTGGTACAACGTCATTAGTCATTCTACTGTGACAGTCTCCCTTG
 TTACCTTGTGTTGTCAAATACACATGAAATTGATAATTCTGATCTTGAGCTAT
 35 TGATTTGATTCTCTCTGATAGTTCTTATCTACCTGCTCATCCTTGAGCCATTCT
 CAGGATGAATTCTGCTGGCAGACAAAAGGCTTTCTACCTGTGGAGCCCACCTGACAGTG
 GTCATAGTGTCTATGGGACTTTGCTTTCTATGTCAGTGACGCCAAGTCCAGTCATTCT
 TGACACTGATAAAAGTGGCTTCCATATTACACCCGGTATCCCCATGTTGAATCCCTGA
 TCTATAGTTACGAAACAAAGATGTAATGCCCTACGAAGGACATGGAATAACTTATG
 40 TAATATTGTTAA (SEQ ID NO: 138)

AOLFR75 sequences:

MEGKNQTNISEFLLGFSWQQQVLLFALFLCLYLTLGLFGNLLILLAIGSDHCLHTPMYFFLA
 NLSLVDLCLPSATVKMLLNIQTQTQTISYPGCLAQMYFCMMFANMDNFLLTVMAHYDRYVAI
 45 CHPLHYSTIMALRLCASLVAAPWVIAILNPLLHTLMMMAHLHFCSDNVIHFFCDINSLLPLSCSD
 TSLNQLSVLATVGLIFVVPSCVILVSYILIVSAVMKVPSAQGKLKAFSTCGSHLALVLFYGA
 GVYMSPLSNHSTEKDSAASVIFMVVAPVLPFIYSLRNNELKTLKTLRPGAVAHAACNPSTL
 GGRGGWIMRSGDRDHPG (SEQ ID NO: 139)

50 ATGGAAGGGAAAAATCAAACCAATATCTCTGAATTCTCCTGGGCTTCTCAAGTTGGC
 AACAAACAGCAGGTGCTACTCTTGCACTTTCTGTGTCTCTATTAAACAGGGCTTTGGA
 AACTTACTCATCTGCTGGCATTGGCTGGATCACTGCCCTCACACACCCATGTATTCTT
 CCTGCCAATCTGCTCTGGTAGACCTCTGCCCTCAGGCCACAGTCCCCAAGATGCTAC
 TGAACATCCAAACCCAAACCCAAACCATCTCCTATCCCGGCTGCTGCTCAGATGTATT
 55 CTGTATGATGTTGCCAATATGACAATTCTCTCACAGTGATGGCATATGACCGTTAC
 GTGCCCATCTGTCACCCATTACATTACTCCACCATATGGCCCTGCGCCTCTGTGCGCTCTCT

5 GGTAGCTCACCTGGGTATTGCCATTGAAACCCCTCTGCACACTCTTATGATGGCC
ATCTGCACTCTGCTCTGATAATGTATCCACCATTCCTCTGTGATATCAACTCTCTCC
CCTCTGTCTGTTCCGACACCAAGTCTTAATCAGTTGAGTGTCTGGTACGGTGGGCTGA
TCTTTGTGGTACCTTCAGTGTGATCCTGGTATCCTATATCCTCATTTCTGCTGTGATG
AAAGTCCCCCTGCCAAGGAAAACCAAGGCTTCTACCTGTGGATCTCACCTGCCCT
GGTCATTCTTTCTATGGAGCAAACACAGGGGTCTATATGAGCCCCCTATCCAATCACTCT
ACTGAAAAAGACTCAGCCGCATCAGTCATTTATGGTTAGCACCTGTGTTGAATCCAT
TCATTTACAGTTAAGAAACAATGAACAGGGGACTTTAAAAAAAGACCTTAAGCCGGC
CGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTGGGAGGCCAGGGCGGGTGGATCA
10 TGAGGTCAGGAGATCGAGACCATCCTGGCTAA (SEQ ID NO: 140)

AOLFR76 sequences:

15 MENNTEVSEFILLGLTNAPELQVPLFIMFTLILYLTLLTGNLGMIIILLLDSHLHTPMYFFLSNLSA
GIGYSSA VTPKVLTGLLIEDKAISYSACAAQMFFCAVFATVENYLLSSMA YDRYAAVCNPLHY
TTTMTTRVCACLAIGCYVIGFLNASIQIGDTFRLSFCMSNVIIHFFCDKPAVITLTCSEKHISELIL
VLISSFNVFALLVTLISYLFILITILKRHTGKGYQKPLSTCGSHLIAIFLFYITVIIIMYIRPSSSHSM
DTDKIASFYTMIIIPMLSPIVYTLRNKDVKNAFMKVVEKAKYSLDSVF (SEQ ID NO: 141)

20 ATGGAGAATAATACAGAGGTGAGTGAATTACCTCTGCTTGGTCTAACCAATGCCAGAA
CTACAGGTTCCCTCTTATCATGTTACCTCATCTACCTCACTCTGACTGGAACCT
GGGGATGATCATATTAACTCTGCTGGACTCTCATCTCCACACTCCCATGTA
CTTCTCA
25 GTAACCTGTCCTTGAGGCATTGGTACTCTCAGCTGTCACTCCAAAGGTTAAC
TGG
GTTGCTTATAGAAGACAAAGCCATCTCTACAGTGCCTGCTGCTCAGATGTT
CTTGT
GCAGTCTTGCCTACTGTGGAAAATTACCTCTGCTCTAAC
TGGCTATGACCGCTACGCAG
CAGTGTGTAACCCCCCTACATTATACCA
CACCACCATGACAAACACGTGTGTGCTGCTGCTGGC
TATAGGCTGTTATGTCATTGGTTCTGAATGCTCTATC
CAAATTGGAGATACATITGCC
TCTCTTCTGCATGTCCAATGTGATT
CATCACTTTCTGTGACAAACCAGCAGTCATTACT
CTGACCTGCTCTGAGAAACACATTAGTGAGTTGATT
CTTGTCTTATATCAAGTT
AAATGTC
30 CTTTTTGCACTCTGTTACCTGATT
CCTATCTGTCATATTGATCACCATTCTTAAGAG
GCACACAGGTAAAGGGATACCA
CAGAAGCCATTATCTACCTG
GGTCTCACCTCATTGCCATT
TTCTTATT
TTATATAACTGT
CATCATG
TACATACG
ACCAAG
TTCCAG
TCATCC
ATGG
CACAGACAAAATT
GCATCTG
GTTCTAC
ACTATG
ATCAT
CCCCAT
GCTCAG
TCTTATAGT
CT
ATACC
CTGAGGA
ACAAAG
ACGT
GAAGA
ATGC
ATT
CATGA
AGGTT
GTTG
GAGA
AGG
CAA
AT
ATT
CT
TAGAT
TCAGT
CTT
TAA (SEQ ID NO: 142)

AOL FB77 sequences:

40 MGDVNQSVASDFILVGLFSHSGSRQLLFLSVAVMFVIGLLGNTVLLFLIRVDSRLHTPMYFLS
QLSLFDIGCPMVTPKMASDFLRLGEGATSYGGGAAQIFFLTLMGVAEGVLLVLM SYDRYVAVC
QLPQYPVLMRRQVCLLMMGSSWVGVLNASIQTSLHFPYCASRIVDHFFCEVPALLKLSA
DTCA YEMALSTSGVLILMLPLSLIATSYGHVLQAVLSMRSEARHKA VTTCSSHTVVGLFYGA
AVFMYMVP CAYHSPQQDNVVSLF YSLVTPTLNPLIYSLRNPEVWMALVKVLSRAGLRQMC
(SEQ ID NO: 143)

45 ATGGGGATGTGAATCAGTCGGTGGCCTCAGACTCATTCTGGTGGGCCTTCAGTC
CAGGATCACGCCAGCTCCTCTCCCTGGTGGTGTCACTGTTGTCAAGGCCTCTGGC
AACACCAGTTCTCTCTTGATCCGTGTGGACTCCCGCTCCACACACCCATGTACTTCT
GCTCAGCCAGCTCTCCCTGTTGACATTGGCTGCCCCATGGTCACCATCCCCAAGATGGCA
TCAGACTTCTGCAGGGAGAAGGTGCCACCTCTATGGAGGTGGTGCAGCTCAAATATTCT
50 TCCTCACACTGATGGGTGTGGCTGAGGGCGTCTGTTGGTCCTCATGTCTTATGACCGTTA
TGTTGCTGTGTGCCAGCCCCCTGCAGTATCCTGTACTTATGAGACGCCAGGTATGTCTGCTG
ATGATGGGCTCCTCTGGGTGGTAGGTGTGCTCAACGCCCTCATCCAGACCTCCATCACCC
TGCATTTCCTACTGTGCCTCCCGTATTGTGGATCACTTCTCTGTGAGGTGCCAGCCCTA
CTGAAGCTCTCCTGTGCAGATACCTGTGCCTACGGAGATGGCGCTGTCCACCTCAGGGGTGC
TGATCCTAATGCTCCCTCTTCCCTCATGCCACCTCCTACGGCCACGTGTTGCAGGCTGTT
55 CTAAGCATGCGCTCAGAGGGAGGCCAGACACAAGGCTGTCACCACCTGCTCCTCGCACATCA
CGGTAGTGGGCTCTTATGGTGCCGCCGTGTTCATGTACATGGTGCCTTGCGCCTACCA

CAGTCCACAGCAGGATAACGTGGTTCCCTTCTATAGCCTGTCACCCCTACACTCAAC
 CCCCTTATCTACAGTCTGAGGAATCCGGAGGTGTGGATGGCTTGGTCAAAGTGCTTAGCA
 GAGCTGGACTCAGGCAAATGTGCTGA (SEQ ID NO: 144)

5 **AOLFR78 sequences:**

MSPDGNHSSDPTEFVLAGLPNLNSARVELSVFLLVYLLNLGNVLIVGVVRADTRLQTPMYF
 FLGNLSCLEILLTSVIIPKMLSNFLSRQHTISFAACITQFYFYFFLGASEFLLAVMSADRYLAICH
 PLRYPLMSGAVCFRVALACWVGGLVPVLGPTVAVALLPFCKQGAVVQHFFCDSGPLRLAC
 TNTKKLEETDFVLASLVIVSSLITAVSYGLIVLAVLIPSASGRQKAFSTCTSHLIVVTLFYGSAI
 10 FLYVRPSQSGSVDTNWAVTVITFVTPLNPFIYALRNEQVKEALKDMFRKVVAGVLGNLLD
 KCLSEKAVK (SEQ ID NO: 145)

ATGAGTCCTGATGGGAACCACAGTAGTGATCCAACAGAGTTGTCCTGGCAGGGCTCCCA
 15 AATCTCAACAGCGCAAGAGTGGATTATTTCTGTTCTTCTGTCTATCTCCTGAATCT
 GACAGGCAATGTGTTGATTGTTGGGGGGGGTAAGGGCTGATACTCGACTACAGACCCCTAT
 GTACTTCTTCTGGTAACCTGTCCTGCCTAGAGATACTGTCACTTCTGTATCATTCCAA
 AGATGCTGAGCAATTCTCTCAAGGCAACACACTATTCCTTGTGATGTATCACCCA
 ATTCTATTTCTACTTCTTCTCGGGGCTCCGAGTTCTACTGTTGGCTGTATGTCCTGCGG
 20 ATCGCTACCTGGCCATCTGTCACTCTCTCGCTACCCCTGCTCATGAGTGGGCTGTGTG
 CTTCTGTTGGCCTTGGCTGCTGGCTTGTGTAAGCAGGGTGTGTTGACAGCACTTCTGCGACA
 GTGGCCACTGCTCCGCTGGCTGACCCAACACCAAGAAGCTGGAGGAGACTGACTTTGT
 CCTGGCCTCCCTCGTCAATTGTACTTCTGCTGATCACTGTCGTGTCCTACGGCCTCATG
 25 TGCTGGCAGTCCCTGAGCATCCCCCTGCTTCAGGCCGTAGAAGGCCCTCTACACCTGTAC
 CTCCCACTTGATAGTGGTGACCCCTCTATGGAAGTGCCTTCTATGTGCGGCCAT
 CGCAGAGTGGTCTGGACACTAAGTGGCAGTGACAGTAATAACGACATTGTGACAC
 CACTGTTGAATCCATTCACTATGCCCTACGTAATGAGCAAGTCAGGAAGCTTGAAGGA
 CATGTTAGGAAGGTAGTGGCAGGCGTTAGGAAATCTTACTTGATAAAATGTCTCAGT
 30 GAGAAAGCAGTAAAGTAA (SEQ ID NO: 146)

AOLFR79 sequences:

MTPGELALASGNHTPKFILQGFSNYPDLQELLFGAILLIYAITVGNLGMALIFTDSHLQSP
 MYFFLNVLSDLICYSSVTPKLLVNFLVSDKSISFEGCVVQLAFFVVHVTAESFLASMA
 35 YDRFLAICQPLHYGSIMTRGTCLQLVAWSYAFGGANSIAQTGNVFALPFCGPQLTHYYCDIPPLH
 LACANTATARVVLVFSALVTLLPAAVILTSYCLVLAIGRMRSVAGREKDLSTCASHFLA
 IAI FYGTVVFTYVQPHGSTNNTNGQVSVFYTIIPMLNPFIYSLRNKEVKGALQRKLQVNIFPG
 (SEQ ID NO: 147)

40 ATGACACCTGGAGAACTAGCCCTGCCAGTGGCAACCACACCCAGTCACCAAGTTCATCT
 TGCAGGGATTCTCCAATTATCCAGACCTCCAGGAGCTCTCTCGGAGGCCATCCTGCTCAT
 CTATGCCATAACAGTGGTGGCAACTGGGAATGATGGCAGTCATCTTCACAGACTCCCAT
 CTCCAAGCCAATGTATTCTCCTCAATGTCCTCTCGTTCTGATATTGTTACTCTTCT
 GTGGTCACACCTAACGCTCTGGTCAACTCCTGGCTCTGACAAGTCCATCTTTGAGG
 GCTGTGTGGCCAGCTCGCCTCTTGTAGTGCATGTGACAGCTGAGAGCTTCTGCTGGC
 45 CTCCATGGCCTATGACCGCTTCTAGCCATCTGTCAACCCCTCATTATGGTTCTATCATGA
 CCAGGGGGACCTGCTCCAGCTGGTAGCTGTCTCATGCAATTGGTGGAGCCAACCTCCGC
 TATCCAGACTGGAAATGTCTTGCCTTGCTTCTGTTGGCCCAACCAAGCTAACACACTAC
 TACTGTGACATACCAACCCCTCTCCACCTGGCTGTGCCAACACAGCCACAGCAAGAGTGG
 TCCTCTATGTCTTCTGCTCTGGTCACCCCTCTGCTGCTGAGTCATTCTCACCTCCTACT
 50 GCTTGGCTTGGTGGCCATTGGGAGGATGCGCTCAGTAGCAGGGAGGGAGAAGGACCTCT
 CCACCTGTGCTCCCACATTCTGGCATTGCCATTTCATGGCACTGTGGTTTCACCTAT
 GTTCAGCCCCATGGATCTACTAACAAACCAATGCCAAGTAGTGTCCGTCTTACACCA
 TCATAATTCCCATGCTCAATCCCTCATCTATAGCCTCCGCAACAAAGGAGGTGAAGGGCGC
 TCTGCAGAGGAAGCTTCAGGTCAACATCTTCCGGCTGA (SEQ ID NO: 148)

55

AOLFR80 sequences:

MEGINKTAKMQFFFRRPSPDPEVQMLIFVVFLMMYLTSLGNATIAVTQINHSLHTPMYFFLA
 NLAVLEIFYTSSITPLALANLLSMGKTPVSITGCGTQMFFFVFLGGADCVLLVVMAYDRFIAICH
 PLRYRLIMSWSLCVELLVGSLVLGFLSLPLTILIFLPFCHNDEIYHFYCDMPAVMRLACADTR
 5 VHKTALYIISFIVLSIPLSISIYVFIVVAILRIRSAEGRQQAYSTCSSHILVLLQYGCTSFYIYSPS
 SSYSPEMGRVVSVAYTFITPILNPLIYSLRNKELKDALRKALRKF (SEQ ID NO: 149)

10 ATGGAAGGAATAAAATAAAACTGCAAAGATGCAGTTTCTTCGTCATTCTCACCTGACC
 CTGAGGTCCAGATGCTGATTTGTGGCTTCCTGATGATGTATCTGACCAGCCTCGGTGG
 AAATGCTACAATTGCACTGTCAGATCAATCATTCCCTCCACACCCCCATGTA
 15 TCCTGGCTAATCTGGCAGTTCTAGAAATCTTCTATACATCTTCATACCCATTGGCCTTG
 GCAAACCTCCTTCATGGCAAACACTCCTGTTCCATCACGGGATGTGGCACCCAGATGT
 TTTCTTGTCTTCTGGGTGGGCTGATTGTCTGCTGGTAGTCATGGCTTATGACCGG
 TTTATAGCGATCTGTCACCCTCTGCATACAGGCTCATCATGAGCTGGCTTGTGTGG
 AGCTGCTGGTAGGCTCCTGGTCTGGGTTCTGTTGTCACTGCCACTCACCATTAAATC
 TTCCATCTCCCATTGCAACATGATGAGATCTACCACTCTACTGTGACATGCCAGT
 CATGCGCTGGCTTGCAAGACACACCGCTTACAAGACTGCTCTGATATCATCAGCTC
 ATCGTCCTTAGCATCCCCCTCTCATTGATCTCCATCTCTATGTCATCGTGGTAGCCAT
 20 TTTACGGATCCGGTCAGCAGAAAGGGGCCAGCAAGCCTACTCTACCTGCTCTCACATC
 TTAGTGGCTCCTCTGCACTATGGCTGCACCAGCTTATATACTTGTCCCCAGTTCCAGCTA
 CTCTCCTGAGATGGGCCGGGTGGTATCTGTCCTACACATTATCACTCCATTAAAC
 CCCTTGATCTATAGTTGAGGAACAAGGAACGTAAAGATGCCCTAAGGAAAGCATTGAGA
 AAATTCTAG (SEQ ID NO: 150)

AOLFR81 sequences:

MGVKNHSTVTEFLSGLTEQAEQLPLFCLFLGIYTVTVVGNLMSIIRLNRLHTPMYYFLSS
 LSFLDFCYSSVTPKMMKLWMESHLIVPETRSPRMSNQTLVTEFILQGFSEHPEYRVFLFSCF
 LFLYSGALTGNVLITLAITFNPGHLAPMYFFLLNLATMDIICSSIMPKALASLVSEESSISYGGC
 30 MAQLYFLTWAASSELLLTVMAYDRYAAICHPLHYSSMSKVFCSGLATAVWLCAVNTAIH
 TGLMLRLDFCGPNVIIHFFCEVPPLLLSCSSTYVNGVMIVLADAFYGVNFLMTIASYGFIVSSI
 LKVKTAWGRQKAFSTCSSHLLTVCMYYTAVFYAYISPVSGYSAGKSKLAGLLYTVLSPTLNPL
 IYTLRNKEVKAALRKLFPPFRN (SEQ ID NO: 151)

35 ATGAAGCTGTGGATGGAGAGTCACCTGATAGTCCCAGAAACCCGTCAGCCCAAGGATG
 ATGAGTAACCAGACGTTGGTAACCGAGTTCATCTGCAGGGCTTTGGAGCACCCAGAAAT
 ACCGGGTGTTCTTATTCACTGCTGTTCTCTACTCTGGGGCCCTCACAGGTAAATGTC
 CTCATCACCTGGCCATCACGTTCAACCCCTGGGCTCCACGCTCTATGTA
 40 CACTTGGCTACTATGGACATTATCTGCACCTCTCCATGCCAAGGCCTGGCCAGT
 CTGGTGTGGAAAGAGAGCTCCATCTCTCACGGTATGCCCTATGACGGTACGCAGC
 CATCTGCCACCCGCTGCATTACAGCAGCATGAGCAAGGTGTTCTGCAGGGCTGGCC
 ACAGCCGTGTGGCTCTGCACCGTCAACACGCCATCCACACGGGCTGATGCTGCGCT
 TGATTTCTGTGGCCCAATGTCATTATCCATTCTCTGCAGGTCCCTCCCTGTCGCTT
 45 CTCTCCTGCAGCTCCACCTACGTCAACGGTGTATGATTGTCCTGGGGATGCTTCTACG
 GCATAGTGAACCTCTGATGACCATCGCTCTATGGCTCATGTCCTCCAGCATCCTGAA
 GGTGAAGACTGCCTGGGGAGGCAGAAAGCCTCTCCACCTGCTCTCCACCTCACCGTG
 GTGTGCATGTATTACACCGCTGTCTACGCCTACATAAGCCCGGCTCTGGCTACAGCG
 CAGGGAAAGAGCAAGTTGGCTGGCTGCTGTACACTGTGCTGAGTCCTACCCCAACCC
 50 CATCTATACTTGAGAAACAAGGAGGTCAAAGCAGCCCTAGGAAGCTTTCCCTTCTC
 AGAAATTAA (SEQ ID NO: 152)

AOLFR82 sequences:

MQLNNNVTEFILLGLTQDPFWKKIVFVIFRLYLGTLLGNLLIIISVKASQALKNP
 55 SDTCLSTSIAPRMIVDALLKTTISFSECMIQVFSHVFGCLEIFILILTA
 SQWVCGVLMAVA WVGS CVHSLVQI FLALSLPFCGPVNHCFCDLQPLLKQACSETYV
 VVNL

VSNSGAICAVSYVMLIFSYVIFLHSRNHSAEVIKKALSTCVSHIIVVILFFGPCIEMYTCPATVFP
MDKMIAVFYTVGTSFLNPVIYTLKNTEVKSAMRKLWSKKLITDDKR (SEQ ID NO: 153)

5 ATGCAACTGAATAATAATGTGACTGAGTTCATTCTGCTTGATTGACACAGGATCCTTTT
GGAAGAAAATAGTGTGTTATTCTTCTACTTGGAACACTGTTGGTAATT
GCTAATCATTATTAGTGTCAAGGCCAGGCCAGGCACTTAAGAACCAATGTTCTTCTCCCT
TTCTACTTATCTTATCTGATACTTGCCTCTACTTCCATAGCCCCTAGAATGATTGTGGA
TGCCTTGAAGAACAACTATCTCCITCAGCGAGTGCATGATCCAAGTCTTTCATCC
10 CATCTGTAAAGCCCCTGCACTACATGACCATCATAAGCCAGTGGCTGTGGTGTGTTGATG
GCTGTGGCCTGGGTGGGATCCTGTGCATTCTTAGTCAGATTCTTCTGCCTGAGTT
GCCATTCTGTGGCCCCAATGTGATCAATCACTGTGACTTGCAGCAGCCCTGTTGAAA
CAAGCCTGTTCAAGAACCTATGTGGTTAACCTACTCCTGGTTCCAATAGTGGGCCATT
15 GTGCAGTGAGTTATGTCATGCTAATATTCTCCTATGTCATCTTCTGCATTCTGAGAAC
CACAGTGCTGAAGTGATAAAGAACACTTCCACATGTGTCCTCCACATCATTGTGGTCA
TCTTGTCTTGACCTTGCAATTATATGTACACATGCCCTGCAACCGTATTCCCCATGGAT
AAGATGATAGCTGTATTATACAGTGGAACATCTTCTCAACCCGTGATTACACGCT
GAAGAATACAGAAGTGAAGAAGTGCATGAGGAAGCTTGGAGCAAGAAATTGATCACAGA
TGACAAAAGATAA (SEQ ID NO: 154)

20

AOLFR83 sequences:

MGNWTAATVTEFVLLGFSLSREVELLLLVLNLLPTFLTLGNLLIISTVLSCSRLHTPMYFFLCNL
SILDILFTSVISPKVLANLGSRDKTISFAGCITQCYFVFLGTVEFLLTVMWSYDRYATICCPLRYT
25 TIMRPSVCIGTVVFSWVGGFLSVLFPTILISQLPFCGSNIINHFFCDSGPLLALACADTTAIELMDF
MLSSMVILCCIVLVAYSYTYIILTIVRIPSASGRKKAFNTCASHLTIVIIPSGITVFIYVTPSQKEYL
EINKIPLVLSSVVTPLNPFYIYTLRNDTVQGVLRDVVVRVRGVFEKRMRAVLRSLSSNKDHQ
GRACSSPPCVYSVKLQC (SEQ ID NO: 155)

30 ATGGGTAACGGACTGCAGCGGTGACTGAGTTGTTCTGCTGGGTTTCCCTGAGCAGGG
AGGTGGAGCTGCTGCTCCTGGTCTGCCACGTTCTGCTGACTCTCTGGGAA
CCTGCTCATCATCTCCACTGTGCTCTGCTCCCGCTCCACACCCCCATGTACTTCTTCT
TGTGCAACCTCTCATCCTGGACATCCTCTCACCTCAGTCATCTCCAAAGTGTGGCC
AACTTAGGATCTAGGGATAAAACCATCTCCTTGGGATGTATCACCCAGTGTCTATTCT
ACTTTTCTGGGACAGTTGAGTTCTCTGCTGACGGTCACTGCTATGACCGTTATGCC
35 ACCATCTGCTGCCCTGCGGTACACCAACATCATGAGACCTCTGCTGCTTGGGACCG
TTGTATTCTCTGGGAGGGCTTCTGTCTGTCTTCTCAACCCTCTCATCTCCAG
CTGCCCTCTGTGGCTCCAATATCATTAACCACTCTCTGTGACAGTGGACCCCTGCTGGC
CCTGGCCTGTGCAGACACCACTGCCATCGAGCTGATGGATTATGCTTCTCCATGGTC
ATCCTCTGCTGCATAGTCTCGTGGCTATTCTATACGTACATCATCTGACCATAGTGC
40 CATTCTCTGCAAGTGGAGGAAGGAAGGGCTTAAACCTGTGCTTCCCACCTGACCAT
GTCATCATCTAGTGGCATCACTGTGTTATCTATGTGACTCCCTCCCAGAAAGAATATCT
GGAGATCAACAAAGATCCCTGGGCTGAGCAGTGTGGTGAACCTCCTCAACCCCTT
ATATATACTCTGAGGAATGACACAGTGCAGGGAGCCTCAGGGATGTGGTCAGGGTT
45 CGAGGAGTTTGAAGAGGATGAGGGCAGTGTGAGAAGCAGATTACCTCCAACAAA
GACCACCAAGGAAGGGCTGCTCTCTCCACCATGTGCTATTCTGAAAGCTCCAGTGT
AG (SEQ ID NO: 156)

AOLFR85 sequences:

50 MGAKNNVTEVLFGLFESREMQHTCFVVFVFLHVLTVLGNLLVIITINARKTLKSPMYFFLSQL
SFADICYPSTTIPKMIADTFVEHKIISFNGCMTQLFSAHFFGGTEIFLLTAMAYDRYVAICRPLHY
TAIMDCRKCGLLAGASWLAGFLHSILQTLTVQLPFCGPNEIDNFFCDVHPLLKLACADTYMV
GLIVVANSGMISLASFFILISYVILLNRLSQQSEDRRKA VSTCGSHVITVLLVLMPPMFMYIRPS
TTLAADKLIIIFNIVMPPLLNPILYTLRNNNDVKNAMRKLFRVKRSLGEK (SEQ ID NO: 157)

55 ATGGGTGCCAAGAACATGTGACTGAGTTGTTTATITGCCTTTGAGAGCAGAGAGA
TGCAGCATACTGCTTGTGGTATTCTCCTCTTCATGTGCTACTGCTCTGGGAACCTT

5 CTGGTCATCATCACCATCAATGCTAGAAAGACCTGAAAGTCTCCCCTGATTTCTTCTGAGCCAGTTGCTTGTGACATATGTTATCCATCCACTACCATAACCAAGATGATTGCTGACACTTTGTGGAGCATAAGATCATCTCCTCAATGGCTGCATGACCCAGCTCTTCTGCCACTTCTTGGTGGCAGTGGAGATCTTCCTCCTACAGCCATGGCCTATGACCGCTATGTGGCCATCTGTAGGCCCTGCACTACACAGCCATCATGGATTGCCGGAAGTGTGGCCTGCTAGCGGGGCCTCTGGTTAGCTGGCTTCTGCATTCCATCCTGCAGACCCCTCCTCACGGITCAGCTGCCTTTGTGGGCCAATGAGATAGACAACCTCTCTGTGATGTTCATCCCTGCTCAAGTTGGCCTGTGCAGACACCTACATGGTAGGTCTCATCGTGGTGGCAACAGCGGTATGATTCTTGTAGCATCCTTTTATCCTTATCATTCCTATGTTATCATCTTACTGAACCTAACAGCCA10GTCATCTGAGGACCGCGTAAGGCTGCTCCACATGTGGCTCACACGTAATCACTGTCCTTTGTTCTCATGCCCTCATGTTATGTACATTGTCCTCCACCAACCCCTGGCTGCTGACAAACTATCATCCTCTTAAACATTGTGATGCCACCTTGCTGAACCCCTTGATCTACACTAAGAACAAACGATGTGAAAAATGCCATGAGGAAGCTGTTAGGGTCAAGAGGAGCTTAGGGAGAAGTGA (SEQ ID NO: 158)

AOLER86 sequences:

20 MQLVLLLMFLVFIGNTAPAFSVTLESMDIPQNTEFFMLGLSQNSEQRVLVVFLLIYVVTVC
GNMLIVVTITSSPTLASPVYFFLANLSFIDTFYSSSMAPKLIADSLYEGRTISYECCMAQLFGAHF
LGGVEIILLTVMAYDRYVAICKPLHNTTIMTRHLCAMLGVVAWLGGFLHSLVQLLLVLWLPFC
GPNVINHFACDLYPLLEVACTNTYVIGLLVVANSGLICLLNFLMLAASYIVILYSLRSHSADGRG
KALSTCGAHFIVVALFFVPCIFTYVHPFSTLPIDKNMALFYGILTPMLNPLIYTLRNEEVKNAMR
KLFTW (SEQ ID NO: 159)

25 ATGCAATTAGTTCTATTACTTATGTTCTCCITGTCTTTAGGCAACTGCACCTGCATT
CTCAGTGACCTTGGAAATCTATGGACATACCACAAAATATCACAGAATTTCATGCTGGGG
CTCTCACAGAACTCAGAGGTACAGAGAGTTCTTTGCTGATCTATGTGG
TCACGGTTGTGGCAACATGCTCATTGTTGACTATCACCTCCAGCCCCACGCTGGCTTC
CCCTGTGTATTTCCTGGCAACCTATCCTTATTGACACCTTATTCTCTATGGC
30 TCCTAAACTCATTGCTGACTCATTGTATGAGGGGAGAACCATCTCTTATGAGTGCTGCATG
GCTCAGCTTTGGAGCTCATTTTGGGAGGTGTTGAGATCATTCTGCTCACAGTGATGG
CTTATGACCGCTATGTCCTGACAAACTACCATCATGACCAAGGCA
TCTCTGTGCCATGCTGTAGGGTGGCTTGGCTGGGGCTTCCTGCAATTGGITCAG
CTCCTCTGGCCTTGGTGCCTGCCCCCTGTGGCCCAATGTGATCAATCATTGCTGTGA
35 CTTGTACCCCTTGCTGGAAGTTGCCTGCACCAATACGTATGTCATTGGTCTGCTGGTGGTT
GCCAACAGTGGTTAATCTGCCTGTAACCTCCTCATGCTGGCTGCCTCCTACATTGTCAT
CCTGTAACCTCTGAGGGTCCCACAGTGCAGATGGGAGATGCAAAGCCCTCTCCACCTGTGGA
GCCCACTTCATTGTTGCTTGTGCTTGTGCTTGTGACACCTATGTGCAATTGTCATCCATT
TCTACTTACCTATAGACAAAAATATGGCATTATTATGGTATTCTGACACCTATGTGAA
40 TCCACTCATTTACCCCTGAGAAATGAAGAGGTAAAAATGCCATGAGAAAGCTCTTACA
TGGTAA (SEQ ID NO: 160)

AOLFR87 sequences:

45 MNIAQLSLGFIDLGIPSVLQKII LTIIILFKMYVSNCPAIHRKINYPNTKLDFEQVNNTIEFIL
LLGLTQNAEAQKLLFAVFTLIVFLTMVDNLIIVVTITSPALDSPVYFFLSFFSFIGCSSSTMAP
KMIFDLLTEKKTISFSGCMTQLFVEHFFGGVEIILVVMA YDCYVAICKPLYYLITMNRQVCGL
LVAMA WVGGFLHALIQMLLIVWLPFCGPVIDHFICDLFPLLKLSCTDTHVFLGFVAANSGLM
CMLIFSILITSYVLILCSQRKALSTCAFHITVVVLFFVPCILVYLRPMITFPIDKAVSVFYTVVTPM
LNPLIYTLRNTEVKNAMQQLWSQITWGNLCD (SEQ ID NO: 161)

50 ATGAATAACATAGCTCAACTTAGTCTGGGTTATAGATTAGGGATTCCATCAGTGTAC
AGAAAATAATCCTGACCAAAATTATTTATTGTCAAAATGTATGTGTCAAATTGCAATCC
TTGTGCTATTACAGAAAAATCAATTATCCAAATACCAAACGGATTTCGAGCAAGTGAAC
AACATAACGGAATTCATCTTGCTTGGCTGACACAGAACGAGAGGCACAGAAACTCTTGT
TTGCTGTGTTACACTCATCTACTTCTCACCATGGTAGACAACCTAATCATTGTGGTGACA
55 ATCACCACCAGCCCAGCCCTGGACTCCCCCGTGTATTTTTCTGTCITTCITTCCTTCAT
AGATGGCTGCTCCTCTTCTACCATGGCCCCAAAATGATATITGACTTACTCACTGAAAAG

AAAACTATTCCCTCAGTGGGTGCATGACCCAGCTTGTAGAACATTCTTGGGGAG
 TTGAGATCATTCTGCTCGTGGTATGGCCTATGACTGCTATGTGGCCATCTGCAAGCCCC
 5 GTACTACCTGATCACAAATGAACAGGCAGGTATGTGGCCTCTGGTGGCCATGGCATGGTC
 GGGGATTCTTCACGCTCTGATTCAAATGCTTTAATAGTCTGGCTGCCCTCTGTGGCC
 CAATGTCATTGCACCATTCATCTGTGACCTTTCCCTCTGCTAAAACCTCCTGCACGTGACA
 10 CTCACGTCTTGGACTCTTGTGCCAACAGTGGGCTATGTGTATGCTCATTTTCT
 ATTCTTATTACCTCTACGTCTAACAGCCTGCTCACAGCGGAAGGCTCTCTACCTGCGC
 CTTCCATATCACTGTAGTCGTCTATTCTTGTCTGCCGTATATTGGTGTACCTCGACCCA
 TGATCACCTCCATTGATAAAAGCTGTGTCTGTGTTTATACTGTGTAACACCCATGTTA
 AACCCCTTAATCTACACCCCTAGAAACACAGAGGTGAAAATGCCATGAAGCAGCTCTGG
 AGCCAAATAATCTGGGTAACAATTGTGTGATTAG (SEQ ID NO: 162)

AOLFR88 sequences:

MWQKNQTSLADFILEGLFDDSLTHLFLFSLTMVFLIAVSGNTLTILLICIDPQLHTPMYFLLSQ
 15 LSLMDLMHVSTIILKMATNYLSGKKSISFVGCAQHFLYLCAGGAECFLLAVMSYDRYVAICH
 PLRYAVLMNKKVGLMMAVMSWLGAVNSLIHMAILMHFPFCGPRKVYHFYCEFPVVKLV
 GDITVYETTVYISSILLLPFLISTSYVFLQSVIQMRSRGSKRNAFATCGSHLTVVSLWF
 GACIFS YMRPRSQCTLLQNKVGSVFYSIITPTLNSLIYTLRNKDVAKALRRVLRRDV
 20 ITQCIQLQLWLP RV (SEQ ID NO: 163)

ATGTGGCAGAAGAACATCAGACCTCTGGCAGACTTCATCCTTGAGGGGCTTCGATGACT
 CCCTTACCCACCTTTCTCTTCTGACCATGGTGGTCTTCCTTATTGCGGTGAGTGGC
 AACACCCCTCACCAATTCTCCTCATCTGCATTGATCCCCAGCTTCATACACCAATGTATT
 25 CTCAGGCCAGCTCTCCCTATGGATCTGATGATGCTCCACAATCATCCTGAAGATGGC
 ACCAAACTACCTATCTGGCAAGAAATCTATCTCCTTGAGGGCTGTGCAACCCAGCACT
 TCTATTGTGTCTAGGTGGTCTGAATGTTTCTCTAGCTGTCTATGACCGCTAT
 GTGCCATCTGTCTGCCACTGCGCTATGCTGTGCTCATGAACAAAGAAGGTGGGACTGATGA
 TGGCTGTCTGTCTGGTGGGACTCCGTGAACCTCCCTAATTGACATGGCATTGAT
 30 GCACTTCCCTTCTGTGGGCTCGGAAGTCTACCAACTTCTACTGTGAGTTCCAGCTGTG
 TGAAGTTGGTATGTGGCAGCATCACTGTGTATGAGACCACAGTGTACATCAGCAGCATT
 CCTCCCTCTCCCCATCTCCTGATTCTACATCCTATGTCCTCATCCTCAAAGTGTCA
 35 GATGCGCTCATCTGGAGCAAGAGAAATGCCCTTGCCACTGTGGCTCCACCTCACGGTG
 GTTCTCTTGGTTGGCTGCTGATCTCTCATGAGACCCAGGTCCCAGTGCAC
 ATTGCGAACAAAGTGGTCTGTGTTACAGCATCATTAGCCCACATTGAATTCTCTG
 ATTATACCTCCGGAATAAAGATGTAGCTAAGGCTCTGAGAAGAGTGCTGAGGAGAGAT
 GTTATCACCCAGTGCATTCAACGACTGCAATTGTGGTGGCCCGAGTGTAG (SEQ ID NO:
 164)

AOLFR89 sequences:
 40 MLDPSISSHTLYLHSFPQGLRKGTMWQKNQTSLADFILEGLFDDSLTHLFLFSLTMVFLIAVS
 GNTLTILLICIDPQLHTPMYFLLSQLSLMDLMHVSTIILKMATNYLSGKKSISFVGCAQHFLY
 CLGGAECFLLAVMSYDRYVAICHPLRYAVLMNKKVGLMMAVMSWLGAVNSLIHMAILMH
 PFCGPRKVYHFYCEFPVVKLVCGDITVYETTVYISSILLLPFLISTSYVFLQSVIQMRS
 GSKRNAFATCGSHLTVVSLWF
 45 GACIFS YMRPRSQCTLLQNKVGSVFYSIITPTLNSLIYTLRNKDVA
 KALRRVLRRDVITQCIQLQLWLP RV (SEQ ID NO: 165)

ATGCTGGACCCAGTATTCCAGTCACACTCTTATCTCCACTCTCTGTTCTCAGGGATT
 GAGAAAGGGACAATGTGGCAGAAGAACATCAGACCTCTGGCAGACTTCATCCTGAGGG
 50 GCTCTCGATGACTCCCTACCCACCTTTCTCTGACCATGGTGGTCTTCCTTAT
 TGCGGTGAGTGGCAACACCCCTACCAATTCTCCTCATCTGCATTGATCCCCAGCTTCATACA
 CCAATGTATTCTGCTCAGCCAGCTCTCCCTCATGGATCTGATGCTGTCTCCACAACCAT
 CCTGAAGATGGCTACCAACTACCTATCTGGCAAGAAATCTATCTCCTTGAGGGCTGTG
 ACCCAGCACTCCTCATTTGTGTCTAGGTGGTCTGAATGTTTCTCTAGCTGTCTG
 CTATGACCGCTATGTGCTCATCCACTGCGCTATGCTGTGCTCATGAACAAAGAAG
 GTGGGACTGATGATGGCTGTCTGATGGTGGCTCATGGTGGGGCATCCGTGA
 55 ACTCCCTAATTCAACAGCAGTCTACCACTTCTACTGTGA
 TGGCGATCTTGTGCACTTCCCTTCTGTGGCCTCGGAAAGTCTACCACTTCTACTGTGA

5 GTTCCCAGCTGTTGAAGTTGGTATGTGGCAGACACTGTTATGAGACACCAGTGTAC
 ATCAGCAGCATTCTCCTCCTCCCCATCTTCCTGATTCTACATCCTATGTCCTCATCCTT
 CAAAGTGTCAATTCAAGATGCGCTCATCTGGGAGCAAGAGAAAATGCCTTGCACATTGTGGCT
 CCCACCTCACGGTGGTTCTCTTGGTTGGTGCATCTCTCCATGAGACCCAGG
 10 5 TCCCAGTGCACCTATTGAGAACAAAGTTGGTCTGTGTCTACAGCATCAITACGCCA
 CATTGAATTCTCTGATTATACTCTCCGAATAAAAGATGTAGCTAAGGCTCTGAGAAGAGT
 GCTGAGGAGAGATGTTATCACCCAGTGCATTCAACGACTGCAATTGTGGTTGCCCGAGTG
 TAG (SEQ ID NO: 166)

10 **AOLFR90 sequences:**

15 MFSMTTEALNNFALGCTNLLMTMIPQIDLKQIFLCPNCRLYMIPVGAFIFSLGNMQNSFVTEF
 VLLGLSQNPNVQEVFVVFVFLFVYIAVGNNMLIVVTILSSPALLVSPMYFFLGFLSFLDACFSSVI
 TPKMIVDSDLVVTKTISFEGCMMQLFAEHFFAGVEVIVLTAMAYDRYVAICKPLHYSSIMNRL
 20 CGILMGVAWTGGLLHSMIQILFTFQLPFCGPNVINHFMCDLYPLLEACTDTHIFGLMVVINSG
 FICIINFSLLLVSYAVILLSRTHSSEGRWKALSTCGSHIAVVIFFVPCIFVYTRPPSAFSLDKMA
 AIFYIILNPLLNPLIYTFRNKEVKQAMRRIWNLMMVSDEKENIKL (SEQ ID NO: 167)

25 ATGTTCTCAATGACAACAGAACACTCAATAATTTCGACTTGGATGTACCAACTTGTAA
 TGACTATGATACCACAAATTGATCTGAAGCAAATTTCCTTGTCTTAATTGAGACTATA
 30 CATGATCCCTGTTGGAGCTTCATCTTCCTGGAAACATGCAAACAAACAAAGCTTGTAA
 ACTGAGTTGTCCTCCTGGACTTCACAGAAATCCAATGTTAGGAAATAGTATTGTTG
 TATTTTGTCTGTCTACATTGCAACTGTTGGGGCAACATGCTAATTGTTAGTAACCATTCTC
 AGCAGCCCTGCTCTCTGGTGTCTCTAATGACTTTCTTGGCTTCTGTCTTCTGGA
 TCGTGTCTCTCATCTGTCACTACCCAAAGATGATTGAGACTCCCTCTATGTAACAAAA
 35 ACCATCTCTTGAAAGGCTGCATGATGCAAGCTTTGCTGAACACTCTTGTCTGGGGTGG
 AGGTGATTGTCCTCACAGCCATGGCCTATGATCGTTATGTCAGCTGGCATTGCAAGCCCTTGCA
 TTACTCTCTATCATGAACAGGAGGCTGTGGCATTCTGATGGGGTAGCCTGGACAGGG
 GGCCTCTTGCAATTCCATGATAAAATTCTTTACTTCCAGCTCCCTTTGTGGCCCCAA
 TGTCTCAATCACTTATGTTGACTTGTACCTGGTTACTGGAGCTTGCCTGCACTGATAACTC
 40 ACATCTTGGCCTCATGGTGGTCATCAACAGTGGGTTATCTGCATCATAAACITCTCCTG
 TTGCTTGTCTCTATGCTGTCACTTGCTCTCTGAGAACACACAGTTCTGAAGGGCGCTG
 GAAAGCTCTCCACCTGTGGATCTCACATTGCTGTTGTGATTGTCTTGTCCCAGTCA
 TATTTGTATATACACGACCTCATCTGTTCTGACAAAATGGCGGAATATTAT
 45 ATCATCTTAAATCCCTGCTCAATCCTTGATTTACACTTCACTGAGGAAATAAGGAAGTAAAC
 AGGCCATGAGGAGAATATGGAACAGACTGATGGTGGTTCTGATGAGAAAGAAAATATTA
 AACTTAA (SEQ ID NO: 168)

AOLFR91 sequences:

50 MGNWSTVTEITLIAFPALLEIRISLFLVVLVVTYTLTATGNITIISLIWIDHRLQTPMYFFLSNLSFL
 DILYTTVITPKLLAACLGEEKTFISFAGCMIQTYFYFFLGTVEFILLA VMSFDRYMAICDPLHYTVI
 MNSRACLLVLCWVGAFLSVLFPTIVVTRLPYCRKEINHFFCDIAPLLQVACINTHLIEKINFLL
 SALVILSSLAFTTGSYVYIISTILRIPSTQGRQKAFSTCASHITVVSIAHGSNIFVYVRPNQNSSL
 YDKVAAVLITVVTPLNPFYSLRNEKVQEVLRETVNRIMTLIQRKT (SEQ ID NO: 169)

55 45 ATGGGAAACTGGAGCACTGTAAGTAAATCACCCCTAATTGCCCTCCAGCTCCGGAGA
 TTGGAATATCTCTCTCGTGGTTCTGTGGTAACCTACACATTAACAGCAACAGGAAACAT
 CACCATCATCTCCCTGATATGGATTGATCATCGCCTGCAAACCTCAATGTTACTCTCTCA
 GTAAATTGTCCTTCTGGATATCTTATACACCACTGTCATTACCCAAAGTTGTTGCCCTGC
 CTCCTAGGAGAAGAGAAAACCATATCTTGTGGTTGCATGATCAAACATATTCTACT
 TCTTCTGGGACGGTGGAGTTATCCTCTTGGCGGTGATGTCCTTGACCGCTACATGGC
 TATCTCGGACCCACTGCACTACACGGTCATCATGAACAGCAGGGCCTGCCCTGCTGGTT
 CTGGGATGCTGGTGGAGCCTCCTGCTGTTGATGTCCTTGACATTGCCCCTCTTCAGGGC
 TACCTTACTGTAGGAAAGAAAATTATCATTTCTCTGTGACATTGCCCCTCTTCAGGGC
 GCTGTATAAAATACTCACCTCATTGAGAAAGATAAACTTCTCTCTGCCCCTGTCATCCT
 GAGCTCCCTGGCATTCACTACTGGTCCTACGTGTACATAATTCTACCATCCTCGTATCC
 CCTCCACCCAGGGCGTCAGAAAGCTTCTACCTGTGCTTCACATCACTGTTGTCTCC

ATTGCCACGGGAGCAACATCTTGTATGTGAGACCCAATCAGAACTCCTCACTGGATT
 ATGACAAGGTGGCCGCTGCCTCATCACAGTGGTGAACCCCTCTCTGAACCTTTATCTA
 CAGCTTGAGGAATGAGAAGGTACAGGAAGTGTGAGAGAGACAGTGAACAGAATCATGAC
 CTGATACAAAGGAAAACCTGA (SEQ ID NO: 170)

5

AOLFR92 sequences:

MRNGTVITEFILLGFPIQQLQTPLFIAIFLTYILLAGNGLIATVWAEPRLQIPMYFFLCNLSFLE
 IWYTTIVIPKLLGTFVARTVICMSCLLQAFFHFFVGTTFLITMSFDRYLTCNPLHHPTIM
 10 TSKLCLQLALSSWVVGFTIVFCQTMILLQLPFCGNVNISHFYCDVGPSSLKACIDTSILELLGVIA
 TILVPGSLLFNMSIYIYILSAILRIPSATGHQKTFSTCASHLTVVSLLYGAVLFMYLRPTAHSSFK
 INKVSVLNTILTPLLNPFIYTIRNKEVKGALRKAMCPKTGHAK (SEQ ID NO: 171)

15 ATGAGAAATGGCACAGTAATCACAGAAATTCTCATCCTGCTAGGCTTCCTGTTATCCAAGGCC
 TACAAACACCTCTCTTATTGCAATCTTCTCACCTACATATTAACCCCTGCAGGCAATGGG
 CTTATTATTGCCACTGTGTGGCTGAGCCCCAGGGTACAAATTCCAATGTACTTCTTCCTTGT
 TAACATTGTCTTCITAGAAATCTGGTACACCACAGTCATCCCCAAACTGCTAGGAACC
 TTTGTAGTGGCAAGAACAGTAATCTGCATGTCCTGCTGCAGGCCCTCTTCCACT
 TCTCGTGGGCACCACCGAGTTCTGATCCTACTATCATGTCCTTGACCGCTACCTCAC
 20 ATCTGCAATCCCCCTCACCAACCCCCACCATCATGACCAAGCAAACCTGCTGCAGCTGGCC
 TGAGCTCTGGTGGCTTACCAATTGTCATTGTCAGACGATGCTGCTCATCCAGTT
 GCCATTCTGTGGCAATAATGTTATCAGTCATTCTACTGTGATGTTGGGCCAGTTGAAA
 GCCGCCTGCATAGACACCCAGCATTTGAACTCCTGGCGTCATAGCAACCATCCTGTGA
 TCCCAGGGTCACTTCTCTTAAATATGATTCTTATATCTACATTCTGTCGCACCTGACAGTTGT
 25 ATTCCTTCAGCCACTGGCCACCAAAAGACTTCTACCTGTGCTGCCTCGCACCTGACAGTTGT
 CTCCCTGCTCTACGGGGCTGTTCTGTCATGTACCTAAGACCCACAGCACACTCCTCCTTA
 AGATTAATAAGGTGGTGTCTGTGCTAAATACTATCCTCACCCCCCTCTGAATCCCTTATT
 TATACTATTAGAAACAAGGAGGTGAAGGGAGCCTAAGAAAGGCAATGACTTGCCCAAAG
 ACTGGTCATGCAAAGTAA (SEQ ID NO: 172)

AOLFR93 sequences:

30 MLMNYSSATEFYLLGFPGSEELHHILFAIFFFFYLVTLMGNTVIIIMIVCVVDKRLQSPMYFFLGHL
 SALEILVTTIIPVVMLWGLLPGMQTIYLSACVVQLFLYLAvgTTEFALLGAMAVDRYVAVCN
 PLRYNIIMNRHTCNFVVLVSWVFGFLQIWPVYVMFQLTYCKSNVNNFFCDRGQLLKSNCN
 35 NTLFTEFILFLMAVFVLFGLIPTIVSNAYIISTILKIPSSSGRRKSFSTCASHFTCVVIGYGSCLFLY
 VKPKQTQAADYNWVVSMLVSVTPFLNPFIITLRNDKVIEALRDGVKRCCQLFRN (SEQ ID
 NO: 173)

40 ATGTTGATGAATTACTCTAGTGCCTGAATTCTCATCCTTGTCTATATTCTCTGGCTCCCTGGCTCTGAAGA
 ACTACATCATATCCTTTGTCTATATTCTCTTCTACTTGCTGACATTAAATGGGAAACA
 CAGTCATCATCATGATTGTCTGTGGATAAACGCTGCAAGTCCCCATGTATTCTCCTC
 GCCCACCTCTGCCCTGGAGATCTGGTCACAACCATATCGTCCCCGTGATGCTTGGG
 GATTGCTGCTCCCTGGGATGCGAGACAATATATTGCTGCTGTGTTGTCAGCTCTTCTG
 TACCTTGCTGTGGGACAACAGAGTTCGCATTACTTGAGCAATGGCTGTGGACCGTTATG
 TGGCTGCTGTAAACCTCTGAGGTACAACATCATTATGAACAGACACACACTGCAACTTTGT
 45 GGTTCTTGTGTCATGGGTGTTGGTTCTTCTCAAATCTGGCCGGTCTATGTCATGTTTC
 AGCTTACTTACTGCAAATCAAATGTGGTGAACAATTCTTGTGACCGAGGGCAATTGCT
 CAAACTATCCTGCAATAATACTCTTCTACGGAGTTATCCTCTTCTAAATGGCTGTTTG
 TTCTCTTGGTTCTTGTACCCCTACAATTGTCCTAACGCTACATCATCTCCACCATCTC
 AAGATCCCGTCATCCTCTGGCCGGAGGAATCTTCTCCACTTGTGCTCTCCACTTCACTG
 50 TGTTGTGATTGGCTACGGCAGCTGCTGTGTTCTACGTGAAACCCAAGCAAACGCGAGGCA
 GCTGATTACAATTGGTAGTTCCCTGATGGTTCACTGAGTAACCTCTTCTCAATCTT
 CATCTTCACCCCTCGGAATGATAAAGTCATAGAGGCCCTCGGGATGGGGTGAAACGCTGC
 TGTCAACTATTAGGAATTAG (SEQ ID NO: 174)

AOLFR94 sequences:

METWVNQSYTDGFFLLGIFSHSTADLVLFSVVAVFTVALCGNVLLIFLIYMDPHLHTPMYFF
 LSQLSLMDLMLVCTNPKMAANFLSGRKSISFVGCGIQIGLFVCLVGSEGLLGLMAYDRYVA
 ISHPLHYPILMNQRVCLQTGSSWAFGIIDGLIQMVMVVMNFPYCGLRKVNHFFCEMLSLLKAC
 5 VDTSLFEKVIFACCVFMLLFPFSIIVASYAHILGTVLQMHSQAQAWKKALATCSSHLTAVTLYG
 AAMFIYLRRPRHYRAPSHDKVASIFYVLTPLMLNPLIYSLRNREVMGALRKGLDRCRIGSQH
 (SEQ ID NO: 175)

10 ATGGAGACGTGGGTGAACCAGTCCTACACAGATGGCTTCCCTTACAGTGGCCCTCTGT
 ACAGTACTGCTGACCTTGTCCCTCTCCGTGGTTATGGCGGTCTTCACAGTGGCCCTCTGT
 GGGATGTCCCTCTCATCTTCCCTACATCTACATGGACCCCTACCTCACACCCCCATGTACTT
 CTTCCCTCAGCCAGCTCTCCCTCATGGACCTCATGGTGGCTGTACCAATGTGCCAAAGATG
 GCAGCCAACCTCCTGTCTGGCAGGAAGTCCATCTCCCTTGCTGGGCTGTGGCATACAAATTG
 15 GCCTCTTGCTGTCTTGCTGGGATCTGAGGGGCTCTGCTGGACTCATGGCTTATGACCG
 CTATGTGGCCATTAGCCACCCACTCACTATCCCATCCTCATGAATCAGAGGGCTGTCTCC
 AGATTACTGGGAGCTCCTGGCCTTGGGATAATCGATGGCTTGATCCAGATGGTGGTAGT
 AATGAATTCCCCTACTGTGGCTTGAGGAAGGTGAACCATTCTCTGTGAGATGCTATCC
 TTGTTGAAGCTGGCTGTGTAGACACATCCCTGTTGAGAAGGTGATATTGCTTGTGTG
 20 TCTTCATGCTTCTCTCCCATTCTCCATCATGTGGCCTCTATGCTCACATTCTAGGGACT
 GTGCTGAAATGCACTCTGCTCAGGCCTGGAAAAAGGCCCTGGCACCTGCTCCTCCACC
 TGACAGCTGTCAACCTCTTCTATGGGCAGCCATGTTCATCTACCTGAGGCCTAGGCACTA
 CCGGGCCCCCAGCCATGACAAGGTGGCCTCTATCTTCTACACGGCTCTACTCCATGCTC
 AACCCCTCATTTACAGCTTGAGGAACAGGGAGGTGATGGGGCACTGAGGAAGGGCTG
 GACCGCTGCAGGATCGGCAGCCAGCACTGA (SEQ ID NO: 176)

25

AOLFR95 sequences:

MLGSKPRVHLYLPCASQQVSTMGDRGTSNHSEMTDFILAGRVRPELHILLFLFLFVYAMILL
 GNVGMMTIIMTDPLNTPMYFLGNLSFDLFYSSVIEPKAMINFWSNKISFAGCVAQLFLFA
 30 LLIVTEGFLLAAMAYDRFIAICNPLLYSVQMSTRLQLVAGSYFCGCISSVIQTSMTFTLSFCAS
 RAVDHFYCDSRPLQRLSCSDLFIHRMISFSLSCIIILPTIIIVSYMYIVSTVLKIHSTEGHKKAFST
 CSSHLGVSVLYGAFFMYLTPDRFPELSKVASLCYSLVTPMLNPLIYSLRNKDQVQEAALKFLE
 KKNIIL (SEQ ID NO: 177)

35

ATGCTAGGATCCAAACCAAGAGTCATTGTATATTTGCCCTGTGCCCTCTCAACAGGTTTC
 TACCATGGGTGACAGGGGAACAAGCAACTCACTCAGAAATGACTGACTTCATTCTGCAGG
 CTTCAAGGGTACGCCAGAGCTCCACATTCTCTCTGCATTGTTGTTATGCCA
 TGATCCTCTAGGAAATGTTGGATGATGACCATTATTATGACTGATCCTCGGCTGAACAC
 ACCAATGTATTCTCTAGGAAATCTCTCTGCATTGATCTTCTATTCTCATCTGTTATTGA
 ACCCAAGGCTATGATCAACTCTGGCTGAAAACAAGTCTATCTCCTTGCAAGGCTGTGTG
 40 GCCCAGCTTTCTCTTGCCTCTGCCTCTGCATTGACTGAGGGATTCTCTCTGGCGGCCATGGC
 TTATGACCGCTTATGCCATCTGCAACCTCTGCTCTACTCTGTTCAAATGTCCACACGTC
 TGTGTACTCAGTTGGCTGTTCTATTGTTGCTGCATTAGCTCAGTTATTGAGACT
 AGCATGACATTACTTATCTTTGCGCTCTCGGGCTGTGACCACCTTACTGTGATTC
 TCGCCCACTTCAGAGACTGTCTGTTCTGATCTCTTATCCATAGAATGATATCTTCT
 45 TATCATGTATTATTATCTTGCTACTATCATAGTCATTAGTATCTTACATGTATATTGTG
 TCCACAGTTCTAAAGATACATTCTACTGAGGGACATAAGAAGGCCTCTCACCTGCAGCT
 CTCACCTGGGAGTTGTGAGTGTGCTGTATGGTGTCTTTATGTATCTCACTCCTGAC
 AGATTCTGAGCTGAGTAAAGTGGCATCCTTATGTTACTCCCTAGTCACTCCATGTTGA
 ATCCTTGATTTACTCTGAGGAACAAAGATGTCCAAGAGGCTCTAAAAAAATTCTAGA
 50 GAAGAAAAATTATTCTTG (SEQ ID NO: 178)

AOLFR96 sequences:

MICENHTRVTEFILLGFTNNPEMQVSLFIFLAIYTVTLLGNFLIVTVTSVDLALQTPMYFFLQN
 LSLLEVCFILVMVPKMLVLDLVSPrKIIISFVGCGTQMYFFFFFGSSECFLSMMAYDRFVAICNP
 55 LHYSVIMNRSLCLWMAIGSWMSGVPVSMLQTAWMMALPFCGPNAVDHFFCDGPPVLKLVTV
 DTTMYEMQALASTLLFIMFPFCLILVSYTRIIILRMSSATGRQKAFSTCSSHLIVVSLFYGTASL

TYLRPKSNQSPESKKLVSLSYTVITPMLNPIIYGLRNNEVKGAVKRTITQKVQLQKLDVF (SEQ ID NO: 179)

5 ATGATCTGTGAAAATCACACCAAGAGTCACTGAATTATTCTTCTTGGTTTACAAACAAACC
 CCGAGATGCAAGTTCCCTCTTATTCTTCTGCCATTATACAGTCACCTTGTGGC
 AACTTCTTATTGTACAGTTACAGTGTGGATCTGCACCTCAAACACCCATGTACTTCTT
 TCTTCAAAATCTGTCACTTCTGAAGTATGTTCACCTGGTTATGGTGC
 TAGATCTAGTGTCCCCAAGGAAATTATCTCTTGTGGCTGTGGTACCCAGATGTACTT
 CTTCTCTTCTTGGCAGITCTGAATGTTCTCTCCATGATGGCTTATGATCGCTTGT
 10 GCCATCTGTAACCCCTCCATTATTCACTGATAATGAACAGGTCCCTATGCTTGTGGATG
 GCCATAGGCTCTGGATGTCGGTGTCTGTCTATGCTACAGACAGCTGGATGATGG
 CCCTCCTTCTGTGGACCAAATGCCGTGGACCACTTTCTGTGATGGTCCCCAGTGT
 AAACTAGTCACAGTGGATACAACCATGTATGAAATGCAAGCACTGCCTCCACACTCCTG
 TTATCATGTTCCCTTGTCTCATTTGGTTCCACACCCGATTATCATAACAATTCTG
 15 AGGATGTCCTCTGCCACTGGCCAGAAGGCATTCTACTTGTCTCACACCTCATTGT
 GGTGTCCTCTTCTACGGAACAGCCAGTGTGACCTACCTGGCCAAATCAAACCAAGTCC
 CCTGAGAGCAAGAAGCTAGTGTCAATTGCTACACTGTCAACACCTATGCTAAACCCCA
 TCATCTACGGCCTGAGGAACATGAAGTGAAAGGGCTGTCAAGAGGACAATCACTAAA
 AAGTCTTACAGAAGTTAGATGTGTTTGA (SEQ ID NO: 180)

20

AOLFR97 sequences:

MTEFHLQSQMP SIRLIFRRLSLGRIKPSQSPRCSTS FMV VPSFSIAEH WRRMKGANLSQGMFEL
 LGLTTDPQLQRLLFVFLGMYTATLLGNLVMFLLIIVSATLHTPMYSLLKSLSLDFCYSSTVV
 25 PQTLVNF LAKRKVISYFGCMTQMFFYAGFATSECYLIAAMA YDRYAAICNPLLYSTIMSPEVC
 ASLIVGSYSAGFLNSLIHTGCIFSLKFCGAHVTHFFCDGPPILSLCVDTSLCEILLFIFAGFNLLS
 CTLTILISYFLILNTILKMSA QGRFKAFSTCASHLTAICLFFGTTLFM YLRRPRSSYSLTQDRTVA
 VIYTVVIPVLPNPLMYSLRN KDVKKALIKVWGRKTME (SEQ ID NO: 181)

30 ATGACAGAGTTTCACTGCAAAGCCAAATGCCCTCAATAAGACTCATCTT CAGAAGGCTGT
 CCTTAGGCAGAAATTAAACCCAGTCAGAGCCCCAGGTGTTCAACCTCATTATGGTGGTGC
 TTCTTCTCCATCGCAGAGCACTGGAGAAGGATGAAAGGGCAAACCTGAGCCAAGGGAT
 GGAGTTTGA GCTCTGGGCTCACC ACTGACCC CAGCTCCAGAGGCTGCTCTCGTGGT
 TTCCCTGGGCA TGTACACAGCCACTCTGCTGGGAACCTGGTCA TGTCTCTGATCCATG
 TGAGTGC CACACACCCATGTACTCCCTCTGAAGAGCCTCTCTTGGATTTC
 35 TGCTACTCCTCCACGGTTGTGCCAGACCCCTGGTGAACTCTTGGCCAAGAGGAAAGTGA
 TCTCTTATTGGCTGCATGACTCAGATGTTCTATGCGGGTTTGCCACCA GTGAGTGC
 TATCTCATCGCTGCCATGGCCTATGACCGCTATGCCGCTATTGTAACCCCTGCTCTACTC
 AACCATCATGTCCTGAGGTCTGTGCCTCGCTGATTGTGGCTCCTACAGTGCAGGATTC
 CTCAATTCTTTATCCACACTGGCTGTATCTTAGTCTGA AATTCTGCGGTGCTCATGTC
 40 CACTCACTCTCTGTGATGGGCCACCCATCCTGCTTGTGTAGACACACTCACTGT
 GTGAGATCCTGCTCTCATTTGCTGGTTCAACCTTTGAGCTGCACCCCTCACCCT
 ATCTCCTACTTCTTAATTCTAACACCATCCTGAAAATGAGCTGGCCAGGGCAGGTTA
 AGGCATTTCACCTGTGCATCCCACCTCACTGCCATCTGCTCTTGGCACAACACTT
 45 TTTATGTACCTGCGCCCCAGGTCCAGCTACTCCTGACCCAGGACCGCACAGTTGCTGTCA
 TCTACACAGTGGTATCCCAGTGTGAACCCCTCATGTACTTTGAGAAACAAGGATGT
 GAAGAAAGCTTAATAAAAGGTTGGGGTAGGAAAACAATGGAATGA (SEQ ID NO: 182)

AOLFR98 sequences:

50 MRGFNKT TVVTQFILVGFSSLGELQLLLFI LYLTLVANVTIMA VIRFSWTLHTPM YGFLFI
 LSFSECYTFVIIPQLLVHLLSDTKTISFMACATQLFFLGFACTNCLLIAVMGYDRYVAICHPLR
 YTLLINKRLGLELISLSGATGFFIALVATNLICDMRFCGPNRVNHYFCDMAPVIKLA
 CTDTHVKE LALFSLSLVIMVPFLILISYGFIVNTILKIPSAEGKKAFVTCASHLT
 VVVFHYGCASIYLRPKSK SASDKDQLVAVTYTVVTPLLNPLVYSLRNKEVK
 TALKRVLGMPVATKMS (SEQ ID NO: 183)

55 ATGCGAGGTTCAACAAAACCACTGTGGTACACAGTTCACTCTGGTGGGTTCTCCAGCC
 TGGGGGAGCTCCAGCTGCTGCTTTGTCACTTTCTCTCTTACACTGACAATCCTGGTG

5 GCCAATGTGACCATCATGGCCGTTATCGCTTCAGCTGGACTCTCACACTCCCATGTATG
 GCTTTCTATTCTCATCCCTTCATTTCTGAGTCCTGCTACACTTTGTCATCATCCCTCAGCTGC
 TGGTCCACCTGCTCTCAGACACCAAGACCATCTCCTCATGGCCTGTGCCACCCAGCTGTT
 CTTTTCCCTGGCTTGTGCTGCACCAACTGCCTCCTCATTGCTGTGATGGGATATGATCGCT
 10 5 ATCTAGCAATTGTGACCCCTGAGGTACACACTCATCAAACAAAAGGCTGGGTTGGA
 GTTGATTCTCTCTCAGGAGCCACAGGTTCTTATTGCTTGGTGGCCACCAACCTCATTT
 GTGACATGCGTTTGTGGCCCAACAGGGTAACCACTATTCTGTGACATGGCACCTGT
 TATCAAGTTAGCCTGCACTGACACCCATGTGAAAGAGCTGGCTTATTAGCCTCAGCATC
 CTGGAATTATGGTGCCTTCTGTAATTCTCATATCCTATGGCTCATAGTTAACACCAT
 15 10 CCTGAAGATCCCCTCAGCTGAGGGCAAGAAGGCCTTGTACCTGTGCCACATCTCACT
 GTGGTCTTGTCCACTATGGCTGTGCCCTATCATCTATCGCGGCCAAGTCCAAGTCTGC
 CTCAGACAAGGATCAGTGGTGGCAGTGACCTACACAGTGGTTACTCCCTACTTAATCCT
 CTTGTCTACAGTCTGAGGAACAAAGAGGTAAGACTGATTGAAAAGAGTTCTTGGAAATG
 CCTGTGGCAACCAAGATGAGCTAA (SEQ ID NO: 184)

15 **AOLFR99 sequences:**

20 MERVNETVVREVIFLGSSLARLQQLLFVIFLLYLFTLGTNAIIISTIVLDRALHIPMYFFLAILSC
 SEICYTFIIVPKMLV DLLSQKKTISFLGCAIQMFSFLGCSHSFLAVMGYDRYIAICNPLRYSV
 LMGHGVCMGLVAAACACGFTVAQIITSLVFHLFYSSNQLHFFCDIAPV LKLA SHHHNHSQIV
 25 IFMLCTLVLAIPLLLILVSYVHILSAILQFPSTLGRCKAFSTCVSHLIIVTVHYGCASIFIYLRPQSNY
 SSSQDALISVSYTIIPLFNPMTYSLRNKEFKSALCKIVRRTISLL (SEQ ID NO: 185)

30 ATGGAGCGGGTCAATGAGACTGTGGT GAGAGAGGGTACATCITCCTCGGCTTCTCATCCCTGG
 CCAGGCTGCAGCAGCTGCTTTGTTATCTCCTGCTCTGACAGGGCCCTTCATATCCCATGTA
 35 25 AATGCAATCATCATTCCACCATTGCTCTGAGATTGCTACACCTTCATCATTGTA
 CCCCAGATGCTGGTTGACCTGCTTCTGCTGGCAGTCATGGGTTATGATCGTTACAT
 AGCCATCTGTAACCCACTCGCCTACTCAGT GCTAATGGGACATGGGGTGTGATGGGACTA
 40 30 GTGGCTGCTGCCTGCTGGCTTCACTGTTGCA CAGATCATCACATCCTTGGTATTCA
 CCTGCCTTTTATCTCCAATCAACTACATCACCTCTCTGACATTGCTCCTGTCC
 AGCTGGCATCTCACCATAACCACTTGTGACATTGCTACATGCTCTGTACATTGTC
 45 35 CTGGCTATCCCTATTGTTGATCTGGTGTCCATGTTCACATCCTCTGTGCC
 ACTTCA GTTCCTTCCACACTGGTAGGTGCAAAGCTTTCTACCTGTGATCTCACCTCATTATTG
 TCACTGICCACTATGGCTGTGCCCTTATCTACTTAAGGCCTCAGTCAA
 AGCCAGGATGCTCTAATATCAGTACACTATTATAACTCCATTGTTCAACCC
 50 40 AACATGTTAGCTGAGAAATAAAGAGTTCAA
 ACTCAGCTCTTGTAAAATTGTGAGAAGAACATTTCCCTGTTGAA
 TCCCCTGTTGTA (SEQ ID NO: 186)

40 **AOLFR101 sequences:**

45 MDTGNWSQVAEFLGPHLQGVQIYLFLLLL
 IYLMTVLGNLLFLVVCLDSRLHTPMYHFVSI
 LSFSELGYTAATIPKMLANLLSEKKTISFSGCLLQIYFFHSLGATECYLLTAMAYDRYLAICRPL
 HYPTLMPTLCAEIAIGCWGLLAGP
 VVEISLISRLPFCGPNIQHVFCDFPPVLSLACTDTSINV
 LVDFVINSCKILATFL
 LILCSYVQI
 ICTLVLRIPSAAGKRKAISTCASHFTVVLIFYGSILSMYVQLK
 KSYSLDYDQALAVVYSV
 LTPFLNPFYSLRNKEIKEA
 VRRQLKRIGILA (SEQ ID NO: 187)

50 ATGGACACAGGAACTGGAGGCCAGGTAGCAGAATT
 CATCATCTTGGGCTTCCCCCATCTCC
 AGGGTGTCCAGATTATCTCTCCTCTTGTGCTCTCATTTACCTCATGACTGTGTTGGGA
 AACCTGCTGATATTCCCTGGTGGTCTGCC
 GACTCCGGCTTCACACACCCATGTACCA
 TTGTCAGCATTCTCTCC
 TTCTCAGAGCTGGCTATACAGCTGCC
 ACCATCCCTAAGATGCTG
 GCAAACCTGCTCAGTGAGAAAAAGACCA
 ATTTCATTCTGGGTTGCTCCTGCAGATCTATT
 TCTTCACTCC
 CTGGAGCGACTGAGTGCTATCTCTGACAGCTATGGCCTACGATAGGTA
 TTAGCCATCTGCC
 GGGCCCTCCACTACCC
 AACCC
 ACTGACCC
 AACACTTGTGAGAG
 ATTGCCATTGGCTGTTGGGAGGCTGGCTGGCCAGTAGTTGAA
 ATTCTGATT
 CACGCCTCCC
 ATTCTGTGGCC
 AACATCGCATT
 CAGCAC
 GCTTGTGACTT
 CCCTCTGTG
 CTGAGTTGGCTTGCACTGATA
 CGTCTATA
 AAATGCTTAG
 ATTTGTTATA
 AAATTCTCTG

5 CAAGATCTAGCCACCTCCCTGCTGATCCTCTGCTCCTATGTGCAGATCATCTGCACAGTGC
 TCAGAATTCCCTCAGCTGCCGGCAAGAGGAAGGCCATCTCACGTGCTCCACTTCAC
 TGTGGTCTCATCTTCTATGGGAGCATCCTTCCATGTATGTGCAGCTGAAGAAGAGCTAC
 TCACTGGACTATGACCAGGCCCTGGCAGTGGTCACTCAGTGCACACCCTCCTCAACC
 CCTTCATCTACAGCTGCGCAACAAGGAGATCAAGGAGGCTGTGAGGAGGCAGCTAAAGA
 GAATTGGGATATTGGCATGA (SEQ ID NO: 188)

AOLFR102 sequences:

10 MPVGKLVFNQSEPTEFVFRRAFTTATEFQVLLFLLYLMILCGNTAIWVVCUTHSTLRTPMYF
 FLSNLSFLELCYTTVVVPLMLSNILGAQKPKISLAGCGAQMFVTLGSTDCAFLLAIMAYDRYVAI
 CHPLHYTLIMTRELCTQMLGGALGLFPLSQLTALIFTLPFCGHHQEINHFLCDVPPVRLACA
 DIRVHQAVLYVVSILVLTIPFLLICVSYVFITCAILSIRSAEGRRAFSTCSFHLTVVLQYGCCSL
 VYLRPRSSSTSEDEDSQIALVYTFVTPLLNPLLYSLRNKDVKGALRSAIIRKAASDAN (SEQ ID
 NO: 189)

15 ATGCCTGTGGGGAAACTTGTCTCAACCACTGAGCCCCTGAGTTGTGTTCCGTGCGT
 TCACCACAGCCACTGAATTCCAGGTCTTCTCTTCTCTCTCTCTACTTGATG
 ATCCTCTGTGGCAACACAGCCATCATCTGGTGGTGTGACACACAGCACCCCTCCGCACCC
 CGATGTATTCTCTTGTCCAACCTGTCTTCTGGAACTCTGCTACACACCACCGTGGTAGTA
 20 CCCTTGATGCTTCCAACATTGGGGCCAGAACGCCCATTCTGTTGGCTGGATGTGGGG
 CCCAAATGTTCTTGTCAACCTCGGAGCACGGACTGTTCTCTGGCAGTCATGGCC
 TATGACCGCTATGTGGCTATCTGCCACCCGCTGCACTACACCCCTCATGACCCGCGAGC
 TGTGACCGAGATGCTGGTGGGGCCCTGGGCTGGCCCTCTTCCCTCCCTGAGCTCAC
 CGCCTTAATCTCACCCCTGGCCCTTGCGGCCACCCACAGGAAATCAACCACTTCCCTGCG
 25 ATGTGCCTCCCGTCTGCGCCTGGCCTGGCTGACATCCGCGTGCACCGAGGCTGCTCTA
 TGTGAGCATCTCGTGTGACCATCTCTCTGCTCATCTGCGTCTCCTACGTGTTCA
 TCACCTGTGCCATCCTGAGCATCCGTTCTGCCAGGGCCGGCCGGCTCTCCACCTG
 CTCCCTCCACCTCACCGTGGCTGTGAGTATGGCTGCTGAGCAGCCTCGTGTACCTGCGTC
 30 CTCGGTCCAGCACCTCAGAGGATGAGGACAGCCAAATCGCCTGGCTACACCTTGTCA
 CCCCTTACTCAACCCCTTGCTTACAGCCTAGGAACAAGGATGTCAAAGGTGCTGTGAGG
 AGTGCCATTATCCGTAAAGCAGCCTCTGACGCCACTGA (SEQ ID NO: 190)

AOLFR103 sequences:

35 MAEMNLTVTEFLIAFTEYPEWALPLFLLLFMYLITVLGNLEMILILMDHQLHAPMYFLLSH
 LAFMDVCYSSITVPQMLAVLLEHGAALSYTRCAAQFLFTFFGSIDCYLLALMAYDRYLAVCQ
 PLLYVTILTQQRSLVAGAYVAGLISALVRTVSAFTLSFCGTSEIDFIFCDLPPLLKLTGESYT
 QEVLIIMFAIFVIPASMVVILVSYLFIVAIMGIPAGSQAKTFSTCTSHLTAVSLFFGTLIFMYLRG
 NSDQSSEKNRVVSVLYTEVIPMLNPLIYSLRNKEVKEALRKILNRAKLS (SEQ ID NO: 191)

40 ATGGCAGAGATGAACCTCACCTGGTACCGAGTTCCCTTATTGCATTCACTGAATATC
 CTGAATGGGCACTCCCTCTCTTCTTGTATTATTTATGTATCTCATCACCGTATTGGGG
 AACTTAGAGATGATTATCTGATCCTCATGGATCACAGCTCCACGCTCCAATGTATTCT
 TCTGAGTCACCTCGCTTCTGATGGACGTCTGACTCATCTACGTGCCCCAGATGCTGG
 CAGTGTGCTGGAGCATGGGCAGCTTATCTTACACACGCGTGTGCTGCTCAGTTCTTCT
 45 GTTCACCTCTTGGTCCATCGACTGCTACCTCTTGGCCCTCATGGCCTATGACCGCTACT
 TGGCTGTGCTGGCAGCCCTGCTTATGTGACCATCTGACACAGCAGGCCCCGCTTGAGTCT
 TGTGGCTGGGGCTTACGTTGCTGGTCTCATCAGTGCCTGGTGCAGCTCAGCCTTC
 ACTCTCTCTTGTGAGACCAGTGTGAGATTGACTTTATTTCTGTGACCTCCCTCTGTT
 AAAGTTGACCTGTGGGGAGAGCTACACTCAAGAAAGTGTGATTATTATGTTGCCATT
 50 GTCATCCCTGCTTCCATGGTGGTATCTTGGTGTCTACCTGTTATCATCGTGGCCATCAT
 GGGGATCCCTGCTGGAAAGCCAGGCCAAGACCTTCTCCACCTGCACCTCCACCTCACTGCT
 GTGTCACCTCTTGTGACCTCATCTCATGTACTGAGAGGTAACTCAGATCAGTCTTC
 GGAGAAGAATCGGGTAGTGTGCTTACACAGAGGTACATCCCCATGTTGAATCCCTC
 ATCTACAGCCTGAGGAACAAGGAAGTGAAGGAGGCCCTGAGAAAAATTCTCAATAGAGCC
 55 AAGTTGTCTAA (SEQ ID NO: 192)

AOLFR105 sequences:

5 MQGLNHTSVSEFILVGSAFPHLQLMLFLLMYLFTLLGNLLIMATVWSERSLHMPMYLFLC
 ALSITEILYTVAIIPRMLADLLSTQRSIAFLACASQMFFSFGFTHSFLLTVMGYDRYVAICHPL
 RYNVLMSLRGCTCRVGCSWAGGLVMGMVVTSAIFHLAFCGHKEIHHFFCHVPPLKLACGDD
 10 VLVVAKGVLVCITALLGCFLILLSYAFIVAAILKIPSAEGRNKAFTSTCASHLTVVVHYGFAS
 VIYLKPKGQPSPEGDTLMGITYTVLTPFLSPIIFSLRNKELKVAAMKKTCFTKLFPQNC (SEQ ID
 NO: 193)

15 ATGCAGGGGCTAAACCACACCTCCGTCTGAATTCATCCTCGTTGGCTTCTGCCTTCCC
 CCACCTCCAGCTGATGCTCTTCCTGCTGATGACCTGTCAGCCTGCTGGCA
 ACCTGCTCATCATGCCACTGTCGGAGCGAGCGCAGCCTCCACATGCCATGCTTCT
 CCTGTGTGCCCTCTCCATCACCGAGATCCTACACCGTGGCCATCATCCCGCGATGCTG
 GCCGACCTGCTGTCCACCCAGCGCTCCATGCCCTCTGGCCTGTGCCAGTCAGATGTTCTT
 CTCCCTCAGCTCGCTTCAACCCACTCCTCCTGCTCACTGTCATGGGCTACGACCGCTACG
 20 TGGCCATCTGCCACCCCTCGTTACAACGTGCTCATGACCTGCGGGGCTGCACCTGCCG
 GGTGGGCTGCTCTGGCTGGCTGGTATGGGATGGTGGTACCTGGGACCTGGGCA
 CACCTGCCCTCTGTGGACACAAGGAGATCCACCATTTCTCTGCCACGTGCCACCTCTGTT
 GAAGTTGGCCTGTGGAGATGATGTGCTGGTGGTGGCAAAGGCGTGGGCTGGTGTAT
 CACGGCCCTGCTGGGCTGTTCTCATCCTCCTCTCATGCCATCGTGGGCC
 25 TCTTGAAGATCCCTCTGCTGAAGGTGGAACAAGGCTTCTCCACCTGTGCCCTCTCACCT
 CACTGTGGTGGTCGTGCACTATGGCTTGCCTCCGTATTACCTGAAGGCCAAAGGTCCC
 CAGTCTCCGAAGGAGACACCTGATGGGATCACCTACACGGCCTCACACCCCTCTCA
 GCCCCATCATCTCAGCTCAGGAACAAGGAGCTGAAGGTGCCATGAAGAAAGACTTGCCTT
 CACCAAACCTTCCACAGAACTGCTGA (SEQ ID NO: 194)

AOLFR106 sequences:

30 METANYTKVTEFVLTLSQTPEVQLVLFVIFLSFYLFILPGNIICTISLDPLHTSPMYFLLANLA
 FLDIWYSSITAPEMLIDFFVERKIISFDGCAIQLFLHFAGASEMFLLTVMAFDLYTAICRPLHYA
 TIMNQRLCCILVALSWRGGFIHSIIQVALIVRLPFCGPNELDSYFCDITQVVRACANTFPEELVM
 ICSSGLISVVCLIAALLMSYAFLLALFKKLSGSGENTNRAMSTCYSHITIVLMFGPSIYIYARPDFD
 SFSLDKVVSVFNTLIFPLRNPIYTLRNKEVKAAMRKLVTKYILCKEK (SEQ ID NO: 195)

35 ATGGAAACTGCAAATTACACCAAGGTGACAGAAATTGTTCTCACTGGCTATCCCAGACTC
 CAGAGGTCCAACACTAGTCTTATTTGTTATTTCTATCCTCTATTGTTCATCCTACAGAGGA
 AATATCCTTATCATTGACCATCAGTCAGACCTCATCTGACCTCTCTATGTT
 GTGGCTAATCTGGCTTCTGTGATATTGGTACTCTTCCATTACAGCCCTGAAATGCTCA
 TAGACTTCTTGTGGAGAGGAAGATAATTCTTGTGATGGATGTCATTGACAGCTCTT
 CTACACTTTGCTGGGGCTTCCACTATGTCACCATCATGAATCAACGCTCTGCTGTATCCTG
 40 CTGCTATCTGGCAGCCCTCCACTATGTCACCATCATGAATCAACGCTCTGCTGTATCCTG
 GTGGCTCTCTCTGGGGGGCTTCATTCTTGTGATGACAGTTACTCTGTGACATCACACAGGTG
 GACTTCTTCTGTGGGGCCAACTGAGTTAGACAGTTACTCTGTGACATCACACAGGTG
 CCGGATTGCTGTGCAACACCTCCCAGAGGAGTTAGTGTGATCTGTGAGTGTGGCTG
 ATCTCTGTGGTGTGTTGATTGCTCTGTTAATGTCCTATGCCCTCTGGCTTGTCAA
 45 GAAACTTTCAGGCTCAGGTGAGAATACCAACAGGGCCATGCCACCTGCTATTCCCACATT
 ACCATTGTGGTGCTAATGTTGGCCATCCATCACATTATGCTGCCATTGACTCGTT
 TTCCCTAGATAAAAGTGGTGTGTTCAATACTTAATATCCCTTACGTAATCCCATTA
 TTTACACATTGAGAAACAAGGAAGTAAAGGCAGCCATGAGGAAGTGGTCACCAAATATA
 TTTGTGTAAGAGAAGTGA (SEQ ID NO: 196)

AOLFR107 sequences:

50 MELWNFTLGSFILVGILNDGSPELLCATITILYLLALISNGLLLAITMEARLHMPMYLLLQ
 LSLMDLLFTSVVTPKALADFLRENTISFGGCALQMFLALTMGGAEDLLLAFMAYDRYVAICH
 PLTYMTLMSSRACWLMVATSWILASLSALIYTIVYTMHYPFCRAQEIRHLLCEIPHLLKVACAD
 TSRYELMVYVMGVTFIPLSLAAILASYTQILLTVLHMPNSNEGRKKALVTCSSHLTVVGMFYGA
 55 ATFMVLPSSFHSTRQDNIISVFYTIVTPALNPLIYSLRNKEVMRALRRVLGKYMPLAHSTL
 (SEQ ID NO: 197)

ATGGAGCTCTGGAACCTCACCTGGGAAGTGGCTCATTGGTGGGGATTCTGAATGACA
 GTGGGTCTCTGAACGTCTGTGCTACAATTACAATCCTATACTTGTGGCCCTGATCAG
 CAATGGCCTACTGCTCCTGGCTATCACCATGGAAGCCGGCTCCACATGCCCATGTACCTC
 5 CTGCTTGGCAGCTCTCTCATGGACCTCCTGTTACATCTGTTGTCACCTCCAAAGGCCCT
 TCGGACTTTCTGCGCAGAGAAAACACCATCTCCTTGGAGGCTGTGCCCTCAGATGTC
 CTGGCACTGACAATGGGTGGTGTGAGGACCTCTACTGCCCTCATGGCCTATGACAGGT
 ATGTGGCCATTGTACATCCTCTGACATACATGACCTCATGAGCTCAAGAGCCTGCTGGCT
 CATGGTGGCCACGTCCTGGATCCTGGATCCCTAAGTGCCCTAATATATACCGGTATACC
 10 ATGCACTATCCCTCTGCAGGGCCCAGGAGATCAGGCATCTCTGTGAGATCCCACACT
 TGCTGAAGGTGGCCTGTGCTGATACCTCCAGATATGAGCTCATGGTATATGTGATGGGTGT
 GACCTTCCCTGATTCCCTCTCTGCTGCTATACTGCCCTCCTACACAAATTCTACTCACTG
 TGCTCCATATGCCATCAAATGAGGGAGGAAGAAAGCCCTGTCACCTGCTCTCCACCT
 15 GACTGTGGTGGATGTTCTATGGAGCTGCCACATTGATGTCTTGGCCAGTTCCCTGAA
 ACAGCACCAGACAAGACAACATCATCTGTTTACACAAATTGTCACTCCAGCCCTGAA
 TCCACTCATCTACAGCTGAGGAATAAGGAGGTATGCCAGGGCCTGAGGAGGGCCTGGG
 AAAATACATGCTGCCAGCACACTCCACGCTCTAG (SEQ ID NO: 198)

AOLFR108 sequences:

20 MCSFFLCQTGKQAKISMGEENQTFVSKFIFLGLSQDLQTQILLFILFLIIYLLTVLGNQLIILIFLD
 SRLHTPMYFFLRNLSFADLCFSTSIVPQVLVHFLVKRKTISFYGCMTQIVFLLVGCTECALLAV
 MSYDRYVAVCKPLYYSTIMTQRVCLWLSFRSWASGALVSLVDTTSFTFHPYWGQNIINHYFCE
 PPALLKLASIDTYSTEMAIFSMGVVILLAPVSLILGSYWNIISTVIQMGSGEGRLKAFSTCGSHLI
 25 VVVLFYGSGIFTYMRPNSTTKELDKMISVFYAVTPMLNPIYSLRNKDVKGALRKLVGRKC
 FSHRQ (SEQ ID NO: 199)

ATGTGTCTTTCTTGTGCCAACAGTAAACAGGCAAAAATATCAATGGGAGAAGAAA
 ACCAACCTTGTGTCACAGTTATCTCCTGGTCTTCACAGGACTTGCAAGACCCAGAT
 30 CCTGCTATTATCCTTTCTCATCATTATCTGCTGACCGTGCTTGGAAACCAAGCTCATCA
 TCATTCTCATCTCCTGGATTCTCGCCTTCACACTCCATGTATTCTTCTAGAAATCTCT
 CCTTGCAGATCTCTGTTCTACTAGCATTGTCCTCAAGTGTGTTCACTCTTGGTA
 AAGAGGAAAACCATTCTTTATGGGTGTATGACACAGATAATTGCTTTCTCTGGTTG
 GGTGTACAGAGTGTGCGCTGCTGGCAGTGATGTCCTATGACCGGTATGTGGCTGTGCAA
 35 GCCCTGTACTACTTACCATCATGACACAACGGGTGTGTCCTGGCTGTCTCAGGTCT
 GGGCAGGGGGCACTAGTGTCTTAGTAGATACCAGCTTACTTCCATCTCCCTACTG
 GGGACAGAATATAATCAACTACTTTGTGAACCTCCTGCCCTCTGAAGCTGGCTTCC
 ATAGACACTTACAGCACAGAAATGCCATCTTCAATGGCGTGGTAATCCTCTGGCCC
 CTGTCTCCCTGATTCTGGTTCTATTGAATATTATCTCCACTGTTATCCAGATGCAGTCT
 40 GGGGAAGGGAGACTCAAGGCTTTTCCACCTGTGGCTCCCATCTTATTGTTGTCCTCTT
 CTATGGGTAGGAATATTCACCTACATGCGACCAAACCTCAAGACTACAAAGAAACTGGA
 TAAAATGATATCTGTGTTCTATACAGCGGTGACTCCAATGTTGAACCCCCATAATTATAGC
 TTGAGGAACAAAGATGTCAAAGGGGCTCTCAGGAAACTAGTTGGGAGAAAGTGTCTCT
 CATAGGCAGTGA (SEQ ID NO: 200)

AOLFR109 sequences:

45 MLRNGSIVTEFILVGFQQSSTSTRALLFALFLALYSLTMAMNGLIIFITSWTDPLNNSPMYFFLG
 HLSLLDVCFITTIPQMLIHLVVRDHIVSFVCCMTQMYFVFCVGVAECILLAFMAYDRYVAICY
 PLNYVPIISQKVCVRLVGTAWFFGLINGIFLEYISFREPFRRDNHIESFFCEAPIVIGLSCGDPQFSL
 50 WAIFADAIVVILSPMVLTVTSYVHILATILSKASSSGRGKTFSTCASHLTVVIFLYTSAMFSYMN
 PHSTHGPDKDKPFSLLYTIITPMCNPIIYSFRNKEIKEAMVRALGRTRLAQPQSV (SEQ ID NO:
 201)

55 ATGCTAAGGAATGGCAGCATAAGTACGGAAATTATCCTCGGGCTTCAGCAGAGCTCCA
 CTTCCACACAGAGCATTGCTCTTGCCTCTCTGCCCCCTACAGCCTCACCATGCCATG
 AATGGCCTCATCATCTTATCACCTCTGGACAGACCCCAAGCTCAACAGCCCCATGTACT
 TCTCCTCGGCCATCTGTCTCTCTGGATGTCTGCTCATCACCACTACCATCCACAGATG

TTGATCCACCTCGTGGTCAGGGACCACATTGTCCTTGTATGTTGATGACCCAGATGT
 ACTTTGTCTTCTGTGTGGTGTGGCGAGTGCATCCTCTGGCTTCATGGCCTATGACCGT
 TATGTTGCTATCTGCTACCCACTTAACATATGTCGGCATATAAGCCAGAAGGCTGTGTC
 GGCTTGTGGGAACCTGCCTGGTCTTGGGCTGATCAATGGCATCTTCTCGAGTATATTTC
 5 ATTCCGAGAGGCCCTCCGCAGAGACAACCACATAGAAAGCTTCTGTGAGGGCCCCATA
 GTGATTGGCCTCTCTGTGGGGACCCCTCAGTTAGTCTGTGGCAATCTTGCCGATGCCA
 TCGTGGTAATTCTCAGCCCCATGGTGCCTACTGTCACCTCCTATGTGCACATCCTGGCACC
 ATCCTCAGCAAAGCCTCCCTCAGGTCGGGGAGACTTCTACTTGTGCTCTCACC
 10 TGACTGTGTCATCTTCTACACTCAGCTATGTTCTTACATGAACCCCCACAGCACA
 CATGGCCTGACAAAGACAAACCTTCTCCCTGTACACCACATTACCCCCATGTGCA
 ACCCCATCATTTATAGTTCCGACAAGGAAATTAGGAGGCCATGGTGAGGGCACTTG
 GAAGAACCAAGGCTGGCCAGCCACAGTCTGTCTAG (SEQ ID NO: 202)

AOLFR110 sequences:

15 MKIANNTVVTTEFILLGLTQSQDIQLLVFLILIFYLILPGNFLIIFTIRSDPGLTAPLYLFLGNLAFL
 DASYSFIVAPRMLVDLSEKKVISYRCITQLFFLHFLGGEGLLLVMMAFDRLAICRPLHCST
 VMNPRACYAMMLALWLGGFVHSIIQVVLILRLPFCGPQLDNFFCDVRQVIKACTDMFVVEL
 LMVFNSGLMTLLCFLGLLASYAVILCHVRAASEGKNKAMSTCTRVIIILMF GPAIFIYMCPR
 20 RALPADKMVSFHTVIFPLMNPMIYTLRNQEVTSMKRLLSRHVVVCQVDFIIRN (SEQ ID NO:
 203)

ATGAAGATAGCAAACAAACACAGTAGTGACAGAAATTATCCTCCTGGTCTGACTCAGTCTC
 AAGATATTCACTCTGGTCTTGTGCTGATCTTAATTCTACCTTATCATCCTCCCTGGA
 25 AATTCTCATTATTCACCATAAAGGTCAAGCCCTGGCTCACAGCCCCCTCTATTATT
 TCTGGCAACTTGGCCTCTGGATGCTCCTACTCCTCATTGTGGCTCCAGGATGTTGG
 TGGAACCTCCTCTGAGAAAAGGTAACTCCTACAGAGGCTGCATCACTCAGCTCTTTT
 CTTGCACTTCCTGGAGGGAGGGATTACTCCTGTTGATGCCACTCCATTATCCAGGTGGCTCATCCTC
 ATCGCCATCTGCCGGCTCTGCACTGTTCAACTGTCATGAACCCTAGAGCCTGCTATGCAA
 30 TGATGTTGGCTCTGTGGCTTGGGGTTGTCCACTCCATTATCCAGGTGGCTCATCCTC
 CGCTGCCTTTGTGGCCAAACAGCTGGACAACCTCTGTGATGTCCAGCAGGTCA
 TCAAGCTGGCTTGCAACGATGTTGGTGGAGCTCTAATGGCTTCAACAGTGGCCT
 GATGACACTCCTGTGCTTCTGGGGCTCTGGCTCCTATGCAGTCATCCTCTGCCATGTTG
 35 GTAGGGCAGCTCTGAAGGGAAAGAACAGGCCATGTCCACGTGCAACCACCTGTCATTA
 TTACTCTTATGTTGGACCTGCTATCTCATCACATGTGCCCTTCAGGGCTTACCA
 GCTGACAAGATGGTTCTCTTACACAGTGATCTTCCATTGATGAATCCTATGATTAA
 TACCCCTCGAACCAAGGAAGTGAAAACCTCATGAAGAGGTTATTGAGTCGACATGTAGTC
 TGTCAAGTGGATTATAATAAGAAACTGA (SEQ ID NO: 204)

AOLFR111 sequences:

40 MCYIYLIFKEWTLIFYFSLLLQLITPAIMANLTIVTEFILMGFSTNKNMCILHSILFLIYL CALM
 GNVLIIMITLDHHLHTPVYFFLKNLSFLDLCLISVTAPKSIANSLIHNNISFLGCVSQVFLSS
 ASAELLLLTVMMSFDRTAICHPLHYDVIMDRSTCVQRATVSWLYGGGLIAVMHTAGTFSLSYCG
 SNMVHQFFCDIPQLLAISCSENLIREIALILINVVLD FCCFIVIITVHFSTVKKIPSTEGQSKAY
 SICLPHLLVVLFLSTGFIAYLKPAESPSILDAVISVFYTMPLPFTNPIIYSLRNKAICVALGMLIKG
 45 KLTKK (SEQ ID NO: 205)

ATGTGTTATATATATTAATTTAAAGAGTGGACATTGATATTTACTTCAGTCTTCTCCT
 TTCTCGAGATTACTCCTGCAATAATGGCAAATCTCACAACTCGTACTGAATTATCCTTA
 50 TGGGGTTTCTACCAATAAAATATGTGCAATTGCAATTGCAATTCTCTTGTGATTTAT
 TTGTGTCCTGATGGGAATGTCCTCATTATCATGATCACAACTTGGACCATCATCTCC
 ACACCCCCGTGTATTCTCTGAAAGAATCTATCTTGGATCTCTGCCTTATTCAGTC
 ACGGCTCCCAAATCTATGCCAATTCTTGATACACAACAACTCCATTTCATTCTGGCTG
 TGTTTCCCAGGTCTTGTGTTCTCAGCATCTGCAGAGCTGCTCCCTCACGGTGA
 55 TGTCCTTGCACCGCTACTGCTATATGTCACCCCTGCACTATGATGTCATCATGGACAGG
 AGCACCTGTGTCAAAGAGCCACTGTGTCITGGCTGTATGGGGCTGATTGCTGTGATGC
 ACACAGCTGGCACCTCTCCTATCCTACTGTGGTCAACATGGCCATCAGTCTCTGT

5 GACATTCCCCAGTTATTAGCTATTCTGCTCAGAAAATTAAAGAGAAATTGCACTCA
 TCCTTATTAATGTAGTTGGATTCTGCTGTTATTGTACATCATCATTACCTATGTCCAC
 GTCTTCTCTACAGTCAGAAGATCCCTCCACAGAAGGCCAGTCAAAAGCCTACTCTATT
 GCCTTCCACACTGCTGGTGTGTTATTCTTCACTGGATTCACTGCTTATCTGAAGCCA
 5 GCCTCAGAGTCTCCTCTATTGGATGCTGTAATTCTGTGTTACACTATGCTGCC
 AACCTTAAATCCCATTATACAGTTGAGAAACAAGGCCATAAAGGTGGCTGGGGATG
 TTGATAAAGGGAAAGCTCACCAAAAAGTAA (SEQ ID NO: 206)

AOLFR113 sequences:

10 MKFWHGFSHLNPMFSSFLYLSPWINTTIQAWLNLCSLALPVWAMSGAGFLSCCYWHTCSP
 SVTCSSSQSSDWMLQLCTHLCTLSVFFPSWSCGIQLPLSLRCLIFSVRRKPFLQDASFRPTSS
 TPWGACECYLLTAMAYDRYLACRPLHYPIIMTTLCAKMAAACWTCGFLCPISEVILASQLPF
 CAYNEIQHIFCDFPPLLSLACKDTSANILVDFAINAFILITFFFIMISYARIIGAVLKIKTASGRKK
 15 AFSTCASHLAVVLIFFGSIIFMYVRLKKSYSLTLRTLAIYVSLTPMVNPITYSLRNKEIIKAIR
 TIFQKGDKASLAHL (SEQ ID NO: 207)

20 ATGTGTCAACAAATCTTACGGGATTGCATTCTTCATACATCATTTGTGCAATTAAACAGGA
 AAAAAGTCTCACTTGTGATGCTGGGTCCAGCTTATAACCACACAATGGAAACCCCTGCC
 CTTCCCTCCTGTGGTATCCAGGACTGCAATCTTCACATCTTGGCTGGCTATCTCACTGA
 GTGCCATGTACATCATAGCCCTGTTAGGAAACACCATCATCGTACTGCAATCTGGATGGA
 TTCCACTCGGCATGAGCCCATGTTAGGCTTCTGTGTTCTGGCTGTGGACATTGTTA
 TGCCCTCCTCGGTGGTACCCAGATGGTGAGCATCTCTGCTCAGGAGACAGCTCAATCAG
 CTTAGTGCCTGTTCACTCAGATGTTTGTCCACTTAGCCACAGCTGTGGAGACGGGG
 CTGCTGCTGACCATGGCTTACCGCTATGTAGCCATCTGCAAGCCTTACACTACAAGA
 25 GAATTCTCACGCCCTCAAGTGATGCTGGGAATGAGTATGGCCATCACCACATCAGAGCTATCAT
 AGCCATAACTCCACTGAGTTGGATGGTAGTCATCTACCTTCTGTGGCTCCAATGTGGTT
 GTCCACTCCACTGTGAGCACATAGCTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCA
 GCAGTCTCTACAGTCTGATTGGTTCTCTCTATGGTGGGCTCTGATGTGGCCTTCATTGCT
 30 GCCCTCTATATCTTAATTCTCAAGGCAGTATTGGTCTCTCCTCAAAGACTGCTCAGTTGAA
 AGCATTAAAGCACATGTGGCTCCATGTGGGGTTATGGTTTGACTATCTACCTGGATG
 GCATCCATCTATCGGGCCTGGTGGGGCAGGATGTTAGTGCCTTGACACACCAAGTCCTGC
 TAGCTGACCTGTACGTGATCATCCCAGCCACCTAAATCCCACATCTATGGCATGAGGAC
 CAAACAACTGCGGGAGAGAATATGGAGTTCTGATGCTGTCCTTTGACCATTCAAAC
 CTGGGTTCATGA (SEQ ID NO: 208)

35

AOLFR114 sequences:

MERINHTSSVSEFILLGLSSRPEDQKTLFVLFLIVYLVITGNLLIIAIRFNPHLQTPMYFFLSFLS
 LTDICFTTSVPKMLMNFLSEKKTISYAGCLTQMYFLYALGNSDSCLAVMAFDRYVAVCDPF
 40 HYVTTMSHHCVLLVAFSCSFPHLHSLLHTLLLNRITFCDNSNVIIHFLCDLSPVLKLS
 EIVQMTEAPIVLVTRFLCIAFSYIRILTVLKIPSTSGKRKAFSTCGFYT
 PSTYAVKDHVATIVYTVLSSMLNPFISLRNKLQGLRKLMSKRS (SEQ ID NO: 209)

45 ATGGAAAGAACATCAACCAACACCAGCAGTGTCTCCGAGTTATCCTCCTGGACTCTCCTCCC
 GGCTGAGGACCAAAAGACACTCTTGTCTCTCCTCATCGTGTACCTGGTCAACCATAAC
 AGGGAACCTGCTCATCATCTGGCCATTGCTCAACCCCCATCTCAGACCCCTATGTATT
 TCTTCTGAGTTTCTGTCTCACTGATATTGCTTACAACAAGCGTTGCCCCAAGATG
 CTGATGAACCTCCTGTCAAGAAAAGAAGACCATCTCCTATGCTGGGTGTCTGACACAGATGT
 ATTTCCTATGCCTTGGCAACAGTGCAGCTGCCCTCTGGCAGTCATGGCCTTGACCG
 CTATGTGGCCGTCTGTGACCCCTTCACTATGTCACCAACATGAGCCACCAACACTGTGTC
 50 TGCTGGTGGCCTCTCTGCTCATTTCTCACCTCACTCAGCTGACACACTCTGCTG
 AATCGTCTCACCTTCTGTGACTCCAATGTTATCCACCACTTCTCTGTGACCTCAGCCCTGT
 GCTGAAATTGTCTGTCTTCCATATTGTCAATGAAATTGTGCAAGATGACAGAAGCACCT
 ATTGTTTGGTGAACCGTCTCTGCAATTGCTTCTCTTATATACGAATCCTCACTACAGT
 TCTCAAGATTCCCTCTACTTCTGGAAACGCAAAGCCTCTCCACCTGTGGTTTACCTCA
 55 CCGTGGTGAACGCTCTTATGGAAGCATCTCTGTGCTATTACAGCCCCCATCCACCTAC
 GCTGTCAAGGACCAACGTGGCAACAATTGTTACACAGTTGTCACTCCATGCTCAATCCTT

TTATCTACAGCCTGAGAAACAAAGACCTGAAACAGGGCCTGAGGAAGCTATGAGCAAGA
GATCCTAG (SEQ ID NO: 210)

AOLFR115 sequences:

5 MEGFYLRRSHELQGMGKPGRVNQTTVSDFLLLGLSEWPEEQPLFLGIFLGMYLVTMVGNLII
LAISDPHLHTPMYFLANLSLTACFTSASIPKMLANIHTQSQIISYSGCLAQLYFLLMFGGLD
10 NCLLAVMAYDRYVAICQPLHYSTSMSPQLCALMLGVCWLTNCPALMHTLLLTRVAFCAQK
AIPHFYCDPSALLKACSDTHVNELMIITMGLLFLTVPLLLIVFSYVRIFWAVFVISSPGGRWKA
FSTCGSHLTVVLLFYGSLMGVYLLPPSTYSTERESRAAVLYMVIPTLNPFYSLRNRDMDKEALG
KLFVSGKTF (SEQ ID NO: 211)

15 ATGGAAGGTTTATCTGCGCAGATCACACGAACATACAAGGGATGGGAAAACCAGGCAGA
GTGAACCAAACCACTGTTCAACTTCCCTCTGGCATGTACCTGGTACCATGGTGGGAAACCTGCTC
ATTATCCTGGCCATCAGCTCTGACCCACACCTCCATCTCCATGTACTTCTGGCCAA
CCTGTCATTAACGTGATGCCTGTTCACTCTGCCTCCATCCCCAAATGCTGGCCAACATTC
ATACCCAGAGTCAGATCATCTCGTATTCTGGGTCTTGCACAGCTATATTCCCTCCTATG
TTGGTGGCCCTGACAACGTGCTGGCTGTGATGGCATATGACCGCTATGTTGGCCATCT
GCCAACCACTCCATTACAGCACATCTATGAGTCCCCAGCTCTGCACTAATGCTGGGTGT
20 GTGCTGGGTGCTAACCAACTGTCCTGCCTGATGCACACACTGTTGCTGACCCGCGTGGCT
TTCTGTGCCAGAAAGCCATCCCTCATTTCTATTGTGATCTAGTGCCTCTGCAGCTTGC
CTGCTCAGATAACCCATGTAACAGAGCTGATGATCATCACCATGGGCTTGTGTTCTCACT
GTTCCCTCCTGCTGATCGTCTCTCCTATGTCGGCAATTCTGGGCTGTGTTGTCACTC
ATCTCCTGGAGGGAGATGGAAGGCCTCTACCTGTGGCTCTCATCTCACGGTGGTTCTG
25 CTCTCTATGGGTCTCTATGGGTGTGATTACTCCCATCAACTTACTCTACAGAGAG
GGAAAGTAGGGCTGCTGTTCTATATGGTATTATTCCCACGCTAAACCCATTCAATTAT
AGCTTGAGGAACAGAGACATGAAGGAGGCTTGGTAAACCTTTGTCAGTGGAAAAACA
TTCTTTATGA (SEQ ID NO: 212)

AOLFR116 sequences:

30 MDEANHSVVSEFVFLGLSDSRKIQLLLFLFFSVFYVSSLMGNLLIVLTVTSDPRLQSPMYFLLAN
LSIINLVFCSTAPKMTYDLFRKHKTISFGCVCVQIFIHAVGGTEMVLLJAMAFDRYVAICKPLH
35 YLTIMNPQRCLFLVISWIIGIHSVIQLAFVVDLLFCGPNELESDFFCDLPRFIKLACIETYTLGFMV
TANSGFISLASFLILISYIFILVTVQKKSSGGIFKAFSMSAHLVIVVVLVFGPLIFFYIFPFPTSHLD
KFLAIFDAVTPVLPVITYTFRNKEEMMVAMRRRCSQFVNYSKIF (SEQ ID NO: 213)

40 ATGGATGAAGCCAATCACTCTGGTCTCTGAGTTGTGTTCTGGACTCTCTGACTCGC
GGAAGATCCAGCTCCCTCTTCTCTTCTCAGTGTCTATGTATCAAGCCTGATGGGA
AATCTCCTCATTGTGCTAAGTGTGACCTCTGACCTCGTTACAGTCCCCCATGTACTCCT
GCTGGCCAACCTTCCATCATCAATTGGTATTGTGTTCTCCACAGCTCCAAGATGATT
ATGACCTTTCAAGGAAGCACAAGACCATCTCTTGGGGCTGTGAGTTCAGATCTTCTT
TATCCATGCAGTTGGGGAACTGAGATGGTCTGCTCATAGCCATGGCTTTGACCGATAT
GTGGCCATATGTAAGCCTCTCCACTACCTGACCATCATGAACCCACAAAGGTGCATTGTT
TTTAGTCATTCTGGATTATAGGTATTACTCACTCAGTGATTCACTCAGTTGGCTTTGTTGTA
45 GACCTGCTGTTCTGTGGCCCTAATGAATTAGATAGTTCTTGTGATCTCCTCGATTAT
CAAACGGCTTGATAGAGACCTACACATTGGGATTCTGTTACTGCCAATAGTGGATT
ATTCTCTGGCTTCTTTAATTCTCATAATCTTACATCTTATTGGTACTGTTCA
AAAAATCTCAGGTGGTATATTCAAGGCTTCTATGCTGTCAGCTCATGTCATTGTT
50 TGTTTTGGCTTGGCCATTAAATCTTCTATATTCCATTCTCCACATCACATCTG
ATAAAATCCTTGCCATCTTGTGAGTCAGTTACTCTCCGTTGAATCCAGTCATCTA
TTAGAAATAAAGAGATGATGGTGGCAATGAGAAGACGATGCTCTCAGTTGTAATTAC
AGAAAATCTTAA (SEQ ID NO: 214)

AOLFR117 sequences:

55 MNNTIVFVIKIQIEKSDLKYRAISLQEISKISLLFWVLLLVISRLLLAMTLGNSTEVEFYLLGFQA
QHEFWCILFIVFLIIYVTSIMGNSGILLINTDSRFQTLTYFFLQHLAFVDICYTSAITPKMLQSFT

EEKNLILFQGCVIQFLVYATFATSDCYLLAMMAVDPYVAICKPLHYTVIMSRTVCIRLVAGSYI
MGSINASVQTGFTCSLSFCKSNSINHFFCDVPPILALCSNVNDINIMLLVVFVGSNLIFTGLVVIFS
YIYIMATILKMSSAGRKKSFSTCASHLTAVTIFYGTLISYMLQSHSNNSQENMKVAFIFYGTVI
PMLNPLIYSLRNKEVKEALKVIGKKLF (SEQ ID NO: 215).

5

ATGAATAACACTATTGTATTGTCAAAAAATACAAATAGAAAAAGTGACTTGAAATATA
GAGCCATTCTATTGCAAGAAATCTCAAAGATTCCCTCTTCTGGGTCTTCCTGGTC
ATTCTAGACTTTACTAGCCATGACACTAGGAAACAGCACTGAAGTCACTGAATTCTATC
TTCTGGGATTGGTGCCCAGCATGAGTTGGTGTATCCTCTTCTATTGTATTCTCTCATC
10 TATGTGACCTCCATAATGGGTAATAGTGAATAATCTTACTCATCAACACAGATTCCAGAT
TTCAAACACTCACGTACTTTCTACAACATTGGCTTTGTTGATATCTGTTACACTTCT
GCTATCACTCCCAAGATGCTCAAAGCTTACAGAAGAAAAGAATTGATATTATTCAGG
GCTGTGTGATACAATTCTTAGTTATGCAACATTGCAACAGCTGACTGTTATCTCCTGGCT
15 ATGATGGCAGTGGATCCTTATGTTGCCATCTGTAAGCCCCCTCACTATACTGTAATCATGT
CCCGAACAGTCTGCATCCGTTGGTAGCTGGTCATACATGGGCTCAATAATGCCTC
TGTACAAACAGGTTTACATGTTCACTGTCCTCTGCAAGTCCAATAGCATCAATCACTTT
TCTGTGATGTTCCCCCTATTCTGCTCTTCACTGCTCCAATGTTGACATCAACATCATGCTA
CTTGTGTCCTTGTGGGATCTAACTTGATAATTCACTGGGTTGGTCGTATCTTCCATACAT
20 CTACATCATGGCCACCATCCTGAAAATGCTTCTAGTGCAGGAAGGAAAATCCTCTCA
ACATGTGCTTCCCACCTGACCGCAGTCACCATTCTATGGGACACTCTTACATGTATT
GCAGTCTCATTCTAATAATTCCCAGGAAAATATGAAAGTGGCCTTATATTATGGCACA
GTTATTCCCAGTAAATCCTTAACTATAGCTTGAGAAATAAGGAAGTAAAGAAGCTT
TAAAAGTGATAGGGAAAAGTTATTTAA (SEQ ID NO: 216)

25 **AOLFR118 sequences:**

MNHMSASLKISNSSKFQVSEFILLGFGPIHSHWQHWSLPLALLYLSALAANTLILIIWQNPSLQQ
PMYIFLGILCVMVDMGLATTIIPKILAIFWFDAKVISLPECFAQIYAIHFFVGMESGILLCMADFDRY
VAICHPLRYPISVTSSLILKATLFLMVLRNGLFVTPVPLAAQRDYCCKNEIEHCLCSNLGVTSLA
30 CDDRRPNSICQLVLAWLGMGSDSLILSYILILYSLVRLNSAAAALKALSTCSSHLTLILFFYTIV
VVISVTHLTEMKATLIPVLLNVLHNIIPPSLNPTVYALQTKELRAAFQKVLFALTKEIRS (SEQ ID
NO: 217)

ATGAATCATATGTCATCTCTCAAAATCTCCAATAGCTCAAATTCCAGGTCTCTGAGTT
CATCCTGCTGGATTCCCGGGCATTACAGCTGGCAACACTGGCTATCTCTGCCCTGGCA
35 CTACTGTATCTCTCAGCACITGCTGCAAACACCCCTCATCCTCATCATCTGGCAGAACCC
TTCTTACAGCAGCCCATGTTATTTCTTGGCATCCTCTGTATGGTAGACATGGGCTGG
CCACTACTATCATCCCTAAGATCCTGGCCATCTCTGGTTGATGCCAAGGTTATTAGCCTC
CCTGAGTGCTTGTCTCAGATTATGCCATTCACTTCTTGTGGGATGGAGTCTGGTATCCT
ACTCTGCATGGCTTTGATAGATATGTGGCTATTGTCACCCCTTCGCTATCCATCAATTG
40 TCACCACTTCTTAATCTAAAGCTACCCCTGTTCACTGGCTGAGAAATGGCTTATTGTC
ACTCCAGTGCTGTGCTGCAGCACAGCGTGATTATTGCTCCAAGAATGAAATGAAACACT
GCCGTGCTCTAACCTGGGGTACAAGCCCTGGCTGTGATGACAGGAGGCCAACAGCAT
TTGCCAGTTGGTCTGGCATGGCTTGGAAATGGGAGTGATCTAAGTCTTATTACTGTCA
TATATTGATTCTGTACTCTGTACTTAGACTGAACATCAGCTGAAGCTGCAGCCAAGGCC
45 TGAGCACTTGAGTTACATCTCACATCTCACCCCTCATCCTTCTTACACTATTGTTGAGT
TCAGTGACTCATCTGACAGAGATGAAGGCTACTTGATTCAGTTCTACTTAATGTGTG
ACAAACATCATCCCCCTCCCAACCCCTACAGTTATGCACTTCAGACACAAAGAACTTAG
GGCAGCCTTCCAAAAGGTGCTGTTGCCCTACAAAAGAAATAAGATCTTAG (SEQ ID NO:
218)

50

AOLFR119 sequences:

MPLFNSLCWFPTIHVTTPPSFILNGIPGLERVHVVISLPLCTMYIIFLVGNLGLVYLIYEESLHHP
MYFFFHGHLSLIDLTCITTLPNALCIFWFLSLKEINFNACLAQMFFVHGFTGVESGVLMALD
55 RYIAICYPLRYATTLPNIIAKAELATFLRGVLLMIPFPFLVKRLPFCQSNISHTYCDHMSVVKL
SCASIKVNVIYGLMALLIGVFDICCIISLSYTLILKAAISLSSSDARQKAFSTCTAHISAIITYVPA

FFTFFAHRFGGHTIPPSLHIVANLYLLLPTLNPIVYGVTKQIRKSVIKFFQGDKGAG (SEQ ID NO: 219)

5 ATGCCTCTATTAATTCAATTGCTGGTTCCAACAATTGACTGTGACTCCTCCATCTTTAT
 TCTTAATGGAATACCTGGTCTGGAAAGAGTACATGTATGGATCTCCCTCCACTCTGCACA
 ATGTACATCATCTCCTGTGGGAATCTTGGTCTGTACCTCATTATTATGAGGAGTC
 CTTACATCATCCGATGTATTTTTGGCCATGCTCTCCCTCATTGACCTCCCTACCTG
 CACCAACACTCTACCCAATGCACTCTGCATCTCTGGTCAGTCTCAAAGAAATTAACTTCA
 ATGCTTGGCTGGCCCAGATGTTCTTGTTCATGGGTTACAGGTGAGTCTGGGGTGTCT
 10 CATGCTCATGGCTCTAGACCGCTATATAGCCATTGCTACCCCTTGCCTATGCTACCACAC
 TCACCAACCTATCATTGCCAAGGCTGAGCTGCCACCTTCTGAGGGGTGTATTGCTGAT
 GATTCTTCCCATTCTGGTTAACGCTTGCCTTCTGCCAAAGCAATTATCTCCATA
 CGTACTGCGACCACATGTCTGTAGTAAAGCTATCTTGTGCCAGCATCAAGGTCAATGTAAT
 CTATGGCTAATGGTGTCTCCTGATTGGAGTGTGACATTGTTGATATCTTGTCTT
 15 ACACTTTGATCCTCAAGGCAGCGATCAGCCTCTCTCATCAGATGCTCGGCAGAAGGCTT
 CAGCACCTGCACTGCCATATATCTGCCATCATCACCTATGTTCCAGCATTCTCACTT
 TCTTGGCCACCGTTTGGGGACACACAATTCCCCCTCTTCACATCATTGTGGCTAAT
 CTTATCTTCTTCCCCAACTCTAAACCTATTGTTATGGAGTAAAGACAAAACAGAT
 ACGCAAGAGTGTATAAGTTCTCCAGGGTATAAGGGTGCAGGTTGA (SEQ ID NO: 220)

20

AOLFR120 sequences:

25 MQPYTKNWTQVTEFVMMGFAGIHEAHLLFFILFTMYLFTLVENLAIILVVGLDHRLRRPMYF
 FLTHLSCLEIWYTSVTVPKMLAGFIGVDDGKNISYAGCLSQLFIFTFLGATECFLLAAMAYDRY
 VAI CMPLHYGAFVSWGTCIRLAAACWLVLGVFLPIYLLSQLTFCGPVNIDHFSCDASPLLALS
 CSDVTWKETVDFLVSIAVLLASSMVIASVGNIVWTLLHIRSAERWKAFTCAAHLTVVSLF
 YGTLFFMYVQTKVTSSINFNKVVSVFYSVTPMLNPLIYSLRNKEVKALGRVFSLNFWKGQ
 (SEQ ID NO: 221)

30

ATGCAACCATAACCAAAACTGGACCCAGGTAACGTAAATTGTCATGATGGGCTTGCTG
 GCATCCATGAAGCACACCTCCTCTTCTCATACTCTCCTCACCATGTACCTGTTCACCTTG
 GTGGAGAAATTGCCATCATTTAGTGGTGGGTTGGACCACCGACTACGGAGACCCATGTT
 ATTCTTCTGACACACTTGTCTGCCTGAAATCTGGTACACTTCTGTTACAGTGCCAAG
 ATGCTGGCTGGTTTATTGGGGTGGATGGTGGCAAGAAATATCTTATGCTGGTTGCCTAT
 CCCAGCTCTCATCTCACCTTCTGGGGCAACTGAGTGTCTACTGGCTGCCATGCC
 35 TATGATCGTTATGTGCCATTGTATGCCCTCCACTATGGGCTTTGTGTCCTGGGCAC
 CTGCATCCGCTGGCAGCTGCCCTGTTGGCTGGTAGGTTCTCACACCCATCTGCCAATCT
 ACCTCTGCTCAGCTAACATTGTGCCAAATGTCATTGACCATTCTCTGTATGCC
 TCACCCCTGCTAGCCCTGTCGTGCTCAGATGTCACITGGAAAGGAGACTGTGGATTCTGG
 TGTCTCTGGCTGTGCTACTGGCCTCTATGGTCATTGCTGTGCTCTATGGCAACATCGTC
 40 TGGACACTGCTGCACATCCGCTCAGCTGCTGAGCGCTGGAAGGCCTCTCACCTGTGCA
 CTCACCTGACTGTGGTAGCCCTTCTATGGCACTCTTCTTATGTTATGTCAGACCAAG
 GTGACCTCTCCATCAACTCAACAAAGTGGTATCTGTCTACTCTGTTGTCAGGCCAT
 GCTCAATCTCTCATCTACAGTCTAGGAACAAGGAAGTGAAGGGAGCTGGTCAGGTC
 TTTCTCTCAACTTGGAAAGGGACAGTGA (SEQ ID NO: 222)

45

AOLFR121 sequences:

50 MKRKNFTEVSEFIFLGSSFGKHQITLFWVFLTVYILTLVANIIIVTIICIDHHLHTPMYFFLSMLA
 SSETVYTLVIVPRMLLSIFHNQPIISLAGCATQMFFFVILATNCFLLTAMGYDRYVAICRPLRY
 TVIMSKGLCAQLVCGSFGIGLTMALVHVTAMFNLPFCGTVVVDHFCDIYPVMKLSCIDTTINEII
 NYGVSSFVIFVPIGLIFISYVLVISSILQIASAEGRKKTFACTCVSHLTVVIVHCGCASIAYLKPKSES
 SIEKDLVLSVTYTIITPLNPVVYSLRNKEVKDALCRVGRNIS (SEQ ID NO: 223)

55

ATGAAGAGAAAGAACITCACAGAAGTGCAGAATTCAATTCTGGGATTCTAGCTTGT
 GAAAGCATCAGATAACCCCTTTGTGGTTCTAACTGTCACATTAACTCTGGTTGCT
 AACATCATCATTGTGACTATCATCTGCATTGACCACATCTCCACACTCCATGTTATTCTT
 CCTAAGCATGCTGGTAGTTGAGAGACGGTGTACACACTGGTCATTGTGCCACGAATGCTT

TTGAGCCTCATTTTCTAAACCAACCTATCCTCTGGCAGGCTGTGCTACACAAATGTTCTT
 5 TTTGTTATCTGGCCACTAATAATTGCTTCTGCTTACTGCAATGGGTATGACCGCTATG
 TGGCCATCTGCAGACCCCTGAGATACTGTCATCATGAGCAAGGGACTATGTGCCAGCT
 GGTGTGTGGGTCTTGGCATTGGTCTGACTATGGCAGTTCTCCATGTGACAGCCATGTT
 AA 10 AATTGCCGCTCTGTGGCACAGTGGTAGACCACTCTTGTGACATTACCCAGTCATGA
 AACTTCTGCATTGATACCACTATCAATGAGATAATAAATTATGGTGTAAAGTTCATTTGT
 GATTTTGTCGCCATAGGCTGATATTATCTCCTATGTGCCCTGTACCTCTCCATCCTC
 AAATTGCCCTCAGCTGAGGGCCGAAGAAGACCTTGCACCTGTGCTCCACCTCACTGT
 GGTATTGTCACGTGGCTGCTCCATTGCCACCTCAAGCCGAAGTCAGAAAGTTCA
 15 ATAGAAAAAGACCTTGTCTCAGTGCACGTACACCATCATCACTCCCTGCTGAACCTG
 TTGTTACAGTCTGAGAAACAAGGAGGTAAAGGATGCCCTATGCAGAGTTGTGGCAGAA
 ATATTCTTAA (SEQ ID NO: 224)

AOLFR122 sequences:

15 MEWENQTLVEFFLGHHSVPRLELLFFVLIFIMYVILLGNGLLISILDPLHLHTPMYFFLGNL
 SFLDICYTTTSIPSTLVSFLSERKTISFSGCAVQMFLGLAMGTTECVLLGMMAFDRYVAICNPLR
 YPIIMSKNAVPMAVGSWFAGIVNSAVQTTFVVQLPFCRKNVINHSCEILA VMKLACADISGN
 EFLMLVATILFTLMPLLLIVISYLISSILKIHSEGRSKAFSTCSAHLTVIIFYGTILFMYMKPKS
 20 KETLNSDDLDATDKIISMFYGVMPMMNPLIYSLRNKDVKAEAVKHPNRRFFSK (SEQ ID NO:
 225)

ATGGAATGGAAAACCAAACCATCTGGGAATTCTGAAGGGACATTCTGTCACC
 25 CAAGGCTTGAGTTACTCTTGTGCTAATCTCATATAATGTATGTGGTCATCCCTCTGGGG
 AATGGTACTCTCATTTAACAGCATCTGGACATCTGCTACACCACCCCTATGTAATTCTT
 TCTGGGAACCTCTCCTTGAGATCTGCTACACCACCCCTATGTAATTCCCTCACACTAG
 TGAGCTTCCTTCAGAAAGAAAGACCATTCCTTCTGGCTGTGCAGTGCAGATGTTCCCT
 GGCCTGGCATGGGACAACAGAGTGTGCTCTGGCATGATGCCCTTGACCGCTATG
 30 TGGCTATCTGCAACCCCTGAGATATCCCATCATGAGCAAGAATGCCATGTAACCCAT
 GGCTGTTGGTCTGGTTGCAGGGATTGTCAACTCTGCACTACAAACTACATTGTAGTA
 CAATTGCCCTCTGCAGGAAGAATGTCAATCATTCTCATGTGAAATTCTAGCTGTCAT
 GAAGTTGCCCTGTGCTGACATCTCAGGCAATGAGTCCTCATGCTTGTGCCACAATTG
 TTACACATTGATGCCACTGCTCTGATAGTTATCTCTTACTCATTAATCATTCCAGCATCT
 35 CAAGATTCACTCCTCTGAGGGAGAAGCAAAGCTTCTCACCTGCTCAGCCATCTGACT
 GTGGTCATAATATTCTATGGGACCATCCTCTCATGTATATGAAGCCAAGTCTAAAGAGA
 CACTTAATTAGATGACTGGATGCTACCGACAAAATTATATCCATGTTCTATGGGGTGT
 40 GACTCCCATGATGAATCCTTAATCTACAGTCTAGAAACAAGGATGTGAAAGAGGCAGT
 AAAACACCTACCGAACAGAACAGTTCTTAGCAAGTGA (SEQ ID NO: 226)

AOLFR123 sequences:

40 MYRFTDFDVSNISIYLHVLFYTTQQAGDLEHMETRNSAMTEFFLVGLSQYPELQLFLFLCL
 IMYMIILGNSLLIIITILDSDLRHTPMYFFLGNLSFLDICYTSSSIPPMIIFMSERKSISFIGCALQM
 VVSLGLGSTEVCVLLAVMAYDHYVAICNPLRYSIIMNGVLYVQMAAWSWIIGCLTSLLQTVLT
 MMLPFCGNVNDHITCEILALLKLVCSDTINVLMITVTNIVSLVILLLIFISYVFILSSILRINCAE
 45 GRKCAFSTCSAHSIVVILFYGSALFMYMKPKSKNTNTSDEIIGLSYGVVSPMLNPIIYSLRNKEV
 KEAVKKVLSRHLHLLKM (SEQ ID NO: 227)

ATGTACAGATTTACAGATTTGATGTATCAAACATTCAATTACCTGAATCATGTCCTTT
 50 CTATACTACCCAGCAGGCAGGTGACCTAGAACACATGGAGACAAGAAATTACTCTGCCAT
 GACTGAATTCTTCTGGTGGGGCTTCCCAATATCCAGAGCTCCAGCTTCTGTTCTGC
 TCTGCCTCATGTACATGATAATCCTCTGGAAATAGCCTCCTCATTATCATCACCAC
 TTGGATTCTGCCCTCCATCTCCATGTATTCTTCTGGAAACCTCTCATTCTGGACAT
 CTGTTACACATCCTCATCCATTCTCCATGCTTATATTATATTATGTCTGAGAGAAAATCCA
 TCTCCTCATGGCTGTGCTGAGATGGTGTGCTCCCTGGCTGGCTCCACTGAGTGT
 GTCCCTGGCTGTGATGGCCTATGACCACTATGTGGCCATCTGCAACCCACTGAGGTACT
 55 CCATCATCATGAACGGAGTGCTGTATGTCAAATGGCTGCATGGCCTGGATCATAGGCTG
 TCTGACCTCCATTGCAAACAGTTCTGACAATGATGTTGCCTTCTGTGGAAATAATGTC

5 ATTGATCATATTACCTGTGAAATTGGCCCTCTAAAACITGTTGTTAGATATCACCAT
 CAATGTGCTTATCATGACAGTGAACAAATATTGTTCACTGGTATTCTCTACTGTTAATT
 TCATCTCCTATGTGTTATTCTCTCTCATCTGAGAATTAAATTGTCAGGGAAAGAAAG
 AAAGCCTCTCTACCTGTCAGCGACTCGATTGTCATCTTATCTACGGTCAGCCCT
 10 5 TTTATGTACATGAAACCAAGTCAAAGAACACTAATACATCTGATGAGATTATTGGCTG
 TCTTATGGAGTGGTAAGCCCAATGTTAAATCCCATCATCTATAGCCTCAGGAATAAAGAGG
 TCAAAGAGGGCTGAAAGAAAGTCCTGAGCAGACATCTGCATTATTGAAAATGTGA (SEQ
 ID NO: 228)

10 **AOLFR124 sequences:**

MNHVVTEFIILGLKKPELQGIIFFLIVYLVAFLGNMLIIAKIYNNTLHTPMYVFLTLAVV
 DIICITSIPKMLGTMLTSENTISYAGCMYSQLFLFTWSLGAEMVLFTTMAYDRYVAICFPLHYST
 VMNHHMCVALLSMVMAIAVTNSWVHTALIMRLTFCGPNTIDHFFCEIPPLLALSCSPVRINEV
 15 MVYVADITLAIQDFILTCTISYGFIVAILRIRTVEGKRAFKSTCSSHLTVVTLYSPVIYTYIRPASS
 YTFERDKVVAALYTLVPTLNPVMVYSPQNREMQAGIRKVFAFLKH (SEQ ID NO: 229)

20 ATGAATCACAGCGTTGTAAC TGAGTT CATT ATTCTGGCCCTCACCAAAAAGCCTGAACTCC
 AGGGAAATTATCTCCTCTTTCTCATTGTCATCTTGCTTCTCGGCAACATGCTC
 ATCATCATTGCCAAATCTATAACACACCTTGACATGCCATGTATGTTCTCTGAC
 ACTGGCTGTTGGACATCATGCACAAACAGCATCACCGAAGATGCTGGGACCAT
 25 GCTAACATCAGAAAATACCATTTCATATGCAGGGTGCATGTCAGCTCTTGTACA
 TGGTCTCTGGGAGCTGAGATGGTCTCTCACCACCATGGCCTATGACCGCTATGTGGCCA
 TTTGTTCCCTCTCATTACAGTACTGTTATGAACCCACATATGTGTGAGCCTGCTCAGC
 ATGGTCATGGCTATTGCA GT CACCAATTCTGGGTGCACACAGCTCTTATCATGAGGTTGA
 CTTCTGTGGGCCAAACACCATGACCATCTCTGTGAGATACCCCCATTGCTGGCTTTG
 30 TCCGTAGCCCTGTAAGAACATGAGGTGATGGTGTATGTCATATTACCCCTGGCCA
 TAGGGGACTTTATTCTTACCTGCATCTCTATGGTTTATCATTTGTCATCTCCGTATC
 CGCACAGTAGAAGGAAGAGGAAGGCCTCTCAACATGCTCATCTCACAGTGGTG
 ACCCTTACTATTCTCTGTAATCTACACCTATACCGCCCTGCTTCCAGCTATACATTGA
 AAGAGACAAGGTGGTAGCTGCACTCTATACTCTGTGACTCCCACATTAAACCGATGGTG
 TACAGCTTCCAGAATAGGGAGATGCAGGCAGGAATTAGGAAGGTGTTGCATTCTGAAA
 CACTAG (SEQ ID NO: 230)

35 **AOLFR125 sequences:**

35 MTNQTQMMEFLVVRFTENWVLLRLHALLFSIYLTAVLMLNVIILMILDHRLHMMAMYFFLRH
 LSFLDLCLISATVPKSILNSVASTDSISFLGCVLQLFLVVLLAGSEIGILTAMSYDRYAAICCPHLH
 EA VMSRGLCVQLMALSWLNRGALGLLYTAGTFSLNFYGSDELHQFFCDVPALLKLTCSKEHAI
 ISVVAIGVCYAFSCLVCIVVSYVYIFSAVLRISQRQRQSKAFSNCVPHLIVVTFLVTGAVAYL
 40 KPGSDAPSILDLLVSFYSVAPPTLNPVIYCLKNKDIKSALKSVLWNVRSSGVMKDD (SEQ ID
 NO: 231)

45 ATGACCAATCAGACACAGATGGAATTCTTGCTGTGAGATTACTGAGAATTGGGTGC
 TCCTGAGGCTGCATGCTTCTCACTGATCTACCTCACGGCTGTGCTGATGAATT
 GTCATCATTCTCCTCATGATTCTGGACCATCGTCTCCACATGGCAATGTACTTTCTCCG
 ACATTGTCCCTCTAGACCTGTGTCATTTCTGCCACAGTCCCCAAATCCATCCTCAACT
 CTGTCGCCTCCACTGACTCCATCTCTGGGGTGTGTCAGCTCTTGTGGTA
 CTGCTGGCTGGATCAGAGATTGGCATCTTACTGCCATGTCCTATGACCGCTATGCTGCCA
 TCTGCTGCCCTACACTGTGAGGCTGTACAGCAGAGGGCTCTGTGTCAGTTGATGGC
 TCTGCTCTGGCTCAACAGAGGGCTTGGACTCTGTACACAGCTGGAACATTCTCTG
 50 AATTCTATGGCTCTGATGAGCTACATCAGITCTCTGCAGTGTCCCTGCCACTAAAGCT
 CACTGTTCTAAAGAACATGCCATCATTAGTGTGAGTGTGGCATTGGGGCTGTTATGCA
 TTTCTATGTTAGTTGCATTGTAGTTCTATGTGACATTCTCTGCTGTGTTAAGGAT
 ATCACAGAGACAGAGACAATCAAAGCCTTCTCAACTGTGTGCTCACCTCATTGTTGTC
 ACTGTGTTCTGTAAACAGGTGCTGTTCTATTAAAGCCAGGGCTGATGCACCTCTAT
 55 TCTAGACTTGCTGGTGTCTGTGTTCTATTCTGTCGACCTCAACCTGAACCTGTTATCT

ACTGTCTGAAGAACAGGACATTAAATCCGCTCTGAGTAAAGTCCTGTGGAATGTTAGAA
GCAGTGGGTAATGAAAGATGACTAA (SEQ ID NO: 232)

AOLFR126 sequences:

5 MFLYLCFIFQRTCSEEMEEENATLLTEFVLTGFLHQPDCKIPLFLAFLVIYLITIMGNLGLIVLIW
KDPHLHIPMYLFLGSLAFVDASLSSTVTPKMLINFLAKSKMISLSECMVQFFSLVTTVTTECFLL
ATMAYDRYVAICKALYPVIMTNELCIQLLVLSFIGGLHALIHEAFSFRLTFCNSNIIQHFYCDII
10 PLLKISCTDSSINFLMVIFAGSVQVFITGTLISYTIILFTILEKKSIKGIRKAVSTCGAHLLSVSLY
YGPLTFKYLGSASPQADDQDMMESLFYTIVPOLLNPMLYSLRNKQVIASFTKMFKSIV (SEQ ID
NO: 233)

ATGTTCTTACCTTGCTCATTTCAGAGGACATGCAGTGAGGAGATGGAAGAGGAAA
ATGCAACATTGCTGACAGAGTTGTTCTCACAGGATTTACATCAACCTGACTGAAAT
15 ACCGCTCTTCCCTGGCATTCTGGTAATATATCTCATCACCATCATGGGAATCTTGGTCTAA
TTGTTCTCATCTGGAAAGACCTCACCTTCATATCCAATGTAATCTTCTGGGAGTTA
GCCTTGTGGATGCTCGTTATCATTCCACAGTGACTCCGAAGATGCTGATCAACATTCTTAG
CTAAGAGTAAGATGATATCTCTCTGAATGCAATGGTACAATTTTCTTGTAAACACT
20 GTAACCACAGAATGTTCTTGTGGCAACAAATGGCATATGATCGTATGTAAGCCATTGCA
AAGCTTACTTATCAGTCATTATGACCAATGAACTATGCAATTGAGCTATTAGTCTGTCA
TTTATAGGTGGCCTTCTCATGCTTAAATCCATGAAGCTTTCTTCATTGAGATTAAACCTCTG
TAATTCCAACATAATACAACACTTTACTGTGACATTATCCCATTTGTTAAAGATTCTGT
25 CTGATTCCCTCTATTAACTTTCTTAATGGTTTATTTTGCAGGTTCTGTTCAAGTTTACCA
TTGGAACTATTCTTATATCTTATACAAATTATCCTTTACAATCTTGTATCTGTATCTTATAC
AAAGGGATACGAAAAGCTGTCACCTGTCATCTCCACCTGTGGGCTCATCTCTTATCTGTATCTTATAC
30 ATGGCCCCCTCACCTCAAATATCTGGGCTCTGCATCTCCGAAGCAGATGACCAAGATAT
GATGGAGTCTCTATTACACTGTCAAGTTCTTATTAATCCATGATCTACAGCTGA
GAAACAAGCAAGTAATAGCTTCATTACAAAAATGTTCAAAAGCAATGTTAG (SEQ ID
NO: 234)

AOLFR127 sequences:

MSNEDMEQDNITLLTEFVLTGLTYQPEWKMLFLVFLVIYLITIVWNLGLIALIWNDPQLHIPM
YFFLGSALFVDAWISSTVTPKMLVNFLAKNRMISLSECMIQFFSFAFGGTTECFLLATMAYDRY
VAICKPLLYPVMNNSLCIRLLAFLSFLGGFLHALIHEVLIFRLTFCNSNIIHFYCDIPLFMISCTD
35 PSINFLMVFILSGSIQVFTIVTVLNSYTFALFTILKKSVRGVRKAFSTCGAHLLSVSLYYGPLIF
MYLRPASPQADDQDMIDSVFYTIIPLLNPIIYSLRNKQVIDSFTKMKVKNV (SEQ ID NO: 235)

ATGTCGAATGAGGACATGGAACAGGATAATACAACATTGCTGACAGAGTTGTTCTCACA
GGACTTACATATCAGCCAGAGTGGAAATGCCCTGTTCTGGTGTCTGGTATCTAC
40 TCATCACTATTGTGTGGAACCTTGGTCTGATTGCTCTTATCTGAATGACCCACAACCTCAC
ATCCCCATGTACTTTTCTTGGGAGTTAGCCTTGTGATGCTTGTGATCTGCTTATCTGCTGAATGC
AACTCCAAAATGTTGGTTAATTCTTGCATTTGGGAACACTAGAAATGTTCTTGTGCAACAAT
45 ATGATTCAATTCTTGCATTTGGGAACACTAGAAATGTTCTTGTGATCTGCTGAATGC
GGCATATGATCGCTATGTAGCCATATGCAAACCTTACTATATCCAGTGATTATGAACAAT
TCACTATGCATACGGCTGTTAGCCTCTCATTTAGGTGGCTTCCTCCATGCCTTAATTCA
TGAAGTCCTTATATTCAAGATTAACCTCTGCAATTCTAACATAATACATCATTTACTGTG
50 ATATTATACCACTGTTATGATTCTGTACTGACCCCTCTATTAAATTCTAATGGTTTTA
TTTGTCTGGCTCAATTCAAGGTATTCACTGACAGTTCTTAATTCTTACACATTGCT
CTTTCAAAATCCTAAAAAGAAGTCTGTTAGAGGGCGTAAGGAAAGCCTTCCACCTGTG
GAGCCCACCTCTTATCTGTCTTTATATTAGGCCACTTATCTTGTATTGCGCCCT
GCATCTCCACAAGCAGATGACCAAGATATGATAGACTCTGCTTTATACAATCATAATT
CTTGCTAAATCCCATTATCTACAGTCTGAGAAATAACAAGTAATAGATTCAATT
AATGGTAAAAGAAATGTTAG (SEQ ID NO: 236)

AOLFR128 sequences:

55 METQNLTVVTEFILLGLTQSQDAQLLVFLVLIFYLILPGNLIIFTIKSDPGLTAPLYFFLGNLA
LLDASYSFIVVPRMLVDFLSEKKVISYRSCITQLFLHFLGAGEMFLLVVMADFDRYIAICRPLHY

STIMNPRACYALSLVLWLGGFIHSIVQVALILHLPFCGPNQLDNFFCDVPQVIKLAGCTNTFVEL
LMVSNSGLSLLCFLGLLASYAVILCIREHSSEGKSKAISTCTTHIIIIFLMFGPAIFIYTCPFQAFP
ADKVVSFLHTVIFPLMNPVITYTLRNQEVKASMRKLLSQHMFC (SEQ ID NO: 237)

5 ATGGAAACACAGAACCTCACAGTGGTACAGAGAATTCAATTCTCTGGTCTGACCCAGTCTC
AAGATGCTCAACTCTGGTCTTGTGCTAGTCTAATTCTACCTTATCATCTCCCTGGAA
AATTCTCATCATTTCACCATAAAGTCAGACCCCTGGGCTCACAGCCCCCTCTATTCTT
TCTGGGCAACTGGGCTTACTGGATGCATCCTACTCCTCATGTGGTCCCAGGATGTG
GTGGACTTCCTCTGTGAGAAGAGTAATCTCCTATAGAACGTCATCACTCAGCTCTT
10 TCTTGCACTTCTGGAGCGGGAGAGATGTTCCCTCGTGTGATGGCCTTGACCGCTAC
ATCGCCATCTGCCGCCCTTACACTATTCAACCACATGAACCCCTAGACGCTGCTATGCAT
TATCGTGGTCTGTGGCTTGGGGCTTATCCATTCCATTGTACAAGTAGCCCTATCCTG
CACTTGCCCTCTGTGGCCAA'ACCAGCTCGATAACTCTCTGTGATGGTCTCCAACAGTGGCCTG
15 CAAGCTGCCCTGCACCAATACCTTGTGGAGCTCTGTGATGGTCTCCAACAGTGGCCTG
CTCAGCCTCCTGTGCTCCTGGCCTCTGGCCTCTATGCAGTCATCCTCTGTGCTATAAG
GGAGCACTCCCTGAAGGAAAGAGCAAGGCTATTCCACATGCACCAACCCATAATTATCATT
ATATTCTCATGTTGGACCTGCTATTTCATCTACACTGTCATCTTGTGATGAACCTGTTATTATA
TGACAAGGTAGTTCTCTTCCATACTGTCATCTTGTGATGAACCTGTTATTATA
20 CGCTTCGCAACCAGGAGGTGAAAGCTCCATGAGGAAGTTGTTAAGTCACATATGTTTG
CTGA (SEQ ID NO: 238)

AOLFR129 sequences:

25 MALYFSLILHGMSDLFLSTGHPRASCRMEAMKLLNQSQVFILLGLTSSQDVEFLLFALFSVI
YVVTVLGNLLIIVTVFNTPNLNTPMYFLLGNLSFVDMTLASFATPKVILNLLKKQKVISFAGCFT
QIFLLHLLGGVEMVLLVSMAFDRYVAICKPLHYMTIMNKKVCVLLVVTSWLLGLLHSGFQIPF
AVNLPFCGPNVVDSIFCDLPLVTKLACIDTYFVQVVIVANSGIISLSCFILLISYSLILITKHNHSP
GQSKARSTLTAHITVVLFFGPCIYTWFFGNHSVDKFLAVFYTTIPILNPIIYTLRNKEMKISMK
KLWRAFVNSREDT (SEQ ID NO: 239)

30 ATGGCTCTTATTTCACTCATACTCCATGGTATGAGTGATCTTCTTCTCTACAGG
TCATCCAAGAGCGAGCTGTAGGATGGAGGCCATGAAACTATTAAATCAATCTCAAGTGTC
AGAATTCACTTCTGGACTGACCAGCTCCAGGATGTAGAGTTCTCTCTTGCCTCT
TCTCGGTTATCTATGTGGTCACAGTTGGTAACCTTCTTATTATAGTCACAGTGTAAAC
ACCCCTAACCTGAATACTCCCATGTATTTCTCCTGGTAATCTCTCTTGTAGATATGAC
35 CCTTGCTCTTGCACCCCTAACGGTGAATTCTGAACCTGTAAAAAAGCAGAACGGTAATT
TCTTTGCTGGGTGCTTCACTCAGATATTCTCCTTCACTTACTGGGTGGGGTTGAAATGGT
ACTGTTGGTCTCCATGGCTTTGACAGATATGTGGCCATTGTAAGCCCTACACTACATG
ACCATCATGAACAAGAACGGTATGTGTTCTGTGTTAGTGACCTCATGGCTCTGGTCTCC
40 TTCACTCAGGGTTTCAGATACCATTGCTGTGAACCTGCCCTTGTGTTACTAACGCTGCTGTATAGACATATATTGTA
GACAGCATTGTCAGCTCCCTTGGTTACTAACGCTGCTGTATAGACATATATTGTA
ACAGGTAGTCATTGTCACAGTGGCATAATCTCCCTGAGCTGTTCTTACGCTTCAATTGCTTA
TCTCCTACAGTCTGATCCTCATAACCATTAGAACCAACTCTCCTACTGGCAATCTAAAGC
45 CCGTCCACTTGACTGCTCACATCACAGTGGTGAATTCTCTTGTGTTACTAACGCTGCTTCAATTGCTTA
TCTACATTGGCCCTCGGCAACCACTCTGTAGATAAGTCCCTGTGTTTATACCATC
ATCACTCCTATCTGAATCCAATTACTCTGAGAACAAAGAAATGAAGATATCCA
TGAAAAAAACTCTGGAGAGCTTGTGAATTCTAGAGAACAGACTTAG (SEQ ID NO: 240)

AOLFR131 sequences:

50 MASTSNVTELIFTGLFQDPAVQSVCFVFLPVYLATVVGNGLIVLTVSISKSLDSPMYFFLSCLS
LVEISYSSTIAPKFIIDLLAKIKTISLEGCLTQIFFFHFFGVAEILLIVVMAYDCYVAICKPLHYMNI
ISRQLCHLLVAGSWLGGFCHSIIQILVIIQLPFCGPNVIDHYFCDLQPLFKLACTDTFMEGVIVLA
NSGLFSVFSFLILVSSYIVILVNLRNHSAEGRHKALSTCASHITVVLFFGPAIFLYMRPSSTFTED
KLVAVFYTVTPMLNPIIYTLRNAEVKIAIRRLWSKKENPGRE (SEQ ID NO: 241)

55 ATGGCCAGTACAAGTAATGTGACTGAGTTGATTTCACTGGCCTTCCAGGATCCAGCTG
TGCAGAGTGTATGTTGTGGTCTCCCGTGTACCTGCCACGGTGGTGGCAATGG

CCTCATCGTTCTGACGGTCAGTATCAGCAAGAGCTGGATCTCCCATGTAACITCITCCTTA
 GCTGCCTGCTTGGAGATCAGTTATCCTCACTATCGCCCTAAATTCACTCATAGAC
 TTACTTGCCAAGATTAACCATCTCTGGAAGGCTGTCGACTCAGATATTCTTCCA
 CTCTTTGGGGTTGCTGAGATCCTTTGATTGTGGTGTGATGCCATGATTGCTACGTGGCC
 5 ATTGCAAGCCTCTCATTATGAACATTATCAGTCGTCACACTGTGTCACCTCTGGTGGC
 TGTTCTGGCTGGGGCTTTGTCACTCCATAATTAGATTCTCGTTATCATCCAATTGC
 CCTCTGTGGTCCCAATGTGATTGACCACTATTCTGTGACCTCCAGCCTTATTCAAGCTT
 GCCTGCACTGACACCTCATGGAGGGGTTATTGTGGTGGCCAACAGTGGATTATTCTCTG
 10 TCTCTCCTCTCCTCATCTGGTGCCTTATATTGTCATTCTGGTCAACTTGAGGAACCAT
 TCTGCAGAGGGAGGCACAAAGCCCTCCACCTGTGCTTCTCACATCACAGTGGTCATCT
 TGTTTTTGGACCTGCTATCTCCTCATGCGACCTCTCCACTTCACTGAAGATAAA
 CTTGTGGCTGTATTCTACACGGTCATCACCCCATGCTGAACCCATCATTACACACTCAG
 GAATGCAGAGGTGAAAATGCCATAAGAAGATTGTGGAGCAAAAGGAGAATCCAGGG
 15 GGGAGTGA (SEQ ID NO: 242)

AOLFR132 sequences:

MVATNNVTEIFVGFQSNWSEQRVISVMFLMYTAVVLGNGLIVVILASKVLTSPMYFFLSYL
 SFVEICYCSVMAPKLIIFDSFIKRKVISLGKCLTQMFSLHFFGGTEAFLLMVMAYDRYVAICKPL
 20 HYMAIMNQRMCGLLVRIAWGGGLLHSVGQTFIFQLPFCGPNIMDHYFCDVHPVLELACADT
 FFISLLITNGGSISVVSFFVLMASYLILHFLRSHNLEGQHAKALSTCASHVTVVDLFIPCSLVYIR
 PCVTLPADKIVAVFYTVVTPLLNPVIYSFRNAEVKNAMRRFIGGKVI (SEQ ID NO: 243)

ATGGTTGCTACAAACAATGTGACTGAAATAATTCTGGGATTTCCAGAAATTGGAGTG
 25 AGCAGAGGGTCATTTCTGTGATGTTCTCTCATGTACACAGCTGTTGTGCTGGCAATGG
 CCTCATTGTGGTGACCATCCTGGCCAGCAAAGTGTACCTCCCCATGTATTCTTCTCA
 GCTACTTATCCTTGTGGAGATCTGCTACTGTTCTGTGATGGCCCTACACAGATGTTTCCCTCC
 TCCATTATCAAGAGGAAAGTCATTCTCTCAAGGGCTGCCTCACACAGATGTTTCCCTCC
 ATTCTTGTGGCACTGAGGCCTTCTCTGATGGTGTGATGGCCTATGACCGCTATGTGGC
 30 CATCTGCAAGCCCTTGCACTACATGGCCATCATGAACCAAGCGAAATGTGTGGTCTCCTCGTG
 AGGATAGCATGGGGGGGGCCTGCTGCATTCTGTGGGCAAACCTCCTGATTTCAGC
 TCCCCTCTGTGGCCCAAACATCATGGACCAACTACITCTGTGATGTCCACCCAGTGCTGGA
 GCTGGCCTGCGCAGACACCTCTTCATTAGCCTGCTGATCATCACCAATGGCGCTCCATC
 TCCGTAGTCAGTTCTCGTGTGATGGCTTCCACCTGATCATCCTGCACTTCTGAGAAG
 35 CCACAACTTGGAGGGCAGCACAAGGCCCTCTCACCTGTGCTCTCATGTCACAGTTGTC
 GACCTGTTCTCATACCTGCTCCTGGCTATATTAGGCCCTGTGTCACCCCTCCTGAGAAG
 CAAGATAGTTGCTGTATTATACAGTGGTCACACCTCTTAAACCTGTGATTACTCCT
 TCAGGAATGCTGAAGTGAAAATGCCATGAGGAGATTATTGGGGAAAAGTAATTGA
 (SEQ ID NO: 244)

AOLFR133 sequences:

MTEFIFVLSPNQEVRQCFVIFLFLYTAIVLGNFLIVLTVMTSRSLGSPMYFFLSYLSFMEICYS
 SATAPKLISDLAERKVISWWGCMQLFFLHFFGGTEIFLLTVMAYDHYVAICKPLSYTTIMN
 WQVCTVLVGIAWVGGFMHSFAQILLIFHLLFCGPNVINHYFCDLVPLLKACSDTFLIGLLIVAN
 45 GGTLSVISFGVLLASYMVILLHRTWSSEGWCALSTCGSHFAVVILFFGPCVFNSLRPSTTLPI
 DKMVAVFYTVITAILNPVIYSLRNAEMRKAMKRLWIRTLRLNEK (SEQ ID NO: 245)

ATGACTGAATTCATTTCTGGTACTTCTCCAACCAGGAGGTGCAGAGGGTTGCTTTG
 TGATATTCTGTCITGTACACAGCAATTGTGCTGGGAATTCTCATGTGCTCACTGTC
 50 ATGACCAGCAGAAGCCTGGTCCCCATGTACTTCTCTCAGCTACCTCTCCTCATGGA
 GACTGCTACTCCTCCGCTACAGCCCCAAACTCATCTCAGATCTGCTGGCTAAAGGAAA
 GTCATATCTGGTGGGCTGCATGGCACAGCTTCTCTGCACTCTTGTGGCAGTGA
 GATTTCTGCTACTGTGATGCCATGACCACTATGTGGCCATCTGCAAGCCCTCAGC
 TACACCACCATCATGAACGGCAGGTGTACTGTCCTGTAGGAATAGCATGGTGGGA
 GGCTTCATGCATTCTTGCACAAATCCTCTCATCTCACCTGCTCTGTGGCCCCAA
 55 TGTGATCAATCACTATTCTGTGACCTAGTCCCCTCTCAAACCTGCTGCTGACACCT
 TCCTCATTGGTCTGCTGATTGTCATGGAGGCACCTGCTGTGATCAGTTGGGGT

5 CCTCTTAGCATCCTATATGGTCATCTGCTCCATCTGAGAACCTGGAGCTCTGAAGGGTGG
TGCAAAGCCTCTCCACCTGTGGGTCCCATTCGCTGTGGTTATCTTGTCTTGGGCCCTG
CGTCTTCAACTCTGTAGGGCCTCTACCCTCTGCCCATAGACAAGATGGTGCTGTGTTCT
ACACAGTGATAACCGCGATCCTGAACCTGTCACTACTCTGTAGAAAATGCTGAAATGAG
GAAGGCCATGAAGAGGGCTGTGGATTAGGACATTGAGACTAAATGAGAAAATAG (SEQ ID
NO: 246)

AOLFR134 sequences:

10 MTTIILEVDNHTVTRFILLGGFPTRAFQLLFFSIFLATYLLTLENLLIIAIHSDGQLHKPMYFFL
SHLSFLEMWYVTVISPKMLVDFLSDKSISFNGCMTQLYFFVTVCYEIILAIMAFDRYVAIC
NPLRYPVIMTNQLCGTLAGGCWFCGLMTAMIKMVFIAQLHYCGMPQINHYFCDISPLLNVSCE
DASQAEMVDFFLALMVIAPLCVVVASYAAILATIIRIPSAQGRQKAFSTCASHLTVVILFYSMT
LFTYARPKLMYAYNSNKVVSVLYTVIVPLLNPIIYCLRNHEVKAALRKTIHCRGSGPQGNGAFS
S (SEQ ID NO: 247)

15 ATGACCACCATATTCTGGAAGTAGATAATCATACAGTGACAACACGTTCATTCCTCTGG
GGTTTCCAACACGACCAGCCTCCAGCTCTCTTTCTCCATTTCCTGGCAACCTATCTG
CTGACACTGCTGGAGAATCTTCTTATCATCTTAGCTATCCACAGTGATGGGCAGCTGCATA
AGCCCCATGTACTTCTTCTGAGCCACCTCTCTCTGGAGATGTGGTATGTACAGTCATC
AGCCCCAAGATGCTGTTGACTTCCTCAGTCATGACAAGAGTATTCTTCATGGCTGCA
TGACTCAACTTACTTTTGTGACCTTGTCTGCACTGAGTACATCCTCTGCTATCATG
GCCCTTGACCGCTATGTAGCCATTGTAATCCACTACGCTACCCAGTCATCATGACCAACC
AGCTCTGTGGCACACTGGCTGGAGGATGCTGGTCTGTGGACTCATGACTGCCATGATTAA
GATGGTTTTATAGCACAACTTCACTACTGTGGCATGCCCTCAGATCAACTCACTACTTTGTG
ATATCTCTCCACTCTTAACGTCTCCTGTGAGGATGCCCTCACAGGCTGAGATGGTGGACTT
CTCTTGGCCCTCATGGTATTGCTATTCTCTTGTGTTGGTGGCATCTCACGCTGCTA
TCCCTGCCACCATCCTCAGGATCCCTGTCTCAGGGCCGCAAAGGCATTCTCCACCTG
TGCCTCCCACCTGACCGTCGTAATTCTCTTATTCCATGACACTTTCACCTATGCCGTC
CCAAACTCATGTATGCCCTACAATTCCAACAAAGTGGTATCTGTTCTACACTGTCATTGTT
CCACTCTCAACCCCATCATTTACTGTCTGAGGAACCATGAAGTAAGGCAGGCCCTCAGAA
AGACCATACATTGCAAGAGGAAGTGGGCCCCAGGGAAATGGGGCTTCAGTAGTTAA (SEQ
ID NO: 248)

AOLFR135 sequences:

35 MIFPSHDSQAFTSVDMEVGNCTILTEFILLGFSADSQWQPILFGVFLMLYLITLSGNMTLVILIRT
DSHLHTPMYFFIGNLSFLDFWYTSVYTPKILASCVSEDKRISLAGCGAQLFFSCVVAYTECYLL
AAMA YDRHAAICNPLL YSGTMSTA LCTGLVAGSYIGGFLN AIAHTANTFRLHFCGKNIIDHFFC
DAPPLVKMSCTNTRVYEKVL LGVVGF TVLSSIL AILISYVNILL AILRIHSASGRHKAFSTCASHL
40 ISVMLFYGSLLFMYSRPSSTYSLERDKVAALFYTVINPLNPLIYSLRNKDIKEAFRKATQTIQPQ
T (SEQ ID NO: 249)

45 ATGATTTCCCTCTCATGATAGTCAGGTTCACCTCCGTGGACATGGAAGTGGAAATT
GCACCATCCTGACTGAATTCATCTGTTGGTTCTCAGCAGATTCCAGTGGCAGCCGAT
TCTATTTGGAGTGTCTGATGCTCTATTGATAACCTTGTCAAGGAAACATGACCTTGGTITA
TCTTAATCCGAACGTGATTCCACATGCAACACTATGTAATTTCATTGGCAATCTGTCT
TTTTGGATTCTGGTATACCTCTGTGTATACCCCCAAAATCCTGGCCAGTTGTGTCTCAGA
AGATAAGCGCATTCTGGCTGGATGTGGGCTCAGCTGTTTTCTGTGTAGCCT
ACACTGAATGCTATCTCTGGCAGCCATGGCATATGACGCCATGCAGCAATTGTAAACCC
ATTGCTTATTCAAGTACCATGTCCACGCCCTCTGTAAGTGGCTTGTCTGGCTCTACA
TAGGAGGATTGTAAATGCCATAGCCCATACTGCCAATACATTCCGCTGCATTGGTGG
TAAAAAATATCATTGACCACTTTCTGTGATGCACCACCATGGTAAAAATGTCTGTACA
AACACCAGGGTCTACGAAAAAGTCCTGCTTGGTGTGGTGGCTTCACAGTACTCTCCAGCA
TTCTTGCTATCTGATTCCCTATGTCAACATCCTCTGGCTATCCTGAGAATCCACTCAGCT
TCAGGAAGACACAAGGCATTCTCCACCTGTGCTTCCCACCTCATCTCAGTCATGCTCTCTA
50 TGGATCATTGTTATGTATTCAAGGCCTAGTCCACCTACTCCCTAGAGAGGGACAAA
GTAGCTGCTCTGTTACACCGTGTCAACCCACTGCTCAACCTCTCATCTAAGCCTGAG
55

AAACAAAGATATCAAAGAGGCCTTCAGGAAAGCAACACAGACTATACAACCACAAACATG
A (SEQ ID NO: 250)

AOLFR136 sequences:

5 MTMENYSMAAQFVLGGLTQQAEQLQLPLFLGLIYVVTVVGNLGMILLIAVSPLLHTPMYYFL
SSLSFVDFCYSSVTPKMLVNFLGKNTILYSECMVQLFFFVVFVAEGYLLTAMAYDRYVAIC
SPLLYNAIMSSWVCSLLVLAFFLGLSALTHTSAMMKLSFCKSHIINHYFCDVLPLLNLSCSNT
HLNELLFLILAGFNTLVPTLAVAVSYAFILYSILHIRSSEGRSKAFTGTCSSHLMVVIFFGSITFMY
FKPPSSNSLDQEKVSSVFYTTVPMLNPLIYSLRNKDVKKALRKVLVGK (SEQ ID NO: 251)

10 ATGACCATGGAAAATTATTCTATGGCAGCTCAGTTGTCTAGATGGTTAACACAGCAAG
CAGAGCTCCAGCTGCCCTCTTCCCTGTTCTGGGAATCTATGTGGTCACAGTAGTGGG
CAACCTGGGCATGATTCTCCTGATTGCAGTCAGCCCTACTTCACACCCCCATGTACTATT
TCCTCAGCAGCTGTCCCTCGTCGATTCTGCTATTCTCTGTCTGATTACTCCCCAAATGCTG
15 GTGAACCTCCTAGGAAAGAAGAATACAATCCTTACTCTGAGTCATGGTCCAGCTCTTT
TCTTGTGGCTTTGTGGTGGCTGAGGGTTACCTCTGACTGCCATGGCATATGATGCTA
TGTGCCATCTGTAGCCCCTGCTTATAATGCGATCATGCTCTATGGGTCTGCTCACTGC
TAGTGTGGCTGCCCTCTTCTGGGCTTCTCTGCCTTGACTCATACAAGTGCATGATG
AAACTGTCCCTTGCAAATCCCACATTATCAACCATTACTCTGTGATGTTCTTCCCCTCCT
20 CAATCTCTCCTGCTCCAACACACACCTCAATGAGCTCTACTTTTATCATTGGGGGTTA
ACACCTGGTGCCACCCCTAGCTGTTGCTCTCATGCCCTACACGATCCT
CACATCCGCTCCTCAGAGGGCCGGTCCAAAGCTTTGGAACATGCAGCTCTCATCTCATGG
CTGTGGTGTCTCTGGGTCATTACCTCATGTATTCAAGCCCCCTCAAGTAACCTCC
CTGGACCAGGAGAAGGTGTCCTGTGTTCTACACCACGGTGATCCCCATGCTGAACCCCT
25 TAATATACAGTCTGAGGAATAAGGATGTGAAGAAAGCATTAAAGGAAGGTCTAGTAGGAA
AATGA (SEQ ID NO: 252)

AOLFR137 sequences:

30 MSPENQSSVSEFLLGLPIRPEQQAVFFALFLGMYLTTVLGNLLIMLLIQLDSHLHTPMYFFLSH
LALTDISFSSVTPKMLNMNMQTHLAVFYKGCISQTYFFIFFADLDSFLITSMAYDRYVAICHPL
HYATIMTQSQCVMVLVAGSWVIACACALLHTLLAQLSFCADHIIPHYFCDLGALLLSCSDTSL
NQLAIFTAALTAIMPLFLCILVSYGHIGVTILQIPSTKGICKALSTCGSHLSVVTIYYRTIIGLYFLP
PSSNTNDKNIASVIYTAVTPMLNPFIYSLRNKDIKGALRKLLSRSGAVAHAACNLSTLGG (SEQ
ID NO: 253)

35 ATGAGCCCTGAGAACCAAGAGCAGCGTGTCCGAGTTCCCTCCCTGGGCCTCCCCATCCGGC
CAGAGCAGCAGGCCGTTCCTGCCCTGTTCTGGCATGTACCTGACCACGGTGTGG
GAACCTGCTCATCATGCTGCTCATCCAGCTAGACTCTCACCTTCACACCCCCATGTACTTCT
40 TCCTTAGCCACTTGGCCCTCACTGACATCTCCCTTTCATCTGTCACTGCTCTAAAGATGCTG
ATGAACATGCAGACTCAGCACCTAGCCGTCTTACAAGGGATGCATTCACTGACAGACATATT
TTTCATATTTCATGACTTAGACAGTTCTTATCACCTCAATGGCATATGACAGGTAT
GTGCCATCTGTCTACATTAGCCACCATCATGACTCAGAGGCCAGTGTGTCTG
TGGTGGCTGGGCTGGGTCTCGCTGCTGCGTGTGCTCTTGCACTACCCCTCCCTGGCC
45 CAGCTTCCTCTGTGCTGACCACATCATCCCTCACTACTCTGTGACCTTGGTCCCTGCT
CAAGTTGTCCCTGTCAGACACCTCCCTCAATCAGTTAGCAATCTTACAGCAGCATTGACA
GCCATTATGCTTCCATTCTGTGCACTCTGGTTCTTATGGTCACATTGGGTCAACATCCT
CCAGATTCCCTCTACCAAGGGCATATGCAAAGCCTGTCCACTTGTGGATCCACCTCTCA
GTGGTGACTATCTATTACGGACAATTATTGGTCTCTATTCTTCTCCCCATCCAGCAACAC
50 CAATGACAAGAACATAATTGCTCAGTGTGATATACACAGCAGTCACTCCATGTTGAACCCA
TTCATTACAGTCTGAGGAATAAGACATTAAGGGAGCCCTAAGAAAACCTTGTGAGTAGG
TCAGGCGCAGTGGCTCATGCCTGTAATCTCAGCACTTGGGAGGCTGA (SEQ ID NO: 254)

AOLFR138 sequences:

55 MLNFTDVTEFILLGLTSRREWQVLFFIVFLVYIITVVGNIGMMLIKVSPQLNSPMYFFLSHLS
FVDVWFSSNVTPKMLENLFSDKKTISYADCLAQCFFFIALVHVEIFILAAIFDRYTVIGNPLLY
GSKMSRGVCIRLITFPYIYGLTSLATLWTYGLYFCGKIEINHYFCADPPLIKMACAGTFVKEY

TMLLILAGINFTYSLTVIISYLFILIAILRMRSAEGRQKAFSTCGSHPTAVIIFYGTLIFMYLRRPTE
ESVEQGKVMAVFYTTVIPMLNPMIYSLRNKDVKKAMMKVISRSC (SEQ ID NO: 255)

5 ATGCTCAATTCAACCGATGTGACAGAGTTCATTCTTTGGGGCTAACGAGCCGTCGGGAAT
GGCAAGTTCTCTTCATCGTTCTGTGGTCTACATTATCACCGTGGTGGCAATATC
GGCATGATGTTGTTAATCAAGGTCAAGTCAGTCCTCAGCTTAACAGCCCCATGTACTTTCTCA
GTCACTTGTCAATTGTTGATGTGGTTCTTCCAATGTCAACCCCTAAATGTTGGaAAAT
CTGTTATCAGATAAAAAAAACAATTCTATGCTGGCTGTTAGCACAGTGTCTTCTTCAT
TGCTCTTGTCCATGTGGAAATTCTTATTCTGCTCGATTGCCTTGATAGATACACAGTGA
10 TTGGAAATCCTTGTCTTATGGCAGCAAATGTCAAGGGATGTCTGATTGACTGATTAC
TTTCCCTTACATTATGGTTCTGACGAGTCTGACAGCAACATTATGGACTTATGGCTGT
ACTTCTGTGGAAAAATTGAGATCAACCAATTCTACTGTGAGATCCACCTCTCATCAAAT
GGCCTGTGCCGGGACCTTGTAAAAGAATATACAATGCTCATACTTGCAGACATCAAATTC
15 ACATATTCCCTGACTGTAATTATCATCTTACTTATTCATCCTCATTGCCATTGCGAAT
GCGCTCAGCAGAAGGAAGGCAGAAGGCCTTTCCACATGTGGTCCCCTGACAGCTGT
CATCATATTCTATGGTACTCTGATCTCATGTACTCAGACGTCCCACAGAGGAGTCTGTG
GAGCAGGGGAAGATGGTGGCTGTGTTCTATACCACAGTGAATCCCCATGTTGAATCCCATGA
TCTACAGTCTGAGGAACAAGGATGTGAAAAGGCCATGATGAAAGTGAATCAGCAGATCAT
20 GTTAA (SEQ ID NO: 256)

AOLFR139 sequences:

MGFPGIHSWQHWLSLPLALLYLLALSANILILIIINKEAALHQPMYYFLGILAMADIGLATTIMP
KILAILWFNAKTIISLLECFQAQMYAIHCFCVAMESSTFVCMAIDRYVAICRPLRYPHSITESFVFKAN
25 GFMALRNSLCLISVPLLAQRHYCSQNQIEHCLCSNLGVTSLSDDRRINSINQVLLAWTLMGS
DLGLIILSYALILYSVLKLNSPEAASKALSTCTSHLILILFFYTVIIVISITRSTGMRVPLIPVLLNVL
HNVIPPALNPMVYALKNKELRQGLYKVIRLGVKGT (SEQ ID NO: 257)

30 ATGGGATTCCCTGGCATTCACAGTTGGCAGCACTGGCTCTCCCTGCCCTGGCTCTGCTCT
ACCTCTAGCTCTCAGTGCCAACATCCTTATCCTGATCATCATCAACAAAGAGGGCAGCACT
GCACCAGCCTATGTACTATTCTGGGCATCTTGGCTATGGCAGACATAGGCCTGGCTTAC
ACCATCATGCCTAAGATTGGCCATCTTATGGTCAATGCTAAGACCATCAGTCTCTGG
AGTCTTGCTCAGATGTATGCCATACATTGCTTGTGGCATGGAATCAAGTACCTTTGT
35 CTGCATGGCTATTGATAGATATGTAGCCATTGTCGACCGCTACGATATCCATCAATCATC
ACTGAATCTTGTGTTCAAAGCAAATGGGTCATGGCACTGAGAACAGCCTGTGTCTCA
TCTCAGTGCCTCTGTGGCTGCCAGAGGCATTACTGCTCCCAGAACATCAAATTGAGCACTG
TCTTGTTCTAACCTGGAGTCACTAGCCTATCTGTGATGATCGAACATAGCATT
40 AACCAAGGTCTTTGGCTGGACACTCATGGGAAGTGACCTGGTTGATTATTTATCAT
ATGCTCTAACATTACTCTGCTGAAGCTGAACCTCTCCAGAACAGCTGCATCCAAGGCCCT
AAGTACCTGCACCTCCCACCTCATCTAACATTCTCTACACAGTCATATTGTGATT
CCATTACTCGTAGTACAGGAATGAGAGTTCCCCTTATTCCAGTTCTACTTAATGTGCTACA
CAATGTCATTCCCCCTGCCCTGAACCCCATGGTATATGCACTCAAGAACAAAGGAACCTCAGG
CAAGGCTTACAAAGGTACTTAGACTGGGAGTGAAGGGACCTGA (SEQ ID NO: 258)

AOLFR140 sequences:

45 MLTLNKTDLIPASFILNGVPGLEDTQLWISFPFCSMYVVAMVGNCGLYLIHYEDALHKPMYY
FLAMLSFTDLMVCSSTIPKALCFWFHLKDIFDDECLVQMFIFTGMEGVLMALDRYV
AICYPLRYSTILTNPVIAKVGATFLRGVLLIIPFTFLTKRLPYCRGNILPHTYCDHMSVAKLSCG
NVKVNAIYGLMVALLIGGFIDLCITISYTMILRAVVSLSSADARQKAFNTCTAHICAIVFSYTPAF
50 FSFFSHRFGEHIIPPSCHITVANTYLLLPTMNPIVYGVTKQIRDGVIRILSGSKDTKSYSM (SEQ
ID NO: 259)

55 ATGCTAACACTGAATAAAACAGACCTAATACCAAGCTTCATTATTCTGAATGGAGTCCAG
GACTGGAAGACACACAACACTCTGGATTCTCTCCATTCTGCTCTATGTATGTTGTGGCTAT
GGTAGGGAATTGTGGACTCTCTACCTCACTATGAGGATGCCCTGCACAAACCCATG
TACTACTCTTGTGCCATGCTTCTTACTGACCTGTTATGTGCTCTAGTACAATCCCTAA
AGCCCTCTGCATCTCTGGTTCATCTCAAGGACATTGGATTGATGAATGCCCTGTCCAG

ATGTTCTTCATCCACACCTTCACAGGGATGGAGTCTGGGGTGCCTATGCTTATGGCCCTGG
 ATCGCTATGTGGCCATCTGCTACCCCTACGCTATTCAACTATCCTCACCAATCCTGTAATT
 GCAAAGGGTGGGACTGCCACCTTCTGAGAGGGGTATTACTCATTATCCCTTACTTTCT
 5 CACCAAGGCCCTGCCCTACTGCAGAGGCAATATACTTCCCCATACCTACTGTGACCACATG
 TCTGTAGCCAAATTGCTCTGTGGTAATGTCAAGGTCAATGCCATCTATGGTCTGATGGTTG
 CCCTCCTGATTGGGGCTTGACATACTGTATCACCCTCCTATACCATGATTCTCCGG
 GCAGTGGTCAGCCTCTCCTCAGCAGATGCTCGCAGAAGGCCTTAATACCTGACTGCC
 ACATTGTGCCATTGTTCTCTATACTCCAGCTTCTCCTTCTTCCCACCGCTTG
 10 GGGAACACATAATCCCCCTTCTGCCACATCATTGTAGCCAATATTATCTGCTCCTACCA
 CCCACTATGAACCCATTGTCTATGGGTGAAACCAAACAGATACGAGACTGTGTCAA
 GGATCCTTCAGGTTCTAAGGATACCAAATCCTACAGCATGTGA (SEQ ID NO: 260)

AOLFR141 sequences:

15 MSSTLGHNMESPNTDVPSPVFLLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVL
 HKPVYLFCLMSTIDLAASVSTPKLLAIFWCAGHISASACLAQMFFIHAFCMMESTVLLAM
 AFDRYVAICHPLRYATILTDLAHIGVAAVVRGSLMLPCPFLIGRLNFCQSHVILHTYCEHMA
 VVKLACGDRPNRVYGLTAALLVIGVDLFCIGLSYALSAQAVRLSSHEARSKALGTCGSHVC
 VILISYTPALFSFFTHRFGHHPVHILLANVYLLPPALNPVYGVTKQIRKRVVRVFQSGQ
 GMGIKASE (SEQ ID NO: 261)

20 20 ATGTCCAGCACTCTGGCCACAACATGGAATCTCCTAATCACACTGATGTTGACCCCTCTG
 TCTTCTTCCTCCTGGCATCCCAGGTCTGGAACAAATTCTATTGTGGCTCTCACCTCTGTG
 TGTGGCTTAGGCACAGCCACAATTGTGGCAATAACTATTCTGGTGTGTTGCCACTG
 AACAGTCTGCACAAGCCTGTGTACCTTTCTGTGATGCTCTCACCCATGACTTGACTG
 25 GCCTCTGTCCTCACAGTCCAGCTACTGGCTATCTCTGGTGTGGAGGCCGACATATAT
 CTGCCTCTGCCTGCCTGGCACAGATGTTCTCATGCCCTCTGCATGATGGAGTCCACT
 GTGCTACTGGCCATGGCTTGTGATCGCTACGTGGCCATCTGCCACCCACTCCGCTATGCCA
 CAATCCTCACTGACACCATCATTGCCACATAGGGTGGCAGCTGTAGTGCAGGGCTCCCT
 30 GCTCATGCTCCCATTGCTCTCTTATTGGCGTTGAACCTCTGCCAAAGCCATGTGATCC
 TACACACGTACTGTGAGCACATGGCTGTGGTAAGCTGGCTGTGGAGACACCAGGCCA
 ACCGTGTGATGGCTGACAGCTGCACTGTTGGTCAATTGGGTTGACTGTGTTGCATTGG
 TCTCTCCTATGCCCTAAGTGCACAAGCTGTCTGCCTCTCATCCCATGAAGCTCGGTCCA
 AGGCCCTAGGGACCTGTGGTCCCATGTCATCTCATCTTACACCAGCCCTC
 35 TTCTCTTTTACACACCGCTTGGCCATCACGTTCCAGTCCATATTCACATTCTTTGGC
 CAATGTTATCTGCTTGTGCCACCTGCTCTTAATCCTGTGGTATATGGAGTTAACCAAC
 AGATCCGTAAGAGTTGTCAGGGTGTCAAAGTGGCAGGGAAATGGCATTCAAGGCAT
 CTGAGTGA (SEQ ID NO: 262)

AOLFR143 sequences:

40 40 MLGLNGTPFPQPATLQLTGIPGIQTGLTWVALIFCILYIMISIVGNLSILTLVFWEPALHQPMYYFL
 SMLALNDLGVSFSTLPTVISTFCFNYNHVAFNACLVQMFHHTFSFMESGILLAMSLDRFVAICY
 PLRYVTVLTHNRILAMGLGILTKSFTLFPFPVVKRLPFCKGNVLHHSYCLHPDLMKVACGDI
 HVNNIYGLLVIIFTYGMDFSTFILLSYALILRAMLVIIISQEQLRKALNTCMHICA
 VLAFYVPIIAVS
 45 MIHRFWKSAPPVVHVMMSNVYLFVPPMLNPIIYSVKTKEIRKGILKFFHKSQA (SEQ ID NO:
 263)

50 50 ATGCTGGGTCTCAATGGCACCCCTCCAGCCAGCAACACTCCAGCTGACAGGCATTCTG
 GGATACAAACAGGCCCTCACCTGGTTGCCCTGATTCTGCATCCTCACATGATCTCCATT
 GTAGGTAACTCAGCATCTCACTCTGGTGTGGAGGCCCTGCTCTGCATGCCCATGTT
 ACTACTCCTCTCATGCTCGCTCAATGATCTGGAGTGTCTCTACACTTCCACT
 GTGATTCTACTTCTGCTTCAACTACAACCATGTTGCGTTAATGCTTGCCTGGTCCAGAT
 GTCTTCTCATCCACACTTCTCCTCATGGAGTCAGGCATACTGCTGGCCATGAGCTTGGATC
 GCTTGTGGCTATTGTTATCCATTACGCTATGTCAGTGTGTCACTCACAACCGTATATTG
 GCTATGGGTCTGGCATTCCATTACCAAGAGTTTCAACACTCTTCCCTTCCCTTGTGGT
 55 GAAACGACTGCCCTCTGCAAAGCAATGTTTGATCACTCCTACTGTCTCCATCCAGAT
 CTCATGAAAGTAGCATGTGGAGACATCCATGTTAACACATTATGGCTCTTGGTGTGATCA

5 TTTTACCTATGGTATGGACTCAACTTCATCCTGTTCTACGCATTGATCCTGAGAGCC
 ATGCTGGTCATCATATCCCAGGAACAGCGGCTCAAGGCCTCAACACCTGCATGTCACACA
 TCTGTGCAGTGCTGGCTTTATGTGCCATAATTGCTGCTCCATGATTCACCGCTCTGG
 AAAAGTGCCTCACCTGTTCATGTCATGATGTCACATGCTACCTGTTGTAACCACCAT
 GCTCAACCCATCATCTACAGTGTGAAAACCAAGGAGATCCGAAAGGGATTCTCAAGTTC
 TTCCATAAAATCCCAGGCCTGA (SEQ ID NO: 264)

AOLFR144 sequences:

10 MGLFNVTIHPAFFLTLGIPGLESSHWSLGPLCVMYAVALGGNTVILQAVRVEPSLHEPMYYFL
 SMLSFSDVAISMATLPTVLRFLCINARNITFDACLIQMFLIHFMSMMEGIGLLAMSFDRYVAICD
 PLRYATVLTTEVIAAMGLGAAARSFITLFLPLFLIKRLPICRSNVLSHSYCLHPDMMRLLACADISI
 NSIYGLFVLVSTFGMDLFFIFLSYVLILRSVMATASREERLKALNTCVSHILAFLFYVPMIGVS
 TVHRFGKHVPCYIHVLMNSVYLFVPPVNLPIYSAKTKEIRRAIFRMFHIIKI (SEQ ID NO: 265)

15 ATGGGGTTGTTCAATGTCACTCACCTGCATTCTCCTCCTGACTGGTATCCCTGGTCTGGA
 GAGCTCTCACTCCTGGCTGTCAAGGGCCCTCTCGCTGATGTTGCTGGCCCTTGGGGGA
 AATACAGTGTACCTGCAGGCTGTGCGAGTGGAGGCCAGCCTCCATGAGCCCATGTTACT
 TCTGTCCATGTTGCCATCAGTGTGGCCATATCCATGCCACACTGCCACTGTACTC
 CGAACCTCTGCCTCAATGCCCGAACATCACTTTGATGCCGTCTAATTCAAGATGTTCT
 20 TATTCACTTCTTCCATGATGGAATCAGGTATTCTGCTGCCATGAGTTTGACCGCTATG
 TGCCATTGTGACCCCTGCGCTATGCAACTGTGCTCACCACTGAAGTCATTGCTGCAAT
 GGGTTAGGTGAGCTGCTCGAAGCTTCATCACCTTTCCCTTCCCTTCTATTAAAGA
 GGCTGCCTATCTGCAGATCCAATGTTCTTCACTCCTACTGCCGTGACCCAGACATGATG
 25 AGGCTGCCTGTGCTGATATCAGTATCAACAGCATCTATGGACTCTTGTCTTGTATCCAC
 CTTGGCATGGACCTGTTTTATCTCCTCTCCTATGTGCTCATCTCGCTTGTCTGCTATGG
 CCACTGCTCCCGTGAAGAACGCCCTAAAGCTCTCAACACATGTGTCACATATCCTGGC
 TGACTTGCAATTATGTGCCAATGATTGGGTCTCCACAGTGCACCGCTTGGGAAGCAT
 GTCCCAGTCTACATACATGTCTCATGTCAAATGTGACCTATTGTGCCCTGTGCTCAA
 30 CCCCTCATTTAGCGCCAAGACAAAGGAAATCCGCCAGGCCATTTCGCATGTTCAC
 CACATCAAAATATGA (SEQ ID NO: 266)

AOLFR145 sequences:

35 MSVQYSLSPQFMLLSNITQFSPIFYLTSFPGLEGIKHWFIFPFMVMVAISGNCFLIIKTNPRLH
 TPMYYLLSLLALTDLGLCVSTLPTTMGIFWFNSQSIYFGACQIQMFCIHSFSFMESSVLLMMSFD
 RFVAICHPLRYSVIITGQQVVRAGLIVIFRGPVATIPVLLKAFPYCGSVLHSFCLHQEVQLA
 CTDTTFNNLYGLMVVVFTVMLDLVLIALSYGLILHTVAGLASQEEQRRAFQTCTAHLCAVLVF
 FVPMGMSLVHRFGKHAPPAILLMANVYLFVPPMLNPIYSIKTKEIRRAIKLLGLKKASK
 (SEQ ID NO: 267)

40 ATGTCAGTCCAATTCGCTCAGTCCTCAATTGCTGCTATCCAACACATTACTCAGTTAG
 CCCATATTCTATCTCACCAAGCTTCCTGGATTGGAAGGCATCAAACACTGGATTTCATCC
 CCTTTCTTATGTACATGGTGCATCTCAGGAATTGTTCAATTCTGATCATTATAAG
 ACCAACCTCGTCTGCACACACCCATGACTATCTACTATCCTGCTGGCCCTCACTGACCT
 GGGGCTGTGTGTCCACGTTGCCACCACTATGGGGATCTCTGGTTAACCTCCAGAGT
 45 ATCTACTTGGAGCGTGTCAAATCCAGATGTTCTGCATCCACTTTTCTCATGGAGTC
 CTCAGTGCTCCTCATGATGTCCTTGACCGCTTGTGCCATCTGCCACCCCTGAGGTATT
 CGGTCAATTACTGAGCAAGTGGTCAGAGCAGGCCATAATTGTCATCTCCGGGGACC
 TGTGCCACTATCCCTATTGCTCCTCTGAAGGGCTTCCACTGTGGATCTGTGGTCC
 TCTCCCACTCATTTGCCGTGACCAAGGAAGTGATACAGCTGCCGTGACAGATACCACCT
 50 CAATAATCTGTATGGACTGATGGTAGTTCACTGTCATGATGCTGGACCTGGTCTCATC
 GCACTGTCCTATGGACTCATCCTGCACACAGTAGCAGGCCCTGGCCCTCCAAGAGGAGCAGC
 GCCGTGCCTTTCAGACATGCACCGCTCATCTGTGCTGTGCTAGTATTCTTGCCATG
 ATGGGGCTGTCCCTGGTGCACCGTTGGAAAGCATGCCCCACCTGCTATTCACTCTTCTAT
 55 GCCAATGTCTACCTTTGTGCCCTGCTTAACCAATCATATACAGCATTAAGACC
 AAGGAGATCCACCGTGCCATTATCAAACCTCTAGGTCTAAAAAGGCCAGTAAATGA (SEQ
 ID NO: 268)

AOLFR146 sequences:

5 MSQVTNTTQEGLYFILTDIPGFEASHIWISIPVCCLYTISIMGNTTILTVIRTEPSVHQRMYLFLSM
 LALTDLGLTLTTLPTVMQLLWFNVRRISSEACFAQFFFFLHGFSFMESSVLLAMSVDCYVAICCP
 LHYASILTNEVIGRTGLAIICCCVLAVLPSLFLKRLPFCHSHLLRSYCLHQDMIRLVCADIRLN
 SWYGFALALLIIVDPLLIVISYTLILKNILGTATWAERLRALNNCLSHILA VLVLYIPMVGVSMT
 HRFAKHASPLVHVIMANIYLLAPPVMNPIIYSVKNKQIQWGMILNFLSLKNMHSR (SEQ ID NO:
 269)

10 ATGTCCCAGGTGACTAACACCAACACAAGAAGGCATCTACTTCATCCTCACGGACATCCCTG
 GATTGAGGCCTCCACATCTGGATCTCCATCCCCGTCGCTGCTCTACACCACATCCATC
 ATGGGCAATACCACCATCCTCACTGTCACTCGCACAGAGCCATCTGTCACCAGCGCATGT
 ATCTGTTCTCTCCATGCTGGCCCTGACGGACCTGGGCTCACCTCACCCACATCCACA
 GTCATGCAGCTCTCTGGTTAACGTTGCTAGAAATCAGCTGAGGGCTGTTTGCTCAGTT
 15 TTTCTTCCTTCATGGATTCTCCTTATGGAGTCTTCTGTCCTCTGGCTATGTCGTTGACT
 GCTATGTGGCCATCTGCTGTCCTCCATTATGCCCTCATCCTCACCAATGAAGTCATTGGT
 AGAAACTGGGTTAGCCATCATTGCTGCTGTTCTGGCGGTCTCCCTCCCTTTCTTACT
 CAAGCGACTGCCTTCTGCCACTCCCACCTCTCTCGCTCCTATTGCCTCCACCAGGATA
 TGATCCGCCTGGTCTGTCGTCATCAGGCTAACAGCTGGTATGGATTGCTTGCCTTGCCTT
 20 GCTCATTATTATCGTGGATCCTCTGCTCATTGTGATCTCTATACACTTATTCTGAAAAATA
 TCTGGGCACAGCCACCTGGGCTGAGCGACTCCGTCGCCCTCAATAACTGCCTGCCCCACAT
 TCTAGCTGTCCTGGTCTCATTCCATGGTGGTGTATCTATGACTCATGCCTTGCCA
 AGCATGCCTCTCCACTGGTCCATGTTATCATGGCCAATATCTACCTGCTGGCACCCCCGGT
 25 GATGAACCCCCATCATTACAGTGAAAGAACAGATCCAATGGGAATGTTAAATTTC
 CTTCCCTCAAAAATATGCATTCAAGATGA (SEQ ID NO: 270)

AOLFR147 sequences:

30 MPSASAMIIFNLSSYNPGPFILVGIPGLEQFHVWIGIPFCIYIVAVVGNCILLYLIVVEHSLHEPMF
 FFLSMLAMTDLILSTAGVPKALSIFWLGAREITFPGLTQMFFLHYNFVLDLMAFDHYV
 AICSPRLRYTTILTPKTIIKSAMGIFRSFCIILPDVFLLTCLPFCRTRIIPHTYCEHIGVAQLACADISI
 NFWYGFVPIMTVISDVILIAVSYAHILCAVFGLPSQDACQKALGTCGSHVCVILMFYTPAFFSI
 LAHRFGNVSRTFHIMFANLYIVIPPMVYGVTKQIRDVKILLFSKG TG (SEQ ID NO:
 271)

35 ATGCCATCTGCCTCTGCCATGATCATTCAACCTGAGCAGTTACAATCCAGGACCCCTCAT
 TCTGGTAGGGATCCCAGGCCTGGAGCAATTCCATGTGTGGATTGGAATTCCCTCTGTATC
 ATCTACATTGTAGCTGTTGGAAACTGCATCCTCTCACCTCATTGTGGTGGAGCATA
 GTCTTCATGAACCCATGTTCTCTCCATGCTGCCATGACTGACCTCATCTGTCC
 ACAGCTGGTGTGCCTAAAGCACTCAGTATCTTGGTAGGGGCTCGGAAATCACATTCC
 40 CAGGATGCCTTACACAAATGTTCTCCTCACTATAACTTGTCTGGATTGAGGACATC
 ATGGCCATGGCATTGATCACTATGTAGCTATCTGTTCTCCCTGAGATATAACCACCATCTT
 GACTCCCAAGACCATCATCAAGAGTGTATGGCATCTCCTTCGAAGCTTCTGCATCATC
 CTGCCAGATGTATTCTGCTGACATGCCCTCTGCAGGACACGCATCATACCCCCACA
 CATACTGTGAGCATATAGGTGTTGCCAGCTGCCGTGCTGATATCTCCATCAACTCTG
 45 GTATGGCTTTGTGTTCCATCATGACGGTCATCTCAGATGTGATTCTCATGCTGTTCT
 ACGCACACATCCTCTGTGCTGTTGGCCTCCCAAGATGCCTGCCAGAAAGCCCT
 CGGCACATTGTGGTTCTCATGTCGTCATCCTCATGTTTATACACCTGCCCTTTCTCCA
 TCCTCGCCCATCGCTTGGACACAATGTCTCTGCACCTCACATCATGTTGCCAATCTC
 TACATTGTTATCCCACCTGCACTCAACCCATGGTTACGGAGTGAAGACCAAGCAGATCA
 50 GAGATAAGGTTATACTTTGTTCTAAGGGTACAGGATGA (SEQ ID NO: 272)

AOLFR148 sequences:

55 MPTVNHSHTVFHLLGIPGLQDQHMWISIPFFISYVTALLGNSLLIFIILTKRSLHEPMYFLC
 MLAGADIVLSTCTIPQALAIWFFRAGDISLRCITQLFFIHSFISESGILLVMAFDHYIAICYPLR
 YTTILTNALIKKICVTVSLRSYGTIFPIIFLLKRLTFCQNNIIPHTFCEHIGLAKYACNDIRINIWYG

FSILMSTVVLDVVLIFISYMLILHAVFHMPSPDACHKALNTFGSHVCIIILFYGSIFTILTQRFGR
HIPPCIHPLANVCILAPPMLNPITYGIKTQIQEQVVFQFLFIQKQITLV (SEQ ID NO: 273)

5 ATGCCACTGTAAACCACAGTGGCACTAGCCACACAGTCTTCCACTTGCTGGGCATCCCTG
GCCTACAGGACCAGCACATGTGGATTCTATCCCATTCTCATTCTCTACAAAGCGCAGCCTCCATGAACCCATGT
CTTGGGAAACAGCCTGCTCATCTCATTATCCTCACAAAGCGCAGCCTCCATGAACCCATGT
ACCTCTTCTCTGCTGAGCAGACATTGTCTCCACGTGCACCATTCCTAG
GCCTTAGCTATCTCTGGTCCGTGGGGACATCTCCCTGGATCGTGCATCACTCAGCT
CTCTTCATCCATTCCACCTCATCTGAGTCAGGGATCTGCTGGTGTGGCCTTGACC
10 ACTATATTGCCATATGCTACCCACTGAGGTACACCACATTCTACAAATGCTCTGATCAA
GAAAATTGTGTGACTGTCTCTGAGAAGTTATGGTACAATTTCCTATCATATTCTT
TAAAAAGATTGACTTCTGCCAGAATAATTATTACACACCTTGTGAACACACATTGG
CCTAGCCAAATATGCTGATGACATTGAAATAACATTGGTATGGGTTTCCATTCTA
15 ATGTCGACGGTGGCTTAGATGTTGACTAATTCTATTCCTATGCTGATTCTCCATGC
TGTCTCCACATGCCCTCTCCAGATGCTGCCACAAAGCTCTCACACACATTGGCTCCCATG
TCTGCATCATCATCCTCTTATGGGCTGGCATCTCACAACTCTTACCCAGAGGTTGG
CGCCACATCCACCTGTATCCACATCCGCTGCTAATGCTGCATTCTGGCTCCACCTAT
GCTGAATCCCATTATTATGGGATCAAACAGCAAATCCAGGAACAGGTGGTCAGTT
TTGTTTATAAAACAGAAAATAACTTGGTTAA (SEQ ID NO: 274)

20 **AOLFR149 sequences:**
MSNASLLTAFILMGLPHAPALDAPLFGVFLVVYVLTVLGNLLILLVIRVDSHLHTMYYFLTNL
SFIDMWFSTVTPKLLMTLVFPSGRAISFHSCMAQLYFFHFLGGTECFYRVMSCDRYLAISYP
25 LRYTSMMTGRSCTLATSTWLSGLHSAVQAILTFHLPYCGPNWIQHYLCDAPPILKLA
AIEVIFVTVGIVASGCFVLIVLSYVSIVCSILRIRTSEGKHRAFQTCASHCIVVLCFFGPGLFIYLR
PGSRKAVDGVVAVFYTVLTPLLNPVYVTLRNKEVKALLKLKDVAHSQSK (SEQ ID NO:
275)

30 ATGTCCAACGCCAGCCTACTGACAGCGTTCATCCTCATGGGCCTTCCCCATGCCAGCG
TGGACGCCCTCTTGGAGTCCTCCCTGGTTACGTGCTACTGTGCTGGGAACCT
CCTCATCCTGCTGGTGTACAGGGTGGATTCTCACCTCACACCACCATGTA
CTACTTCCTCA
CCAACCTGTCGTTATTGACATGTGGTCTCCACTGTCACGGTGCCAAATTGCTGATGAC
TTGGTGTCTCCAAGTGGCAGGGCTATCTCCCTCACAGCTGCATGGCTCAGCTCTATTCT
TTCACTCCTAGGGGCACCGAGTGTTCCTCATGGTCATGTCTGTGATCGCTACCT
35 GCCCATCAGTTACCGCTCAGGTACACCATGACTGACTGGCGCTCGTACTCTTC
GCCACCAGCACTGGCTCAGTGGCTCTGCACTCTGCTCCAGGCCATTGACTTT
ATTGCCCCTACTGTGGACCCAACTGGATCCAGCACTATTGTGATGCACCGCCCAC
GAAACTGGCTGTGCAGACACCTCAGCCATAGAGACTGTCATTGTGACTGTGAA
GTGGCCTCGGGCTGTTGTCTGATAGTGTCTCTATGTGTCATCGTCTGTTCCATCCT
40 GCGGATCCGCACCTCAGAGGGGAAGCACAGAGCCTTCAGACCTGTGCTCCACTGTATC
GTGGCCTTTGCTTCTTGGCCCTGGTCTTCTACACTGTGCTGACGCCCTCTCAACCC
TGTGGATGGAGTTGTGGCCGTTCTACACTGTGCTGACGCCCTCTCAACCC
ATTCTCAGAGCAAATAG (SEQ ID NO: 276)

45 **AOLFR150 sequences:**
MELGNVTRVKEFIFLGLTQSQQSLVLFFLCLVYMTLLGNLLIMVTVCESRLHTPMYFLR
NLAIDICFSSTTAPKVLLDLLSKKKTISYTSCTMQIFLFHLLGGADIFSLVMAFD
50 HYVTIMSRGQCTALISASWMGGFVHSIVQISLLLPLFCGPNVLDTFYCDVPQVLKLT
LEFLMISNNGLVTTLWFIFLVSYTVLMTLSQAGGGRRKAISTCSPHCGDPAFC
PALHCPPHRKGHLCHLHCHLPSAEPFDLHSEEPGNEVSHEKTEEKTRAF (SEQ ID NO: 277)

55 ATGGAGTTGGAAATGTCACCAGAGTAAAGAATTATATTCTGGACTACTCAATCCC
AAGACCAGAGTTGGCTTGTCTTCTTTATGTCTTGTCATGACGACTCTGCTGGGA
AACCTCCTCATCATGGTACCCGTGACCTGTGAGTCTCGCCTCACACCCCC
GCTCCGCAATCTAGCCATCCTGACATCTGCTTCTCCACA
ACTGCTCTAAAGTCTTGC

5 TGGACCTCTGTCAAAGAAAAAGACCATATCCTATACAAGCTGCATGACACAGATATTCT
 CTTCCACCTCCTGGGGCAGACATTCTCTCTGTGATGGCGTTGACTGCTACA
 TG GCCATCTCAAGCCCCCTGCACTATGTGACCATCATGAGTAGAGGGCAATGCACTGCCCT
 CATCTCTGCCTCTTGGATGGGGGCTTGTCCACTCCATCGTCAGATCTCCCTGTGCTGC
 10 CTCTCCCCTTCTGTGGACCCAATGTTCTGACACTTCTACTGCGATGTCCCCCAGGTCTC
 AAACACTCTGCACTGACACTTTGCTCTGAGTTCTGATGATTCCAACAATGGCCTGGT
 CACTACCCCTGTGGTTATCTCCTGCTTGTCCTACACAGTCATCCTAATGACGCTGAGGT
 CTCAGGCAGGAGGGGGCAGGAGGAAGCCATCTCCACTTGCACCTCCCCACATCACTGTG
 GTGACCCCTGCATTTGTGCCCTGCATCTATGTCTATGCCGCCCTCACTGCCCTCCCCAC
 15 AGAAAAGGCCATCTGTCACTTCACTGTCACTCCCCTGTGTAACCCCTTGATCTACA
 CTCTGAGGAACCAGGAAATGAAGTCAGCCATGAGAAGACTGAAGAGAAGACTCGTGCCTT
 CTGA (SEQ ID NO: 278)

AOLFR151 sequences:

15 MFSPNHTIVTEFILLGLTDDPVLEKILFGVFLAIYLITLAGNLCMILLIRTNSHLQTPMYFFLGHLS
 FVDICYSSNVTPNMLHNFLSEQKTISYAGCFTQCLLIALVITEFYILASMALDRYVAICSPHLHS
 SRMSKNICVCLVTIPYMYGFLSGFSQSLLTFHLSFCGSLEINHFYCADPPLIMLACSDTRVKKMA
 MFVVAGFNLSLFLIILSYLFIAIFRIRSAEGRHKAFSTCASHLTIVTLYGTLFCMYVRPPSE
 KSVEEKITAVFYTFLSPMLNPLYSLRNTDVILAMQQMIRGKSFHKIAV (SEQ ID NO: 279)
 20
 ATGTTCTCCCCAAACACACCATAGTGACAGAAATTCTATTCTCTGGGACTGACAGACGACC
 CAGTGCTAGAGAAGATCCTGTTGGGGTATTCTCTGCGATCTACCTAACACTGGCAGG
 CAACCTGTGCATGATCCTGCTGATCAGGACCAATTCCCACCTGCAAACACCCATGTATTTC
 25 TTCTCTGGCCACCTCTCCTTGTAGACATTGCTATTCTCCAATGTTACTCCAATATGCT
 GCACAATTCTCTCAGAACAGAACGACCATCTCCTACGCTGGATGCTCACACAGTGTCTT
 CTCTCATGCCCTGGTGAATGAGTTTACATCCTGCTCAATGGCATTGGATCGCTA
 TGTAGCCATTGCAAGCCCTTGCATTACAGTCCAGGATGTCAGAACATCTGTGTC
 CTGGTCACTATCCCTACATGTATGGGTTCTAGTGGGTTCTCTCAGTCACTGCTAACCTT
 30 TCACATTATCTCTGTGGCTCCCTGAAATCAATCATTTCTACTGCGCTGATCCTCCTCTTA
 TCATGCTGGCTGCTGACACCCGTGCAAAAAGATGGCAATGTTGAGTTGAGGCTT
 TAATCTCTCAAGCTCTCTCATCATTTCTGCTCTATCTTTCATTGGCAGCGATCTT
 CAGGATCCGTTCTGCTGAAGGCAGGCACAAAGCCTTCTACGTGTGCTCCACCTGACA
 ATAGTCACTTGTTATGGAACCCCTCTGCTACGTACGTAAGGCCTCCATCAGAGAAGT
 35 CTGTAGAGGAGTCCAAAATAACTGCAGTCTTATACTTTTGAGCCAATGCTGAACCC
 ATTGATCTATAGCCTACGGAACACAGATGTAATCCTGCCATGCAACAAATGATTAGGGAA
 AAATCCTTCATAAAATTGCAGTTAG (SEQ ID NO: 280)

AOLFR152 sequences:

40 MDQINHTNVKEFFFLELTRSRELEFFLFVVFVAVYVATVLGNALIVVTITCESRLHTPMYFLLRN
 KSVLDIVFSSITVPKFLVDLLSDRKTISYNDMAQIFFFHFAGGADIFFLSVMAYDRYLAIAKPL
 HYVTMMRKEVVVALVVASWVSGGLHSIIQVILMLPFPFCGPNLDAFYCYVLQVVKLACTDT
 FALELFMISNNGLVTLLWFLLLGSYTVILVMLRSHSGEGRNKALSTCTSHMLVVTLFVPCV
 YIYCRPFMTLPMDDTTISINNTVITPMLNPIYSLRNQEMKSAMQRLQRLGPSESRKWG (SEQ ID
 NO: 281)
 45
 ATGGACCAGATCAACCAACTAATGTGAAGGAGTTCTTCTGGAACTTACACGTTCCC
 GAGAGCTGGAGTTCTTCTGTTGTGGTCTCTTGTGTATGTAGCAACAGTCCTGGG
 AAATGCACTCATTGTGGTCACTATTACCTGTGAGTCCCGCCTACACACTCCTATGTACTTTC
 50 TCCTGCGGAACAAATCAGTCCTGGACATCGTTTCTCATCTATCACCGTCCCCAAGTTCTG
 GTGGATCTTTATCAGACAGGAAAACCATCTCTACAATGACTGCATGGCACAGATCTTT
 TCTTCCACTTTGCTGGGGCAGATATTCTCTCTGTGATGGCTATGACAGATAAC
 CTGCAATGCCAACGCCCCCTGCACTATGTGACCATGATGAGGAAAGAGGGTGTGGGTGGCC
 TTGGTGGTGGCTCTTGGGTGAGTGGTGGTTGCAATTCAATCATCCAGGTAAATTCTGATGC
 TTCCATTCCCTCTGTGGCCCCAACACACTGGATGCCCTACTGTTATGTGCTCCAGGTG
 55 GTAAAACCTGGCCTGCAGTACACCTTGCTTGGAGCTTCTGATCTAACAACACGGAC
 TGGTGACCCCTGCTCTGGTCTCCTGCTCCTGGCTCCTACACTGTCAATTCTGGTGTGCT

5 AGATCCCACTCTGGGGAGGGCGGAACAAGGCCCTCTCACGTGCACGTCCCACATGCTG
 GTGGTGAECTTCACTCGTGCCTGTGTTACATCTACTGCCGCCCTCATGACGCTGCC
 CATGGACACAACCATAATCCATTAATAACACGGTCATTACCCCATGCTGAACCCCATCATC
 TATTCCCTGAGAAATCAAGAGATGAAGTCAGCCATGCAGAGGCTGCAGAGGAGACTTGGG
 CCTTCCGAGAGCAGAAAATGGGGTG (SEQ ID NO: 282)

AOLFR153 sequences:

10 MSKTSVTAFILETGLPHAPGLDAPLFGILVVYVLTVLGNLLILLVIRVDSHLHTPMYFLTNLS
 FIDMWFSVTVPKMLMTLVSPSGRAISFHSCVAQLYFFHFLGSTEFLYTVMSYDRYLAISYPL
 RYTSMMSSGSRCALLATSTWLGSLSLHSAVQTLTFHLPYCGPNQIQHYLCDAPPIKLACADTSA
 NEMVIFVDIGLVASCGFLIVLVSYVSTVCSILRIHTSEGRHRAFQTCAASHCIVVLCFFVXCVFIYL
 PGSRDVVDGVVAIFYTVLTPLLNPVYTLRNKEVKKAVLKL RDKVAHSQGE (SEQ ID NO:
 283)

15 ATGTCCAAGACCAGCCTCGTACAGCGTTCATCCTCACGGGCCCTCCCCATGCCAGGGC
 TGGACGCCCACTCTTGGAACTCTCCTGGTGGTTACGTGCTACTGTGCTGGGAACCT
 CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCATGTACTACTCCTCA
 CCAACCTGCTCTCATTGACATGTGGTCTCCACTGTACGGTGCCCCAAATGCTGATGAC
 CTTGGTGTCCCCAAGCGGCAGGGCTATCTCCTCACAGCTCGTGGCTCAGCTCTATT
 20 TCCACTCCTGGGAGCACCAGTGTTCCTCTACACAGTCATGTCTATGATCGCTACTTG
 GCCATCAGTTACCCGCTCAGGTACACCAGCATGATGAGTGGGAGCAGATGTGCCCTCTGG
 CCACCAGCACTGGCTCAGTGGCTCTGCACTCTGCTGTCAGACCATATTGACTTCCAT
 TTGCCCCTACTGTGGACCCAACAGATCCAGCACTATTGTGTGATGACCGCCATCCTGA
 AACTGGCCTGTGACAGACACCTCAGCCAACGAGATGGTCATCTTGTGGACATTGGCTAGT
 25 GGCCTCGGGCTGCTTTCTCTGATAGTGCTGTTATGTGTCATCGCTGTTCCATCCTGC
 GGATCCACACCTCAGAGGGGAGGCACAGAGCCTTCAGACCTGTGCCCTCCACTGCATCGT
 GGTCTTGTGTTTGTNNCCCTGTGTTCTACACTGTGCTGACACCCCTCTCAACCTGTTGTAC
 TGATGGAGTTGTGCCATTCTACACTGTGCTGACACCCCTCTCAACCTGTTGTAC
 30 ACCCTGAGAAACAAGGAGGTGAAGAAAGCTGTGTTGAAACTGAGAGACAAAGTACAT
 TCTCAGGGAGAATAA (SEQ ID NO: 284)

AOLFR156 sequences:

35 MCWAMPSPFTGSSTRNMRNQSTVTEFIFTGFPQLQDGSLYFFPLFIYTFIIDNLLIFSAVRL
 DTHLGNPMYNFISIFSFLEIWYTTATIPKMLSNLISEKKAISMTCILQMYFFHSLENSEGILLTT
 MAIDRYVAICNPLRYQMIMTPRLCAHLSAGSCLFGFLILLPEIVMISTLPFCGPQIHQIFCDLVP
 VLSLACTDTSMILEDVIHAVTIIITFLIIALSYVRIVTILRIPSSEGRQKAXSTCAGHLMVFLIFFG
 SVSLMYLRFNSNTYPPVLDTAIALMFTVLAPFFNPIYSLRNKDMNNAIKLFCLQKVLNPKGG
 (SEQ ID NO: 285)

40 ATGTGCTGGCTATGCCCTCCATTACAGGTAGCTACTAGAAATATGGAGAGCAGAA
 ACCAATCAACAGTGAATTATCTCACTGGATTCCCTCAGCTTCAGGATGGTAGTCT
 CCTGTACTCTTCTTACTTTCTACATCTATACTTTATTATCATTGATAACTTATTATCCT
 CTCTGCTGTAAGGCTGGACACCCATCTGGCAACCCATGTATAATTATCAGTATATT
 CCTTCTGGAGATCTGGTACACCACAGCCACCATCTCCAAGATGCTCTCCAACCTCATCAG
 45 TGAAAAGAAGGCCATCTCAATGACTGGCTGCATCTGCAGATGTATTCTCCACTCACT
 GAAAACTCAGAGGGATCTGCTGACCACCATGCCATTGACAGATACGTTGCCATCTGCA
 ACCCTCTCGCTATCAAATGATCATGACCCCCCGCTCTGTGCTCACCTCTGAGGTTCC
 TGCCTCTCGGTTCTTCTACCTGCTTCCGAGATTGTGATGATTCCACACTGCCTTCTG
 TGGGCCAACCAAATCCATCAGATCTCTGTGACTTGGTCCCTGTGCTAACGCTGGCTGT
 50 ACAGACACGTCCATGATTGATTGAGGATGTGATTGATCTGCTGTGACCATCATCATTACCT
 TCCTAATCATGCCCTGCTCTATGTAAGAATTGTCAGTGTGATATTGAGGATTCCCTCTTCT
 GAAGGGAGGCAAAAGGCTNTTCTACCTGTGCAAGGCCACCTCATGGTCTCTGATATTCT
 TTGGCAGTGTATCACTCATGTACTTGCCTTCAGCAACACTTATCCACCAAGTTGGACAC
 AGCCATTGCACTGATGTACTGTACTTGCCTCATCTCAATCCCACATTTATAGCCTGA
 55 GAAACAAGGACATGAACAATGCAATTAAAAACTGTTCTGTCTCAAAAGTGTGAACA
 AGCCTGGAGGTTAA (SEQ ID NO: 286)

AOLFR157 sequences:

5 MAMDNVTAVFQFLIGISNYPQWRDTFFTLVLIYLSTLLNGNGFMIFLIHFDPNLHTPIYFFLSNL
 SFLDLCYGTASMPQALVHCFSTHPYLSYPRCLAQTSVSLALATAECLLAAMAYDRVVAISNP
 LRYSVVMNGPVCVCLVATSWGTSVLTAMLILSLRLHFCGANVINHFACEILSLIKLTCSDTSL
 NEFMILITSIFTLLPFGFVLLSYIRIAMAIIRSLQGRLKAFTTCGSHTVVTIFYGSAISMYMKT
 QSKSSPDQDKFISVFYGALTPMLNPLIYSLRKKDVKRAIRKVMLKRT (SEQ ID NO: 287)

10 ATGGCCATGGACAATGTCACAGCAGTGTTCAGTTCTCCTTATTGGCATTCTAACTATCC
 TCAATGGAGAGACACGTTTCACATTAGTGTGATAATTACCTCAGCACATTGTTGGGG
 AATGGATTATGATCTTCTTATTCACTTGTACCTTACCCCCAACCTCCACACTCCAATCTACTTCTT
 CCTTAGTAACCTGTCTTCTTACCTTGTATGGAACAGCTTCAATGCCCAAGGCTTGG
 TGCAATTGTTCTTACCCATCCCTACCTCTTATCCCCGATGTTGGCTCAAACGAGTGTGTC
 TCCTTGGCTTGGCCACAGCAGAGTGCCTCTACTGGCTGCCATGGCCTATGACCGTGTGG
 15 TTGCTATCAGCAATCCCCTGCGTTATTCACTGGTTATGAATGGCCCAGTGTGTCTGCTT
 GGTGCTACCTCATGGGGGACATCACTTGTGCTACTGCCATGCTCATCCTATCCCTGAGG
 CTTCACTTCTGTGGGCTAATGTCATCAACCATTGCTGTGAGATTCTCTCCCTCATTAA
 GCTGACCTGTTCTGATACCAAGCCTCAATGAATTATGATCCTCATCACCAGTATCTCACCC
 TGCTGCTACCATTGGGTTGTTCTCCTCTACATACGAATTGCTATGGCTATCATAAGG
 20 ATTCGCTCACTCCAGGGCAGGCTCAAGGCCTTACCACTGTTGCTCACCTGACCGTGG
 TGACAATCTCTATGGGTGAGCCATCTCATGTATATGAAAACCTCAGTCCAAGTCCCTCCCC
 TGACCAAGACAAGTTATCTCACTGGTTATGGAGCTTGAACACCCATGTTGAACCCCTG
 ATATATAGCCTGAGAAAAAAAGATGTTAACAGGGCAATAAGGAAAGTTATGTTGAAAAGG
 ACATGA (SEQ ID NO: 288)

AOLFR158 sequences:

25 MKAGNFSDTPEFFLLGLSGDPELQPIFLMSMYLATMLGNLLIILAVNSDSHLHTPMYFLLSI
 LSLVDICFTSTTMPKMLVNIQAAQNSINYTGLTQICFVLVFVLENGILVMAYDRFVAICHP
 30 LRYNVIMNPKLCGLLLLSSIVSVDALLHTMLVQLTFCIDLEIPHFFCELAHILKLA
 CSDVLIN NILVYLVTSLLGVVPLSGIIFSYSYTRIVSSVMKIPSAGGKYKAFSICGSHLIVV
 SLYGTGFVYLSS GATHSSRKGAIASVMYTVVTPMLNPLIYSLRNKDMKLKALRK
 LISRIPSFH (SEQ ID NO: 289)

35 ATGAAAGCAGGAAACTCTCAGACACTCCAGAATTCTTCTCTGGGATTGTCAAGGGATC
 CGGAGCTGCAGCCCACCTCTCATGCTGTTCCCTGCCATGTACCTGCCACAATGCTGGG
 GAACCTGCTCATCATCCTGGCGTCAACTCTGACTCCCACCTCCACACCCCATGTACTTCC
 40 TCCTCTCATCCTGTCCITGGTCACATCTGTTCACCTCCACACGATGCCAAGATGCTG
 GTGAACATCCAGGCACAGGCTCAATCCATCAATTACACAGGCTGCCTCACCCAAATCTGCT
 TTGTCCTGGTTTTGTTGGATTGAAATGGAATTCTGGTCATGATGCCATGATCGATT
 TGTGCCATCTGTACCCACTGAGGTACAATGTCATCATGAACCCAAACTCTGTTGGCTG
 45 CTGCTTCTGCTGTCCTCATCGTAGTGTCTGGATGCTCTGTCACACGTTGATGGTGC
 ACAGCTGACCTCTGATAGACCTGAAATTCCCACTTTCTGTGAACACTAGCTCATATTC
 TCAAGCTCGCTGTTCTGATGTCCTCATCAATAACATCCTGGTGTATTGGTACCC
 GTTAGGTGTTGTTCTCTCTGGATCATTTCTTACACACGAATTGTCCTCTGTCA
 TGAAAATTCCATCAGCTGGGGAAAGTATAAAGCTTTCCATCTGGGGTCACATTAA
 CGTTGTTCTGTTATGGAACAGGGTTGGGGTGTACCTAGTTCTGGGGTACCC
 CCTCCAGGAAGGGTGCAATAGCATCAGTGTATACCGTGGTCACCCCATGCTGAACCC
 ACTCATTACAGCCTGAGAAACAAGGACATGTTGAAGGCTTGAAGGAAACTAATATCTAG
 GATACCATCTTCCATTGA (SEQ ID NO: 290)

AOLFR159 sequences:

50 MGPRNQTAVSEFLLMKVTEDPELKLIPFSLMSMYLVTILGNLLILLA
 VISDSHLHTPMYFLLFN LSFTDICLTTTVPKILVNIQAAQNSITYTGLTQICLVL
 VFAGLESCFLAVMAYDRFVAICHPL RYTVLMNVHFGLLILLSFMSTM
 DALVQLSFCNVIEPLFFCEVVQVIKLA
 CSDTLLINNLIYFASSVFGAIPLSGIIFSYSQIVTSVLR
 MPSARGKYKAFSTCGCHLSV
 FSLFYGTAFGVYIS
 55 SAVAESSRITAVASV
 MYTVV
 PQMMNPFIYSLRN
 KEMKKALRK
 LIGRLFPF (SEQ ID NO: 291)

5 ATGGGACCCAGAAACCAAACAGCTGTTTCAAGAATTCTTCATGAAAGTGACAGAGGAC
 CCAGAACTGAAGTTAACCTCTCAGCCTGTTCTGTCCATGTACCTGGTCACCATCCTGG
 GGAACCTGCTCATTCTCCTGGCTGTACTCTGACTCCCACCTCCACACCCCCATGTACTTC
 CTTCTCTTAATCTCTCTTACTGACATCTGTTAACCAACCACAGTCCAAAGATCCT
 10 5 AGTGAACATCCAAGCTCAGAACATCAGAGTATCACACAGGCTGCCACCCAGATCTGT
 CTTGTTCTGGTTTGCTGGCTTGGAAAGTTGCTTCTGAGTCATGGCCTACGACCGCTA
 TGAGGCCATTGCCACCCACTGAGGTACACAGTCCTCATGAATGTCCATTCTGGGGCTTG
 CTGATTCTCTCCATGTCATGAGCACTATGGATGCCCTGGTCAGAGTCTGATGGTATT
 GCAGCTGTCCTCTGCAAAAACGTTGAAATCCCTTGTCTGTGAAGTCGTCAGGTC
 15 10 ATCAAGCTCGCCTGTCATCACCCCATCAACAAACATCCTCATATATTGCAAGTAGTGT
 ATTGGTGCAATTCTCTCTGGAATAATTCTCTTATTCTCAAATAGTCACCTCTGTT
 TGAGAATGCCATCAGCAAGAGGAAAGTAAAGCCTTCCACCTGTGGCTGTCACCTCTC
 TGTTTTCCCTGTTCTATGGGACAGCTTGGGGTGTACATTAGTCTGCTGTTGAGT
 CTTCCGAATTACTGCTGTGGCTTCAGTGATGTACACTGTGGTCCCTCAAATGATGAACCC
 15 15 CTTCATCTACAGCCTGAGAAATAAGGAGATGAAGAAAGCTTGGAGAAACTATTGGTAG
 GCTGTTCCCTTTAG (SEQ ID NO: 292)

AOLFR160 sequences:

20 MPMQLLTDFIIFSIRFIINSMEARNQTAISKFLLGLIEDPELQPVLFLSFLSMYLVTILGNLLILL
 AVISDSHLHTPMYFFLSNLSFLDICLSTTIPKMLVNIQAQNRSITYSGCLTQICFVLFFAGLENC
 LLAAMAYDRYVAICHIPRLRYTVIMNPRLCGLLILLSLTSVNALLSLMVLRLSFCDLEIPLFF
 CELAQVIQLTCSDLTLINNILYFAACIFGGVPLSGIILSYTQITSCVLRMPSASGKHKA
 SIVLLFYGAGLGVYISSVVTDSPRKTAVASVMYSVFPQMVPNFIYSLRNKDMKGTLRKFIGRIP
 SLLWCAICFGFRFLE (SEQ ID NO: 293)

25 25 ATGCCGATGCAGCTGCTTACAGATTATTATCTTCCATCAGATTCACTCATCACACAG
 CATGGAAGCGAGAAACCAAACAGCTATTCAAAATTCTCTCTGGACTGATAGAGGAT
 CCGGAACTGCAGCCCGTCTTTCAGCCTGTCATCTGACTCTCACCTCCACACCCCCATGTACTCT
 30 30 GAACCTGCTCATCCTCTGGCTGTACTCTGACTCTCACCTCCACACCCCCATGTACTCT
 TCCCTCCAATCTCTCTTGGACATTGTTAACGACAACCACGATCCAAAGATGCTG
 GTGAACATCCAAGCTCAGAACCGAGCATCACGTAACGGCTGCCACCCAGATCTGCT
 TTGTCCTGTTGGCTGGCTTGGAAAATTGTCCTTGCAAGCAATGGCCTATGACCGCTAT
 GTGGCCATTGTCACCCCTTAGATACACAGTCATCATGAACCCCCGCTCTGTGGCTG
 TGATTCTCTCTGTTGACTAGTGTGAATGCCCTCTCTCACCTGATGGTGTG
 35 35 AGGCTGTCCTCTGCACAGACCTGGAAATCCGCTCTCTGTGAACGGCTCAGGTCA
 TCCAACTCACCTGTCAGACACCCCTCATCAAAACATCCTGATATATTGCACTGCT
 TTTGGTGGTGTCTCTGTCAGGTTGGGGTGTACATTAGTCTGTTACTGACTC
 GAGAATGCCATCAGCAAGTGGAAAGCACAAGCAGTTCCACCTGTGGGCTCACCTCTCC
 40 40 ATTGTTCTCTGTTCTATGGGCAGGTTGGGGTGTACATTAGTCTGTTACTGACTC
 ACCTAGGAAGACTGCAGTGGCTTCAGTGATGTATTCTGTTCCCTCAAATGGTGAACCC
 TTTATCTATAGTCTGAGGAATAAGGACATGAAAGGAACCTTGAGGAAGTTCATAGGGAGG
 ATACCTCTCTGTTGCTGCCATTGCTTGGATTCAAGGTTCTAGAGTAA (SEQ ID
 NO: 294)

AOLFR161 sequences:

45 MEPRNQTSAQFILLSEKPEQETLLFSLFFCMYLVMVVGNLILAIISIDSHLHTPMYFFLANL
 SLVDFCLATNTIPKMLVSLQTGSKAJSYPCCLIQMYFFHFFIVDSVIIAMAYDRFVAICHPLH
 YAKIMSLRLCRLLVGALWAFSCFISLTHILLMARLVFCGSHEVPHYFCDLTPILRLSCTDTSVNR
 IFILIVAGMVIATPFVCILASYARILVAIMKVPSSAGGRKKAFSTCSSHLSVALFYGTIGVYLCP
 50 50 SSVLTVKEKASAIVMYTAVTPMLNPFYSLRNRLKGALRKLVNRKITSSS (SEQ ID NO: 295)

55 ATGGAACCAAGAAACCAAACCAAGTCATCTCAATTCACTCCTCTGGACTCTCAGAAAAGC
 CAGAGCAGGAGACGCTCTCTTCCCTGTTCTGATGTACCTGGTCATGGCTG
 GAACCTGCTCATCATCCTGCCATCAGCATAGACTCCCACCTCCACACCCCCATGTACTCT
 TCCCTGGCCAACCTGCTCCCTGGTTGATTCTGCTGCCACCAACACCCATCCCTAAGATGCT
 GGTGAGCCTCAAACCGGGAGCAAGGCCATCTTATCCCTGCTGCCATCCAGATGTAC

TTCTTCCATTCTTGGCATCGTGGACAGCGTCATAATGCCATGATGGCTATGACCGGTT
 CGTGGCCATCTGCCACCCATTGCACTACGCCAAGATCATGAGCCTACGCCCTGTCGCCTG
 CTGGTCGGCGCCCTCTGGCGTTTCTGCTCATCTCACTCACATCCTCCTGATGGC
 5 CCGTCTCGTTCTGGCGACCCATGAGGTGCCTCACTACTCTGCGACCTCACTCCATCC
 TCCGACTTCTGACCGACACCTCTGAAATAGGATCTCATCCTCATTGTGGCAGGGAT
 GGTGATAGCCACGCCCTTGTCTGCATCCTGCCCTCATGCTCGCATCCTGTGGCCATCA
 TGAAGGTCCCCTCTGCAGGGCAGGAAGAAAGCCTCTCACCTGCAGCTCCACCTGTC
 10 TGTGGTTGCTCTCTATGGGACCACCATGGCGTCTATCTGTGTCCTCCTCGGTCTCA
 CCACTGTGAAGGAGAAAGCTCTGCGGTGATGTACACAGCAGTCACCCCCATGCTGAATCC
 CTCATCTACAGCTGAGGAACAGAGACCTGAAGGGCTCTCAGGAAGCTGGTCAACAG
 AAAGATCACCTCATCTCCTGA (SEQ ID NO: 296)

AOLFR162 sequences:

15 MMRLMKEVRGRNQTEVTEFLLGLSDNPDLQGVLFALFLIYMANMVGNLGMIVLIKIDLCH
 TPMYFFLSSLSFVDASYSSVTPKMLVNLMAENKAISFHGCAAQFYFFGSLGTECFLLAMMA
 YDRYAAIWNPLLYPVLVSGRICFLIATSFLAGCGNAAIHTGMTFRLSFCGSNRINHFYCDTPPL
 LKLSCSDTHFNGIVIMAFSSFIVISCVMVILISYLCIFIAVLKMPGLEGRHKAFCSTCASYLMAVTIF
 20 FGTILFMYLRPTSSYSMEQDKVVSVFYTVIIPVLNPLIYSLKNKDVKKALKKILWKHIL (SEQ ID
 NO: 297)

25 ATGATGAGACTTATGAAAGAGGTTCGAGGCAGAAATCAAACAGAAGTAACAGAATTCTC
 CTCTAGGACTTCCGACAATCCAGATCTACAAGGAGTCCTCTTGCAATTGTTCTGTTGAT
 CTATATGGCAAACATGGTGGCAATTGGGGATGATTGATTGATTAAGATTGATCTCTGAT
 CTCCACACCCCCATGTTCTCTCAGTAGCCTCTCTTGAGATGCCCTACTCTCT
 TCCGTCACTCCCAAGATGCTGGTAACCTCATGGCTGAGAATAAGGCCATTCTTCTCATG
 30 GATGTGCTGCCAGTTCACTCTTGGCTCTTGGGACTGAGTGCTCCCTGTTGGCC
 ATGATGGCATATGACCGCTATGCAGCCATTGGAACCCCTGCTACCCAGTCTCGTGT
 CTGGGAGAATTGCTTTGCTAATAGCTACCTCTCTAGCAGGTGTGGAAATGCAGC
 CATACATACAGGGATGACTTTAGGTTGCTCTTGTGGTTCTAATAGGATCAACCATTCT
 ACTGTGACACCCCGCCACTGCTCAAACACTCTTGTCTGATACCCACTCAATGGCATTGTG
 35 ATCATGGCATTCTCAAGTTTATTGTCATCAGCTGTTATGATTGCTCATTCCCTACCT
 GTGTATCTTCAATTGCCGCTTGAAGATGCCCTCGTAGAGGGCAGGCACAAAGCCTCTCC
 ACCTGTGCCCTTACCTCATGGCTGACCATATTCTTGGAAACAATCCTCTCATGTACTT
 GCGCCCTACATCTAGCTACTCAATGGAGCAAGACAAGGGTGTCTCTGTCTTATAACAGTA
 ATAATCCCTGTGCTAAATCCCTCATCTATAGTTAAAAAATAAGGATGTAAAAAAGGCC
 TAAAGAAGATCTTATGGAAACACATCTTGTAG (SEQ ID NO: 298)

AOLFR163 sequences:

40 MQRSNHTVTEFILLGFTTDPGMQLGLFVFLGVYSLTVGNSTLIVLICNDSCLHTPMYFFTGN
 LSFLDLWYSSVYTPKILVTCISEDKSISFAGCLCQFFSAGLAYSECYLLAAVAYDRYVAISKPL
 LYAQAMSIKLCALLVAVSYCGGFINSSIITKKTSFNFCRENJDFFCDLLPLVELACGEKGGYK
 IMMYFLLASNVICPAVILASYLEIITSVLRSSSKGYLKAFSTCSSHLSVTLYYGSILYIYALPRS
 SYSFDMDKIVSTFYTVVFPMLNLMYSLRNKDVKEAALKLLP (SEQ ID NO: 299)

45 ATGCAGAGGAGCAATCATACTGACTGAGTTACTGCTGGGCTTCACCACAGACCCA
 GGAATGCAGCTGGCCTCTCGTGGTCTGGCTGGCGTGTACTCTCTACTGTGGTAGGAA
 ATAGCACCCCTCATCGTGTGATCTGTAATGACTCTGCCTCACACACCCATGTATTCTC
 ACTGGAAATCTGTCGTTCTGGATCTCTGGTATTCTCTGTCACACCCAAAGATCCTAGT
 GACCTGCATCTCTGAAGACAAAAGCATCTCCTTGTCTGGCTGCCGTGTCAGTTCTCT
 50 CTGCAGGGCTGGCTATAGTGAGTGCTACCTGCTGGCTGCCGTGGCTTATGACCGCTACGT
 GCCATCTCCAAGCCCCCTGCTTATGCCAGGCCATGTCCATAAAGCTGTGTGCATTGCTG
 GTAGCAGTCTCATATTGTTGGCTTATTAACCTCTCAATCATACCAAGAAAACGTTTC
 CTTAACCTCTGCCGTGAAAACATCATTGATGACTTTCTGTGATTGCTTCCCTGGTGG
 AGCTGGCCTGTGGCGAGAAGGGCGGTATAAAATTATGATGTACTCTCTGCTGCCCTCAA
 55 TGTCATCTGCCCGCAGTGCTCATCCTGCCCTACCTCTTATCATCACCAAGTGTCTGA
 GGATCTCCTCCCAAGGGCTACCTCAAAGCCTCTCACATGCTCCTCCACCTGACCTCT

GTCACITTATACTATGGCTCCATTCTACATCTACGCTCTCCCCAGATCTAGCTATTCTT
TGATATGGACAAAATAGTTCTACATTTACACTGTGGTATTCCCCATGTGAATCTCATG
ATCTACAGCTAAGGAATAAGGATGTGAAAGAGGCTCTGAAAAAAACTCTCCATAA (SEQ
ID NO: 300)

5

AOLFR164 sequences:

MFLTERNTTSEATFTLLGFSDYLELQIPLFFVFLAVYGFSVVGNLGMIVIINKINPKLHTPMYFFLN
HLSFVDFCYSSIIAPMMLVNLVVEDRTISFSGCLVQFFFFCTFVVTELILFAVMAYDHFVAICNP
LLYTVAISQKLCAMLVVVLYAWGVACSLTLACSAKLSFHGFNTIHFFCELSSLISLSDYPSYL
10 SQLLFLTVATFNEISTLILTSYAFIIVTILKMPASGHRKVFSTCASHLTAITFHGTILFLYCV
NSKNRSHRTVKVASFYTVVPLNPLIYSLRNKDVKDAIRKINTKYFHKHRHWYPFNFVIEQ
(SEQ ID NO: 301)

15 ATGTTCTGACAGAGAGAAATACGACATCTGAGGCCACATTCACTCTGGGCTTCTCAG
ATTACCTGAACTGCAAATTCCCTCTTGTATTCTGGCAGTCACGGCTTCAGTGTG
GTAGGGAATCTGGGATGATAGTGTATCAAATTAAACCCAAATTGCATACCCCCATGT
ATTTTCTCAACCACCTCTCCTTGTGGATTCTGCTATTCCCATCATTGCTCCCAGTA
TGCTGGTGAACCTGGTTGAGAAGATAGAACCATTCATTCAGGATGTTGGTGAATT
CTTTTCTTGCACCTTGTAAGTGAATTAAATTCTATTGCGGTGATGGCCTATGACC
20 ACTTTGTGCCATTGCAATCCTCTGCTCACACAGTTGCCATCTCCAGAAACTCTGTGCC
ATGCTGGTGGTTGATTGTATGCATGGGAGTCGCATGTTCCCTGACACTCGCGTGCTCG
CTTAAAGTTATCTTTCATGGTTCAACACAATCAATCATTCTCTGTGAGTTATCTCC
CTGATATCCTCTACCTGACTCTTACAGCCAGTTGCTTCACTGTTGAC
25 TTTAATGAGATAAGCACACTACTCATCATTCTGACATCTATGCATTCACTATTGTCACCA
CCTTGAAGATGCCATTGAGCCAGTGGGACCGCAAAGTCTCTCCACCTGTGCCCTCCACCT
GACTGCCATCACCATTCCATGGCACCATCCTCTCTACTGTTGAC
ACTCCAGGCACACAGTCAAAGTGGCTCTGTGTTTACACCGTGGTATCCCTGTTGAA
TCCCCTGATCTACAGTCTGAGAAATAAGATGTTAAGGATGCAATCCGAAAAATAATCAAT
30 ACAAATATTTCATATTAAACATAGGCATTGGTATCCATTAAATTGTTATTGAACAATA
A (SEQ ID NO: 302)

AOLFR165 sequences:

MAVGRNNTIVTKFILLGLSDHPQMKIFLFLGLYLLTLAWNLSLIALIKMDSHLHMPMYFFL
SNLSFLDICYVSSTAPKMLSDIITEQKTISFVGCAIQYFVFCGMLTECFLLAAMAYDRYAAICN
35 PLYTVLISHLCLKMVVGAYVGGFLSSIETYSVYQHDFCGPYMINHFFCDLPPVLALSCSDTF
TSEVVTFIVSVVVGIVSVLVLISYGYIVAAVVKISSATGRTKAFSTCASHLTAVTIFYGSGFFM
YMRPSSSYSLNRDKVVSIFYALVIPVNPIIYSFRNKEIKNAMRKAMERDPGISHGGPFIFMTLG
(SEQ ID NO: 303)

40 ATGGCTGTAGGAAGGAACAACACAATTGTGACAAATTCTCTGGGACTTCAAGACC
ATCCTCAAATGAAGATTTCCTTTCATGTATTCTGGGCTCTACCTCTGACGTTGGCC
TGGAACCTAACGCCATTGCCCTCATTAAGATGGACTCTCACCTGCACATGCCCATGTACT
TCTCTCTAGTAACCTGTCCTCTGGACATCTGCTATGTGTCCTCACCGCCCCCTAAGATG
CTGTCTGACATCATCACAGAGCAGAAACCATTCCTTGTGGCTGTGCCACTCAGTACT
45 TTGTCITCTGTGGATGGGCTGACTGAATGCTTCTCTGGCAGCTATGCCCTATGACCG
GTATGCTGCAATCTGCAACCCCTTGCTTACACAGTCCTCATATCCCACACTTTGTTAA
AGATGGTGGTTGGCCCTATGTGGTGGATTCTTACAGTCTTCTGAAACATACTCTGT
CTATCAGCATGATTCTGTGGCCCTATATGATCAACCACTTTCTGTGACCTCCCTCAG
50 TCTCTGGCTCTGTCTGCTGATACCTCACAGCGAGGTGGTGCACCTCATAGTCAGTGT
GTCGTTGGAATAGTGTCTGTGCTAGTGGCTCTCATCTTATGGTACATTGTTGCTGCTGT
TGTGAAGATCAGCTCAGCTACAGGTAGGACAAAGGCCTCAGCACTTGTGCCTCTCACCTG
ACTGCTGTGACCCCTCTCTATGGTCTGGATTCTCATGTACATGCGACCCAGTTCCAGCTA
CTCCCTAAACAGGGACAAGGTGGTGTCCATATTCTATGCCTTGGTGAATCCCGTGGTGAAT
55 CCCATCATCTACAGTTAGGAATAAGGAGATTAAGGAGATTAAGGAGATGCCATGAGGAAAGCCATGGAA
AGGGACCCGGGATTCTCACGGTGGACCATTCTGACCTTGGCTAA (SEQ ID
NO: 304)

AOLFR166 sequences:

5 MEMENCTRKEFIFLGLTQNREVSLVLFLLL VYVTTLLGNLLIMVTVCESRLHTPMYFLH
 NLSIADICFSSITVPKVLVDLLSERKTISFNHCFTQMLFHIGGVDFSLVMALDRYVAISKPL
 HYATIMSRDHICLTVAAWLGGFVHSIVQISLLLPLPFCGPNVLDTFYCDVHRVLKLAHTDIFL
 ELLMISNNGLLTLWFFLLL VSYIVILSLPKSQAGEGRRKAISTCTSHITVVTLHFVPCIYVYARP
 FTALPMDKAISVTFTVISPLLNPLIYTLRNHEMKSAMRRLKRRLVPSDRK (SEQ ID NO: 305)

10 ATGGAGATGGAAA ACTGCACCAGGGAAAAGAATTATTTCTTGGCCTGACCCAGAAC
 GGGAAAGTGAGCTTAGTCTTATTCTTCTACTCTTGGGTATGTGACAACCTTGTGGGA
 AACCTCCTCATCATGGTCACTGTTACCTGTGAATCTCGCCTCACACGCCCATGTATTTT
 GCTCCATAATTCTATTGCCGATACTGCTTCTTCCATCACAGTGCCAAGGTTCTGG
 TGACCTCTGTCTGAAAGAAAGACCATCTCCTCAATCATTGCTTCACTCAGATGTTCTA
 TTCCACCTTATTGGAGGGGTGGATGTATTTCTCTTGGGTATGGCATTGGATCGATATG
 15 TGCCATCTCCAAGCCCCTGCACTATGCGACTATCATGAGTAGAGACCATTCGATTGGGCT
 CACAGTGGCTGCCTGGTGGGGCTTGTCCACTCCATCGTCAGAATTCCCTGTTGCTC
 CCACTCCCTTCTGCCGACCCAATGTTCTGACACTTCTACTGTGATGTCCACCGGGTCT
 CAAACTGGCCCATACAGACATTTCATACTGAACACTAAATGATTCCAACAATGGACTG
 CTCACCACACTGTGGTTTCTGCTCCTGGTGTCCATAGTCATATTACATTACCCAA
 20 GTCTCAGGAGGGCAGGAGAGGGCAGGAGGAAGCCATCTCCACCTGCACCTCCCACATCACTGT
 GGTGACCTGCAATTCTGTCACCTTCAGTGTCACTCTCCCTGCTCAACCCCTGATCTAC
 TGGATAAGGCCATCTCTGTCACCTTCAGTGTCACTCTCCCTGCTCAACCCCTGATCTAC
 ACTCTGAGGAACCATGAGATGAAGTCAGCCATGAGGAGACTGAAGAGAAGACTGTGCT
 TCTGATAGAAAATAG *SEQ ID NO: 306)

25

AOLFR167 sequences:

30 MSITKAWNSSS VTMFILLGFTDHPELQALLFVTFLGIYLTTLAWNLA LIFLIRDTHLHTPMYFF
 LSNLSFIDICYSSA VAPNMLTDFFWEQKTISFVGCAAAQFFFFVGMGLSECLL TAMA YDRYAAI
 SSPLLYPTIMTQGLCTR M VVGA YVGGFLSSLIQASSIFRLHFCGPNIHFCDLPPVLA LSCSDT
 FLSQVNVFLVVVTVGGTSFLQLLISYGYIVSAVLKIPSAEGRWKACNTCA SHLMVVTLLFGTAL
 FVYLRPSSSYLLGRDKVVSVFYSLVIPMLNPLIYSLRNKEIKDALWKVLERKKVFS (SEQ ID
 NO: 307)

35 ATGTCCATAACCAAAGCCTGGAACAGCTCATCAGTGACCATGTTCATCCTCTGGGATTCA
 CAGACCATCCAGAACTCCAGGCCCTCCTTTGTGACCTTCTGGCATCTATCTTACCA
 CTGGCCTGGAACCTGCCCTCATTTCTGATCAGAGGTGACACCCATCTGCACACACCA
 TGTACTTCTCTTAAGCAACTTATCTTCAATTGACATCTGCTACTCTCTGCTGTGGCTCC
 AATATGCTCACTGACTTCTCTGGGAGCAGAAGACCATATCATTGTTGGCTGTGCT
 AGTTTTTTCTTGTGGCATGGGTCTGTCTGAGTGCCCTCCTGACTGCTATGGCATAC
 40 GACCGATATGCAGCCATCTCCAGCCCCCTCTACCCACTATCATGACCCAGGGCCTCT
 GTACACGCATGGTGGTGGGCATATGTTGGTGGCTCTGAGCTCCCTGATCCAGGCCAG
 CTCCATATTAGGCTTCACTTTGCGGACCCAACATCATCAACCACTCTCTGCGACCTCC
 CACCAGTCCGGCTCTGCTTGACACCTTCTCAGTCAGTGGTAATTCTCTGCT
 GTGGTCAGTGTGGAGGAACATCGTTCTCAACTCCTTATCTCTATGGTACATAGTGT
 45 CTGGCTCTGAAGATCCCTCAGCAGAGGGCGATGGAAGCCTGCAACACGTGTGCCT
 CGCATCTGATGGTGGTACTCTGCTGTTGGACAGCCCTTCTGTA CTTGCGACCCAG
 CTCCAGCTACTGCTAGGCAGGGACAAGGTGGTGTCTGTTCTATTCTATTGGTGAATCCCC
 ATGCTGAACCCCTCTCATTCAGTGTGGAGGAACAAAGAGATCAAGGATGCCCTGTGGAAG
 GTGTTGGAAAGGAAGAAAGTGTGTTCTAG (SEQ ID NO: 308)

50

AOLFR168 sequences:

55 MEKINNVTEFIFWGLSPEIEK VCFVVFSSFYIILLGNLLIMLTVCLSNLFKSPMYFFLSFLSFV
 DICYSSVTAPKMIVDLLAKDKTISYVGCMQLLGVHFFGCTEIFILTVMAYDRYVAICKPLHYM
 TIMNRETCNKMLLGTWVGGFLHSIIQVALVVQLPFCGPNEIDHYFCDVHPVLKACTETYIVG
 VVVTANS GTIALGSFVILLISYSIILVSLRKQSAEGRRKALSTCGSHIAMVVIFGPCTFMYMRPD

TTFSEDKMWAVFYTIITPMLNPLIYTLRNAEVKNAMKKLWGRNVFLEAKGK (SEQ ID NO: 309)

5 ATGGAAAAAATAAACACGTAACGTGAATTCACTTCTGGGTCTTCTCAGAGCCCAGAGA
 TTGAGAAAGTTGTTGTGGTCTTCTACATAATCATTCTCTGGAAATCTC
 CTCATCATGCTGACAGTTGCTGAGCAACCTGTTAAGTCACCCATGTATTCTTCTAG
 CTCTGTCTTGTGGACATTGTTACTCTCAGTCACAGCTCCAAAGATGATTGTTGACC
 TGTAGCAAAGGACAAAACCACATCTCCTATGTGGGTGCACTGTTGAGACTGCTGGAGTAC
 ATTCTTGGTTGCACTGAGATCTCATCCTACTGTAATGGCTATGATGTTATGTGCT
 10 ATCTGAAACCCCTACATTATATGACCATCATGAACCGGGAGACATGCAATAAAATGTTAT
 TAGGGACGTGGTAGGTGGTTCTACACTCCATTATCCAAGTGGCTGGTAGTCCA
 ACCCTTTGTGGACCCAATGAGATAGATCACTACTTTGTGATGTTACCCCTGTTGAAA
 CTTGCCTGCACAGAAACATACATTGTTGTTGACAGCCAAACAGTGGTACCATG
 CTCTGGGAGTTTGTATCTGCTAATCTCCTACAGCATCATCCTAGTTCCCTGAGAAAG
 15 CAGTCAGCAGAAGGCAGGCAGCAAAGCCTCTCCACCTGTGGCTCCACATTGCCATGGTCG
 TTATCTTTCGGCCCTGTACTTTATGTACATGCGCCCTGATACGACCTTTCA
 AAGATGGTGGCTGTATTTACACCATTACTCCTGTTAAATCCTGATTATACACT
 GAGAAATGAGAAGTAAAGAATGCAATGAAGAAACTGTGGGAGAAATGTTCTTGG
 GGCTAAAGGGAAATAG (SEQ ID NO: 310)

20

AOLFR169 sequences:

MMDNHSSATEFHLLGFPGSQGLHHILFAIFFFYLVTLMGNTVIIVIVCVVDKRLQSPMYFFLSHL
 STEILVTTIIVPMMLWGLFLGCRQYLSLHVSLNFSCTGTMFALLGVMAVDRYVAVCNPLRY
 25 NIIMNSSTCIWVVIVSWVFGFLSEIWPYATFQFTFRKSNSLDHFYCDRGQLLKLSCDNTLLTEFI
 LFLMAVFILIGSLIPTIVSYTYIISTILKIPSASGRRKAFSTFASHFTCVVIGYGSCLFLYVVKPKQTQ
 GVEYNKIVSLLVSVLTPFLNPFIITRNDKVKEALRDGMKRCCQLKD (SEQ ID NO: 311)

30 ATGATGGACAACCACTCTAGTCCACTGAATTCCACCTCTAGGCTTCCCTGGGTCCAAG
 GACTACACCACATTCTTTGCTATATTCTTTCTCTATTAGTGCACATTAAATGGGAAAC
 ACGGTATCATATTGTGATTGTCTGTGGATAAACGTCAGTCAGTCCCCCATGTATTCTTCT
 CAGCCACCTCTCACCCCTGGAGATCCTGGTCACAACCATAATTGTCCCCATGATGCTTGG
 GGATTGCTCTCCTGGGATGCGAGACAGTATCTTCTCTACATGTATCGCTCAACTTTCTG
 TGGGACCATGGAGTTGCATTACTGGAGTGATGGCTGTGGACCGTTATGTGGCTGTGTT
 AACCCCTTGAGGTACAACATCATTATGAAACAGCAGTACCTGTATTGGGTGGAATAGTGT
 35 CATGGGTGTTGGATTCTTCTGAAATCTGCCCATCTATGCCACATTCACTTACCTTC
 CGCAAATCAAATTCTAGACCATTTACTGTGACCGAGGGCAATTGCTCAAACGTCT
 GCGATAACACTCTCTCACAGAGTTATCCTTCTTAATGGCTGTTTATTCTCAATTGGT
 TCTTGATCCCTACGATTGTCTCCTACACCTACATTACTCCACCATCCTCAAGATCCGTC
 40 AGCCTCTGCCGGAGGAAAGCCTCTCCACTTTGCCCTCCACTTCACCTGTGTTGATTG
 GCTATGGCAGCTGCTTCTCTACGTGAAACCCAAGCAACACAGGGAGTTGAGTACAA
 TAAGATAGTTCCCTGTTGGTTCTGTGTTAACCCCCCTCTGAATCCTTCACTTTACTCT
 TCGGAATGACAAAGTCAAAGAGGCCCTCGAGATGGATGAAACGCTGCTGTCAACTCCT
 GAAAGATTAG (SEQ ID NO: 312)

45

AOLFR170 sequences:

MSFTSLIPSLCFSLTLPPFLFCYLSLLPFLSAFLFITRWLALFLSFSVSPVSSVSSSMVLCLYLSVS
 ASPSVCFCSCMQGPILWIMANLSQPSEFVLLGFSSFGEQALLYGPFLMLYLLAFMGNTIIVMVI
 ADTHLHTPMYFFLGNFSLLEILVTMTAVPRMLSDLVPHKVTFTGCMVQFYFHSLGSTSFLIL
 50 TDMALDRFVAICHPLRYGTLMSRAMCVCQLAGAAWAAPFLAMVPTVLSRAHLDYCHGDVNH
 FFCDNEPLLQLSCSDTRLEFWDFLMALTFVLSSFLVTLISYGYIVTTVLRIPSASSCQKAFSTCG
 SHLTLVFIGYSSTIFLYVRPGKAHSVQVRKVVALVTSVLPFLNPFLTCFCNQTVKTVLQGQMQ
 RLKGLCKAQ (SEQ ID NO: 313)

55

ATGTCTTCACTCTCTACACCTCACTCTGTTCTCCCTGACTCTCCATTCTGTTG
 TATCTTCTTATTGCCGTTCTCTGTTCTGTTATCACTCGCTGGCTACTGCCTT
 CTCTCTCTATTCTCTGCTCTGCTCCCTGTTCTGTTCAAGTTCAATGGTTCTCTGTC

TATCTCTCTGTTCTGCCTCTCCGCTGCTTTGTTCTTGCATGCAGGGCCCCATACTG
 TGGATCATGGCAAATCTGAGCCAGCCCTCCGAATTGTCCTCTGGGCTTCTCCTCCTTGG
 TGAGCTGCAGGCCCTCTGTATGGCCCTTCATGCTTATCTTCTGCCTCATGGAA
 5 ACACCATCATCATAGTTATGGTCATAGCTGACACCCACCTACATACACCCATGTAACCTC
 CTGGGCAAATTTCCTGCTGGAGATCTGGTAACCATGACTGCAGTGCCAGGATGCTCT
 CAGACCTGTTGGTCCCCACAAAGTCATTACCTTCACTGGCTGCATGGTCCAGITCTACTTC
 CACTTTCCCTGGGGTCCACCTCCTCATCCTGACAGACATGGCCCTGATCGTTGT
 10 GCCATCTGCCACCCACTGCCTATGGACTCTGATGAGCCGGCTATGTGTGTCAGCTG
 GCTGGGCTGCCGGCAGCTCCTTCAGCCATGGTACCCACTGTCCCTCTCCGAGCTC
 ATCTTGATTACTGCCATGGCGACGTCAACCACTTCTCTGTGACAATGAACCTCTCG
 CAGTTGTCATGCTCTGACACTCGCTGTTGAAATTCTGGACTTTCTGATGGCCTGACCTT
 TGCCCTCAGCTCCTCCTGGTGCACCTCATCTCCTATGGCTACATAGTGACCACTGTGCTG
 15 GGATCCCCTCTGCCAGCAGCTGCCAGAAGGTTCTCCACTTGCAGGGTCTCACCTCACACT
 GGTCTCATCGGCTACAGTAGTACCATTTCTGTATGTCAGGCTGGCAAAGCTCACTCT
 GTGCAAGTCAGGAAGGTGTTGGCCTGGTGAACCTCAGTTCTCACCCCCCTTCATACTC
 TTATCCTTACCTTCTGCAATCAGACAGTTAAACAGTGTACAGGGCAGATGCAGAGGCT
 20 GAAAGGCCTTGCAAGGCACAATGA (SEQ ID NO: 314)

AOLFR171 sequences:

20 MVGNLLIWVTIGSPSLGSLMYFFLAYLSLMDAIYSTAMSPKLMIDLCDKIAISLACMGQLFI
 EHLLGGAEVFLVVMAYDRYVAISKPLHYLNIMNRLVCILLVVAMIGGFVHSVVQIVFLYSLP
 ICGPNVIDHSVCDMYPILLELLCLDTYFIGLTVVANGGIICMVIFTFLISCVGILNFLKTYSQEER
 HKALPTCISHIVVALVFVPCIFMYVRPVSNFPFDKLMTVFSIITMLNPLIYSLRQSEMKNAM
 KNLWCEKLSIVRKRVSPTLNIFIPSSKATNRR (SEQ ID NO: 315)

25 ATGGTGGGAAACCTCCTCATTGGGTGACTACTATTGGCAGCCCTCCTGGGCTCCCTAA
 TGTACTTCTCCCTGCCTACTTGTCACTTATGGATGCCATATACTCCACTGCCATGTCACCC
 AAATTGATGATAGACTTACTCTGTGATAAAATCGCTATTCCCTGTGAGCTGCTGGGTC
 AGCTCTCATAGAACACTTACTTGGTGGTGCAGAGGTCTCCTTGTGGTGTGATGGCCTA
 30 TGATCGCTATGTGGCTATCTCTAACGCCGCTGCACTATTGAACATCATGAATCGACTGGTT
 TGACATCTCTGTTGGTGGCCATGATTGGAGGTTTGTGCACTCTGTGGTCAAATTGT
 CTTCTGTACAGTCTACCAATCTGTGGCCCTGACACCTACTTATAGGACTCACTGTGGTGC
 ACCATTGTGGAACTGTGTGCCTGACACCTACTTATAGGACTCACTGTGGTGC
 35 TGGTGGATAATTGTATGGTCATCTTACCTTCTGCTAATCTCTGTGGAGTCATCTAA
 ACTTCCCTAAACTACAGTCAGGAAGAGAGGCATAAAGCCCTGCCTACCTGCATCTCCA
 CATCATTGTGGITGCCCTCGTTTGTTCCCTGTATTTTATGTATGTTAGACCGTTCCA
 ACTTCCCTTGATAAAATTATGACTGTGTTTATTCAATTATCACACTCATGTTGAATCCT
 TTAATATACTCGTTGAGACAATCAGAGATGAAAGAAATCTCTGGTGTGAA
 40 AAGTTAAGTATAGTTAGAAAAAGAGTATCTCCACACTGAACATATTATTCCCTAGTTCTA
 AGGCAACAAATAGGCGGTAA (SEQ ID NO: 316)

AOLFR172 sequences:

45 MAETLQLNSTFLHPNFFILTGFPGGLGSAQTWLTLVFGPIYLLALLNGNGALPAVVWIDSTLHQPM
 FLLAILAATDLGLATSIAPGLLAVLWLGRPSVPYAVCLVQMFFVHALTAMESGVLLAMACDR
 AAAIGRPLHYPVLVTKACVGYAALALALKAVAIVVPFPLLVAKFEHFQAKTIGHTYCAHMAV
 VELVVGNTQATNLYGLALSLAISGMDILGITGSYGLIAHAVLQLPTREAHAKAFGTCSSHICVIL
 AFYIPGLFSYLAHRFGHHTVPKPVHILLSNIYLLPPALNPLIYGARTKQIRDRLLETFTFRKSPL
 (SEQ ID NO: 317)

50 ATGGCAGAAACTCTACAACCAATTCCACCTTACACCCAAACTTCTCATACTGACTG
 GCTTCCAGGGCTAGGAAGTGCCAGACTGGCTGACACTGGTCTTGGCCATTTATCT
 GCTGGCCCTGCTGGCAATGGAGCACTGCCGGCAGTGGTGGATAGACTCCACACTGCA
 CCAGCCCATGTTCTACTGTTGCCATCTGGCAGCCACAGACCTGGGCTTAGCCACATCT
 ATAGCCCCAGGGTGTGGCTGTGCTGGCTTGGGCCCCGATCTGTGCCATATGCTGTGT
 55 GCCTGGTCCAGATGTTCTTGATCGCACTGACTGCCATGGAATCAGGTGTGCTTGGC
 CATGGCCTGTGATCGTGCCTGGCAATAGGGCTCCACTGCACTACCCCTGTCCGGTACCC

AAAGCCTGCTGGGTTATGCAGCCTGGCCCTGGCACTGAAAGCTGTGGCTATTGTTGTAC
 CTTTCCCAC TGCTGGCAAAAGTTGAGCACTTCCAAGCCAAGACCATAGGCCATACCTA
 TTGTCACACATGGCAGTGGTAGAACACTGGTGGTGGTAACACACAGGCCACCAACTATA
 5 TGGTCTGGCACTTCACTGGCCATCTCAGGTATGGATATTCTGGGTATCACTGGCTCCTAT
 GGACTCATGCCCCATGCTGTGCAGCTACCTACCCGGAGGCCATGCCAAGGCCCTTG
 GTACATGTAGTTCTCACATCTGTGCATTCTGGCCTCTACATACCTGGTCTCTCTCCTAC
 CTCGCACACCGCTTGGTCATCACACTGTCCCAGCCTGTGCACATCCTCTCTCCAAACAT
 CTACTGCTGCTGCCACCTGCCCTCAACCCCTCATCTATGGGCCCCGACCAAGCAGATC
 AGAGACCGACTCCTGGAAACCTCACATTAGAAAAAGCCC GTTGAA (SEQ ID NO: 318)

10

AOLFR173 sequences:

MSHTNVTFHPAVFVLPGIPGLEAYHIWLSIPLCLIVITAVLGNSILIVVIVMERNLHVPMYFFLS
 MLA VMDILLSTTTVPKALAIFWLQAHNIAFDACVTQGFFVHMMFVGESAILLAMAFDRFVAIC
 15 APLRYTTVLTWPVVGRIALAVITRSFCIIFPVIFLLKRLPFCLTNIVPHSYCEHIGVARLACADITV
 NIWYGFSPIVMVILDVILIAVSYSLILRAVFR LPSQDARHKALSTCGSHLCVILMFYVPSFTLL
 THHFGRNIPQHVHILLANLYVAVPPMLNPIVYGVTKQIREGVAHRFFDIKTWCCTSPLGS
 (SEQ ID NO: 319)

20

ATGAGTCACACCAATGTTACCATCTTCACTCCTGCAGTTTGTCCCTCCGGCATCCCTGG
 GTTGGAGGCTTATCACATTGGCTGTCAATACCTCTTGCCCTCATTTACATCACTGCAGTCC
 TGGGAAACAGCATTCTGATAGTGGTTATGTCTGATGGAACGTAACCTTCATGTGCCCATGTA
 TTTCTCCTCTCAATGCTGGCCGTATGGACATCCTGCTGTCTACCACCACTGTGCCCAAGG
 CCCTAGCCATCTTGGCTCAAGCACATAACATTGCTTTGATGCCGTGTCACCCAAAGGC
 TTCTTGTCATATGATGTTGTGGGGAGTCAGCTATCCTGTTAGCCATGGCCTTGTGATCG
 25 CTTTGTGGCCATTGTGCCCCACTGAGATATAACACAGTGCTAACATGGCCTGTTGTGGGG
 AGGATTGCTCTGGCCGTATCACCAGAACATGCTGCTGACATCCTACTGTGAGCATATTGGA
 GAAGCGGCTGCCCTCTGCCTAACCAACATGCTCCTACTGTGAGCATATTGGA
 GTGGCTCGTTAGCCTGTGACATCCTACTGTGTTAACATTTGGTATGGCCTCTCAGTGCCCAT
 TGTCATGGTCATCTGGATGTTATCCTCATCGCTGTGCTTACTCACTGATCCTCCGAGCAG
 30 TGTTTCGTTGCCCTCCCAGGATGCTGGGACAAGGCCCTCAGCACTTGTGGCTCCACCT
 CTGTCATCCCTATGTTATGTTCCATCCTCTTACCTTATTGACCCATCATTTGGCG
 TAATATTCCCTAACATGTCCATATCTGCTGGCCAATCTTATGTGGCAGTGCCACCAATGC
 TGAACCCCATGTCTATGGGTGAGACTAACAGATACGTGAGGGTGTAGCCCACCGGTT
 CTTTGACATCAAGACTTGGTGCTGTACCTCCCTCTGGGCTCATGA (SEQ ID NO: 320)

35

AOLFR175 sequences:

MHFLSQNDLNINLPHLCLHRHSVIAGAFTIHRHMKIFNSPSNSSTFTGFILLGFPCPREGQILLFV
 LFTVVYLLTLMNGNSIICAVHWDRQLHAPMYILLANFSFLEICVVTSTVPSMLANFLSDTKIISF
 40 SGCFQFYFFFSLGSTECCFLAVMAFDRYLAICRPLRYPTIMTRRLCTNLVNCWVLGFIWFLIPI
 VNISQMSFCGSRIIDHFLCDPAPLLTLCCKGPVIELVFSVSLPLPVFMLFLIVGSYALVVRAVL
 RVPSAAGRRAFSTCGSHLAVVSLFYGSVLVMYGSPPSKNEAGKQKTVTLFYSVTPLLNPVI
 YSLRNKDMRKALKFWGT (SEQ ID NO: 321)

45

ATGCATTTCTTCCAAAATGATTAAATATAATCTGATTCCCCATCTATGTTGCACCG
 TCATTCACTGAGTAACTGCTGGCTTTACAATTCACAGGCACATGAAAATCTCAACAGCCCC
 AGCAACTCCAGCACCTCACTGGCTTCACTCCTCTGGCTCCCTGGCCAGGGAGGGGC
 AGATCCTCCTCTTGCTCTTCACTGTTACCTCCTGACCCCTCATGGGCAATGGTTC
 ATCATCTGTGCTGTGCACTGGGATCAGAGACTCCACGCCCATGTACATCCTGCTCGCCA
 ACTTCTCCTCTTGAGATATGTTATGTCACCTCCACAGTCCCCAGCACTGCTGCCAACTTC
 50 CTCTCTGACACCAAGATCATCTCGTTCTCTGGCTGCTCCCTCCAGTTCTACTTTTCTTCTCC
 TTGGGCTCTACAGAAATGCTTTCTGGCAGTTATGGCATTGATCGATACCTTGCCATCTG
 TCGGCCTCTACGCTATCCAACCATATGACCAAGACGTCTGTACCAATCTGTGGTCAATT
 GCTGGGTACTGGTTCTGATCTGGTCTTGTGATTCTATCGTCAACATCTCCAAATGTCCCTC
 TGTTGGATCTAGGATTATTGACCACTTCTATGTGACCCAGCTCTCTTAACACTCACTTG
 55 CAAAAAAAGGCCCTGTGATAGAGCTTGTCTTCTGCTTAAGTCCTGCTGTCTTATGC
 TCTTCTCTCATTGTGGGGCTCATGCTCTGGCTGTGAGAGCTGTGTTGAGGGTCCCTCA

5
GCGAGCTGGGAGAAGAAAGGCTTCTCCACCTGTGGGTCTCACCTGGCTGTGGTTCACTGT
TCTACGGCTCAGTACTGGTCATGTATGGGAGCCACCACATCTAAGAATGAAGCTGGAAAGC
AGAAGACTGTGACTCTGTTTATTCTGTTGTTACCCCACTGCTTAACCCCTGTGATATAGT
CTTAGGAACAAAGATATGAGAAAAGCTCTGAAGAAAATTTGGGAAACATAA (SEQ ID NO:
322)

AOLFR176 sequences:

10	MFFIHSLSVTSVFLTALGPQNRTMHFVTEFVLLGFHGQREMQSCFFSFLVLYLLTLLGNGAIVC AVKLDRLRLHTPMYILLGNFAFLEIWYISSTVPNMLVNILSEIKTISFSGCFLQFYFFFSLGTTECFF LSVMAYDRYLAICRPLHYP SIMTGF CILVCVCWVGGFLCYPVPIVLISQLPFCGPNIIDHLVCD PGPLFALACISAPSTELICYTFNSMIIFGPFLSILGSYTLVIRAVLCIPSGA GRTKAFSTCGSHLMV VSLFYGTLVMVYVSP TSGNPAGMQKII TLVYTAMTPFLNPLIYSLRNKDMKDALKRVLGLTVS QN (SEQ ID NO: 323)
15	ATGTTCTTAAITATTCA TTGGTTACTTCTGTTCTAACAGCTTGGGACCCCAGAA CAGAACAAATGCATT TGACTGAGTTGCTCCTCTGGGTTCCATGGTCAAAGGGAGATG CAGAGCTGCTTCTCTCATT CATCCTGTTCTATCTCCTGACACTGCTAGGGAATGGAGC TATTGTC TGCA GTGAAATTGGACAGGCGGCTCCACACACCCATGTACATCCTCTGGGA AACTTTGCCCTTCTAGAGATCTGGTACATTCCCTCACTGTC CAAACATGCTAGTCAATAT CCTCTCTGAGATTAAAACCATCTCCTCTCTGGTTGCTTCTGCAATTCTATTCTTTTTTC ACTGGGTACAACAGAGTGTCTTTTATCAGTTATGGCTTATGATCGGTACCTGGCCATC TGTCGTCCATTACACTACCCCTCCATCATGACTGGGAAGTTCTGTATAATTCTGGTCTGTG ATGCTGGGTAGGCGGATTCTCTGCTATCCAGTCCCTATTGTTCTATCTCCCAACTCCCT TCTGTGGGCCAACATCATTGACCACTGGTGTGACCCAGGCCATTGTTGCACTGGC CTGCATCTGCTCCTCCACTGAGCTTATCTGTTACACCTCAACTCGATGATTATCTTGG GCCCTTCTCTCCATCTGGATCTTACACTCTGGTCACTAGAGCTGTGCTTGTATTCCC TCTGGTGTGGTCAACTAAAGCTTCTCACATGTGGTCCCACCTAATGGTGGTGTCTC TATTCTATGGAACCTTATGGTGTATGTGAGCCCAACATCAGGGAACCCAGCAGGAAT GCAGAAGATCATCACTCTGGTATACACAGCAATGACTCCATTCTAAATCCCTTATCTAT AGTCTCGAAACAAAGACATGAAAGATGCTAAAGAGAGTCCTGGGTTAACAGTTAGC CAAAACTGA (SEQ ID NO: 324)
20	
25	
30	

AOLFR177 sequences:

35 MSFFFVDLRPMNRSA THIVTEFILLGFPGCWKIQIFLFLFLVIVVLTLLNGN AIIYAVRCNPLLH
TPMFLLGNFAFLEIWIYVSS TIPNMLVNILSKTKAISFGCFLQFYFFFSLGTT ECLFLAVMAYD
RYLAICHPLQYPAIMTVRFCGKLVSFCWLIGFLGYPIPIFYISQLPFCGPNIIDHFLCDMDPLMAL
SCAPAPITECIFYTQSSLVLFFTSMYILRSYILLTAVFQVPSAAGRRKAFSTCGSHLVVVSFLYG
TVMVMYVSPYGIPTLQLKILT L VYSVTPLFNPLIYTLRNKDMKLALRNVLFGMRIRQNS
(SEQ ID NO: 325)

40 ATGCTTCTCTTGTAGACTAAGACCCATGAACAGGT CAGCAACACACATCGTGACAG
AGTTTATTCTCCTGGGATTCCCTGGTTGCTGGAAAGATT CAGATTTCTCTTCTCATTTGTT
TTGGTGATTATGTCTGACCTTGCTGGAAATGGAGCCATCATCTATGCAGTGAGATGCA
ACCCACTACTACACACACCCCCATG TACTTCTGCTGGAAATTTGCCCTCCTGAGATCTG
45 TATGTGTCCCTCACTATT CCTAACATGCTAGTCAACATTCTCTCAAGACCAAGGCCATCTC
ATTTCTGGGTGCTTCCCTCAGTTCTATTTCTCTTCTACTGGAAACA ACTGAATGTCTCT
TTCTGGCAGTAATGGCTTATGATCGATACCTGGCCATCTGCCACCCACTGCAGTACCTGC
CATCATGACTGTAAGGTTCTGTTGTAAGCTGGTCTTCTGTTGGCTTATTGGATTCCCTG
50 GATAACCCAA TCCCATTCTACATCTCCCAACTCCCCCTCTGTTGCTTAATATCATTGAT
CACTTCTGTGTGACATGGACCCATTGATGGCTCTATCCTGTGCCCAAGCTCCATAACTG
AATGTATTCTATACACTCAGAGCTCCCTGTCCCTTTTCACTAGTATGTACATTCTCGA
TCCTATATCCTGTTACTAACAGCTGTTTCAAGGCTCCCTCTGCAGCTGGTGGAGAAAAG
CCTCTCTACCTGTGGTCTCATTTGGGTGTGGTATCTCTTTCTATGGGACAGTCATGGTA
55 ATGTATGTAAGTCTACATATGGGATCCAAC TTTATTGCAAGAGATCTCACACTGGTAT
ATTCAAGTAAACGACTCCTCTTTTAATCCTGTACTATCTCTGTAATAAGGACATGAAA

CTCGCTCTGAGAAATGTCCTGTTGGAATGAGAATTGTCAAAATTGTGA (SEQ ID NO: 326)

AOLFR178 sequences:

5 MVGANHSVVSEFVFLGLTNSWEIRLLLVFSSMFYMASMMGNLILLTVTSDPHLHSPMYFLL
ANLSFIDLGVSSVTSPKMIYDLFRKHEVISFGGCIAQIFFIHVIGGVEMLIAMAFLDRYVAICKP
LQYLTIMSPRMCMFLVAAWVTGLIHSVQLVFVNVLPFCGPNVSDSFYCDLPRFIKLAETDSY
RLEFMVTANSGFISLGSFFILIIYVVIITVLKHSSAGLSKALSTLSAHVSVVVLFFGPLIFVYTW
PSPSTHLDKFLAIFDAVLTPVLPNPIYTFRN (SEQ ID NO: 327)

10 ATGGTTGGGGCAAATCACTCCGTGGTGTCAAGAGTTGTGTTCTGGGACTCACCAATTCTT
GGGAGATCCGACTTCTCCTCTGTGTTCTCCATGTTTACATGGCCAGTATGATGGGA
AACTCTCTCATTTGCTCACTGTGACTTCTGACCCCTCACTGCACCTCCCCATGTATTTCT
GTTAGCCAACCTCTCCTCATGACCTGGGTGTTCTGTCACTTCTCCCCAAATGATT
15 ATGACCTGTTAGAAAAGCACGAAGTCATCTCTTGGAGGCTGCATCGCTAAATCTCTT
CATCCACGTCATTGGCGGTGTTGGAGATGGTGTGCTCATAGCCATGGCTTTGACAGATAT
GTGGCCATATGTAAGGCCCTCCAGTACCTGACCATATGAGGCCAAGAATGTGCATGTTCT
TCTTAGTGGCTGCTGGTGAACGGCCTTATCCACTCTGTAGTTCAATTGGTTTTGAGTA
AACTGCCCTCTGGTCTTAATGATCGGACAGCTTACTGTGACCTTCCCGGTTCAT
20 CAAACTTGCCCTGCACAGACAGCTACCGACTGGAGTTCATGGTTACAGCCAACAGTGGATTC
ATCTCTCTGGGCTCCCTCTTCAACTGATCATTTCTATGTGGTGTGCTCATCTCACTGTTCT
GAAACACTCTCAGCTGGTTATCCAAGGCTCTGTCACCCCTTCAGCTCACGTCACTGTTG
GTAGTTTGTCTTTGGCCTTTGATTTGCTATACGTGGCCATCTCCCTCCACACACCT
GGATAAGTTCTGGCCATCTTGATGCAAGTCTCACTCTGTGTTAAATCCTATCATCTACA
25 CATTAGGAATTGA (SEQ ID NO: 328)

AOLFR179 sequences:

30 MNGMNHSSVSEFVFMGLTNSREIQLLLFVFSLLFYFASMMGNLVTVFTVTMDAHLHSPMYFLL
ANLSIIDMAFCSITAPKMICDIFKKHKAISFRGCITQIFFSHALGGTEMVLLIAMAFLDRYMAICKP
LHYLTIMSPRMCLYFLATSSIIGLIHSVLQLVFVVDLPFCGPNFDSFYCDLPRLLRACNTQEL
EFMVTVNGLISVGSFVLLVISYIFILFTVWKHSSGLAKALSTLSAHVTVVILFFGPLMFYTW
PSPSTHLDKYLAIFDAFITPFLNPVIYTFRNKDMKVAMRRLCSRLAHTKIL (SEQ ID NO: 329)

35 ATGAATGGAATGAATCACTCTGTGGTATCAGAAATTGTATTGATGGGACTCACCAACTCAC
GGGAGATTCACTTCTACTTTGTTCTTGTGTTCTACTTGTGAGCATGATGGGA
AACCTGTCTTCAACTGTAACCATGGATGCTCATCTGCACTCCCCATGTATTTCT
CCTGGCTAACCTCTCAATCATGATATGGCATTGTCAATTACAGCCCCTAAGATGATT
GTGATATTCAAGAACGACAAGGCCATCTCCTTGGGGATGTATTACTCAGATCTCTT
40 TAGCCATGCTCTGGGGCACTGAGATGGTGTGCTCATGCCATGGCTTTGACAGATAC
ATGGCCATATGTAACACCTCTCAACTACCTGACCATCATGAGGCCAAGAATGTGTCTATACT
TTTAGCCACTTCTCTATCATTGGCCTTATCCACTCATGGTCAATTAGTTTGTGGA
GATTACCTTTGTGGTCTTAATATCTTGACAGTTTACTGTGATCTCCCTGGCTCCT
CAGACTTGCTGTACCAACACCCAAGAACGGACTGGAGTTCATGGTCACTGTCAATAGTGGACTC
ATTCTGTGGCTCCCTTGCTGGTAATTCTCTACATCTCATCTGTTACTGTTG
45 GAAACATTCTCTGGTGTCTAGCCAAGGCCCTCTACCCCTGTCAGCTCATGTCAGTGTG
GTCATCTGTTCTTGGCACTGATGTTCTACACATGGCTTCTCCACATCACACACCT
GGATAAAATATCTTGCTATTGATGCAATTACTCCTTCTGAATCCAGTTATCTACA
CATTAGGAACAAAGACATGAAAGTGGCAATGAGGAGACTGTGCACTGCTTGC
TTACAAAGATTGTAA (SEQ ID NO: 330)

50

AOLFR180 sequences:

55 MTNKMYAIYIKNLNYFSFLIVQCLQPTMAIFNNNTSSSNFLTAFPGLECAHVWISIPVCCLYTI
ALLGNSMIFLVIITKRLHCKPMYYFLSMLAADLCLTITLPTVLGVLFHAREISFKACFIQMF
FVHAFLSLESSVLAAMAFDRFVAICNPLNYATILTDRLMVLVIGLVICIRPAVFLLPLLVAINTVSF
HGGHELSPFCYHPEVIKYTYSKPWISSFWGLFLQYLNGLDVLFILFSYVLILRTVLGIVARKK

QQKALSTCVCHICAVTIFYVPLISLSAHLRFHSTPRVLCSTLANTYLLLPPVLPNPIYSLKTKTR
QAMFQLLQSKGSWGFNVRLGRGRWD (SEQ ID NO: 331)

5 ATGACTAATAAAATGTATGCTATATATATAAAGAACATCTTAAATTATTTCTTCCTCATAGT
TCAGTGTCTCAACCAACCATGGCAATATTCAATAACACCACTTCGTCTCCTCAAACCTCC
TCCTCACTGCATTCCCTGGGCTGGAAATGTGCTCATGTCTGGATCTCCATTCCAGTCTGCTGT
CTCTACACCAATTGCCCTCTGGGAAACAGTATGATCATTCTGTATCATTACTAACGGGA
GAACCTCCACAAACCCATGTATTATTCCTCTCCATGCTGGCAGCTGTTGATCTATGTCTGACC
ATTACGACCCCTCCCACTGTGCTGGTCTCTGGTTCATGCCCGGGAGATCAGCTTAA
10 AGCTTGCTTCATTCAAATGTTCTTGTGATGCTTCTCCATTGCTGGAGTCCTCGGTGCTGG
TAGCCATGCCCTTGACCGCTTCGTGGCTATCTGTAACCCACTGAACATGCTACTATCCTC
ACAGACAGGATGGTCTGGTATAGGGCTGGTATCTGCAATTAGACCAAGCAGTTTCTTAC
TTCCCTTCTGTAGCCATAAACACTGTGCTTTCATGGGGTCACGGAGCTTCCATCCA
TTTGCTACCACCCAGAAGTGTCAAATACACATATTCAAACCTGGATCAGCAGTTT
15 GGGGACTGTTCTCAGCTCACCTGAATGGCACTGACGTATTGTTATTCTTTCTCCTAT
GTCCTGATCCTCCGTACTGTTCTGGCATGGGGCCGAAAGAACAAAAAGCTCTCA
GCACTTGTGCTGTACATCTGCACTATTCTATGTGCCACTGATCAGCCTCTCT
TTGGCACACCGCCTTCCACTCCACCCAAAGGGTGTCTGTAGCATTGGCCAATATT
TCTGCTCTTACACCTGTGCTGAACCCATCATTACAGCTGAAGACCAAGACAATCCGC
20 CAGGCTATGTCAGCTGCTCCAATCCAAGGGTTCATGGGGTTAAATGTGAGGGGTCTTA
GGGAAGATGGGATTGA (SEQ ID NO: 332)

AOLFR181 sequences:

25 MSVLNNSEVKLFLLIGIPGLEHAHTWFSIPICLMLYLLAIMGNCTILFIKTEPSLHEPMYYFLAML
AVSDMGLSLSLPTMLRVFLFNAMGISPNAQFAQEFFIHGFTVMESVLLIMSLDRFLAIHNPLR
YSSILTSNRVAKMGLILAIRSILLVIPFPFTLRLKYCQKNLLSHSYCLHQDTMKLACSDNKTNV
IYFFIALCTMIDLALIVLSYVLLKTIISLASLAERLKALNTCVSHICAVLTFYVPIITLAAMHFF
AKHKSPLVVILIADMFLVPPLMNPIVYCVKTRQIWEKILGKLLNVCGR (SEQ ID NO: 333)

30 ATGTCTGTTCTCAATAACTCCGAAGTCAAGCTTCTGATTGGGATCCCAGGACTGG
AACATGCCACATTGGTCTCCATCCCCATTGCTCATGTACCTGCCATCATGGGC
AACTGCACCATCTCTTATTATAAAGACAGAGCCCTCGCTTCTGAGGCCATGTATTATT
CCTGCCATGTTGGCTGTCTGACATGGGCTGCTCTCCCTCCCTACCATGTTGA
GGGTCTCTGTCAATGCCATGGGATTTCACCTAATGCCCTGCTTGTCAAGAATTCTC
35 ATTCAATGGATTCACTGTCAATGGAATCCTCAGTACTTCTAATTATGTCTTGACCGCTTCT
TGCCATTCAACATCCCATAAGATAACAGTCTATCCTCACTAGCAACAGGGTGTAAAGATG
GGACTTATTAGCCATTAGGAGCATTCTCTAGTGATTCCATTCCCTCACCTTAAGGAG
ATTAAAATATTGTCAAAAGAATCTCTTCTCACTCATACTGTCTTCACTCAGGATACCATGA
AGCTGGACTTGGCACTGATTGTTGCTTATGTGCTGATCTGAAGACTATACTCAGCATT
40 ATGCTGGACTTGGCACTGATTGTTGCTTATGTGCTGATCTGAAGACTATACTCAGCATT
TGCACTTTGGCAGAGAGGCTTAAGGCCCTAAATACCTGTGCTCCCACATCTGTGCTGTG
CTCACCTTCTATGTGCCCATCATCACCCCTGGCTGCCATGCATCACTTGCCAAGCACAAA
GCCCTCTTGTGATCCTATTGCAAGATATGTTCTTGTGCGCCGCCCTATGAACCCC
ATTGTGACTGTGAAAGACTCGACAAATCTGGAGAAGATCTTGGGAAGTTGCTTAAT
45 GTATGTGGAGATAA (SEQ ID NO: 334)

AOLFR182 sequences:

50 MTLGSLGNSSSSVATFLSGIPGLERMHIWISIPLCFMYLVSIPGNCTILFIKTERSLHEPMYLFL
SMLALIDLGLSLCTLPTVLGIFWVGAREISHDACFAQLFFIHCFSFLESSVLLSMAFDRFVAICHP
LHYVSILTNTVIGRJGLVSLGRSVALIFPLPMLKRFPYCGSPVLSHSYCLHQEVMKLACADMK
ANSIYGMFVIVSTVGIDSLLILFSYALILRTVLSIASRAERFKALNTCVSHICAVLLFYTPMIGLSV
IHRFGKQAPHLVQVVMGMYLLFPPVMNPIVYSVTKQIRDRTVTHAFCY (SEQ ID NO: 335)

55 ATGACCCCTGGGATCCCTGGAAACAGCAGCAGCAGCAGCGTTCTGCTACCTTCTGCTGAGTG
GCATCCCTGGGCTGGAGCGCATGCACATCTGGATCTCCATCCCACTGTGCTTCACTGTATCT
GGTTCCATCCCGGGCAACTGCACAATTCTTTATCATTAAAACAGAGCGCTCACCTCAT

5 GAACCTATGTATCTCTCCTGTCCATGCTGGCTCTGATTGACCTGGGTCTCTCCCTTGACAC
 TCTCCCTACAGTCCTGGCATCTTTGGGTTGGAGCACGAGAAATTAGCCATGATGCCATGC
 TTTGCTCAGCTCTTTCATTCACTGCTTCTCCTCGAGTCCTCTGTGCTACTGTCTATG
 GCCTTGAACCGCTTGTGGCTATCTGCCACCCCTGCACTATGTTCCATTCTCACCAACAC
 10 AGTCATTGGCAGGATTGGCCTGGCTCTGGTGTAGTAGCAGTCATTTCATT
 CTTTTATGCTAAAGATTCCCTATTGGCTCCCCAGTCTCTCACATTCTTATTGTCT
 CCACCAAGAAGTGTGAAATTGGCCTGTGCCGACATGAAGGCCAACAGCATCACGGCAT
 GTTGTGATCGTCTACAGTGGGTATAGACTCACTGCTCATCCTCTTATGCTCTGA
 TCCTGCGCACCGTGTCCATGCCCTCAGGGCTGAGAGATTCAAGGCCCTAACACCTG
 TGTTCCCACATCTGCTGTGCTCTACACTCCATGATTGGCCTCTGTGATCC
 ATCGCTTGGAAAGCAGGCCACCCACCTGGTCCAGGTGGTATGGGTTTCATGTATCTCT
 CTTCTCCTGTGATGAATCCATTGTCTACAGTGTGAAGACCAACAGATCCGGGATCGA
 GTGACGCATGCCCTTGTACTAA (SEQ ID NO: 336)

15 **AOLFR183 sequences:**

MTNLNASQANHRNFILTGPCTPDKNWLAFLGFLYLTLLNGNTILAVIKVEPSLHEPTYYFL
 SILALTDVSLSMSTLPSMSIYWFNAPQIVFDACIMQMFFIHVGIVESGVLVSMAFDRFVAIRN
 PLHYVSILTHDVIRKTGIVSLTRAFCVVFVPLIKCLPFCHSNVLSHSYCLHQNMMLACASTR
 20 INSLYGLIVVIFTLGLDVLLTLLSYVLTALKTVLGVSRGERLKTLSTCLSHMSTVLLFYVPMGA
 ASMIHRFWEHLSVVHVMVADYLILLPPVLPNIVYSVTKQI (SEQ ID NO: 337)

25 ATGACGAACCTGAATGCATCACAGGCCAACACCAGTAACCTCATCTGACAGGTATCCAG
 GAACGCCAGACAAGAACCCATGGTGTGCCCTTCCCCTGGATTCTACACACTCACACT
 CCTGGAAATGGTACCATCCTAGCTGTATCAAGGTGGAGCCAAGTCTCCATGAGGCCACG
 TATTACTCCCTTCTATCTTGGCTCTCACTGACGTTAGTCTCTCCATGTCCACCTTGGCCTCC
 ATGCTCAGCATCTACTGGTTAATGCCCTCAGATTGTTTGTGATGCATGCATCATGCAGAT
 GTTCTTCATCCATGTATTGGAATAGTAGAATCAGGAGTCTAGTGTCCATGCCCTTGAC
 AGATTGTTGGCCATCCGAAACCCATTACACTATGTTCCATCCTCACTCACGATGTTATCG
 30 AAAGACTGGAATATCTGCTCTCACCGGAGCTGTTGTGGTATTCCCTGTGCCCTCCTT
 ATAAAGTGCCTACCCCTCTGCCATTCCAATGTCTGTCTCATTCACTGTCTCACCAAA
 CATGATGCCCTAGCTGTGCCAGCACCCGATCAACAGCCTCTACGGCCTCATGTCGTC
 ATCTTCACACTGGGCTCGATGTTCTCTCACTCTACTGTCTTATGTAACCTCACGACAGAC
 TGTCGCTGGCATTGTCTCCAGAGGTGAAAGGCTGAAACCCCTCAGCACATGCTCTCAC
 35 ATGTCTACCGTGCTCCTCTTATGTTCTTATGGGTGCTGCCCATGATACCTACTGCTCCG
 TTGGGAGCATTATCACCAAGTAGTGCACATGGTCACTGGTGTGATATACCTACTGCTCCG
 CCTGTGCTAAACCCATTGTCTACAGTGTGAAGACCAAGCAAAATTGA (SEQ ID NO: 338)

AOLFR184 sequences:

40 MSTLPTQIAPNSSTSMAPTFLLVGMPGLSGAPSWTLPLIAVYLLSALGNNTILWIIALQPALHR
 PMHFFFLFLSVDIGLVTALMPTLLGIALAGAHTVPAASACLLQMVFHVSVMESSVLLAMSID
 RALAICRPLHYPALLTNGVISKISLALISFRCLGLHLPLPFLAYMPYCLPQLVTHSYCLHPDVARL
 ACPEAWGAAYSLFVVLSAMGLDPLLIFFSYGLIKVLQGVESREDRWKAGQTCAHLSAVLLF
 YIPMILLALINHPELPIQHTHTLLSYVHFLLPPLINPILYSVKMKEIRKRILNRLQPRKVGGAQ
 (SEQ ID NO: 339)

45 ATGTCAACATTACCAACTCAGATAGCCCCAATAGCAGCACTCAATGGCCCCCACCTCT
 TGCTGGTGGCATGCCAGGCCTATCAGGTGCACCCCTCTGGTGGACATTGCCCTCATG
 TGTCTACCTCTCTGCACTGGAAATGGCACCACCTCTGGATATTGCCCTGCAGGCC
 GCCCTGCACCGCCAATGCACCTCTCCTCTTGTCTAGTGTGTCTGATATTGGATTGGT
 50 CACTGCCCTGATGCCACACTGCTGGCATGCCCTTGCTGGTGTCTCACACTGCCCTGCC
 TCAGCCTGCCTCTACAGATGGTTTATCCATGTCTTCTGTCTATGGAGTCCTCTGTCTT
 GCTGCCATGTCCATTGATCGGGCACTGGCATCTGCCGACCTCTCACTACCCAGCGCTC
 CTCACCAATGGTGTAAATTAGCAAATCAGCCTGGCATTCTTCTGATGCCCTGGGTCTCC
 ATCTGCCCTGCCATTCTGCTGGCTACATGCCCTACTGCTCCCACAGGTCTAACCCAT
 55 TCTTATTGCTTGATCCAGATGTGGCTCGTTGGCCTGCCAGAAGCTTGGGTGAGCCT
 ACAGCCTATTGTGGTCTTCAGCCATGGTTGGACCCCTGCTTATTCTCTCCTAT

5 GGCCTGATTGGCAAGGTGTTGCAAGGTGTTGAGTCCAGAGAGGATCGCTGGAAGGCTGGT
 CAAACCTGTGCTGCCCACCTCTGCAGTGCCTCTTCTATATCCCTATGATCCTCCTGGC
 ACTGATTAACCACATCTGAGCTGCCAATCACTCAGCATAACCATACTCTCTATCCTATGTCC
 ATTCCTCTCCTCATTGATAAAACCTATTCTCTATAGTGTCAAGATGAAGGAGATTAGA
 5 AAGAGAAACTCAACAGGTTGCAGCCCAGGAAGGTGGTGGTGCAGTGA (SEQ ID NO:
 340)

AOLFR185 sequences:

10 MFYPILNDISTKNNSNIMSCCNILFIKTVIEILVYNQTQSPWYPVPSKSLVYNNNTCFDCYHLQR
 VDCVPSRDHINQSMVLASGNSSHPVSFILLGIPGLESFQLWIAFPFCATYAVAVGNITLLHVR
 IDHTLHEPMYLFLAMLAITDVLVSSSTQPKMLAIFWFHAEIHQYHAACLIQVFFIHAFFSVEGVL
 MAMALDCYVATCFPLRHSSILTPSVVIKLTIVMLRGLLWVSPFCFMVSRMPFCQHQAIQSYC
 EHMAVLKLVCADTSISRGYGLFVAFSVAGFDMIVIGMSYVMILRAVLQLPSGEARLKAFSTRA
 SHICVILALYIPALFSFLTYRFGHDVPRVVHILFANLYLLIPPMILNPIYGVRTKQIGDRVIQGCCG
 15 NIP (SEQ ID NO: 341)

20 ATGTTCTACCCCATTGAAATGACATAAGTACGAAAAACAAACAGTAACATCATGTCATGTT
 GTAACATATTATTAAACAGTTGAAATTATTCTAGTTATAATCAAACCCAATCACC
 CTGGTATCCAATAGTCCCATCCAAAAGCCTTGTATATAATAAAACACTTGTGTTGATTGTT
 ATCATCTGCAGAGAGTAGATTGCGTCCCAGCAGAGACCATATAACCAGTCCATGGTGCT
 GGCTTCAGGGAACAGCTCTCTCATCCTGTGCTCTCATCCTGCTTGAATCCCAGGCCTG
 GAGAGTTCCAGTTGGAATTGCTTCTGCTGCTGCTGCCACGTATGCTGTGGCTGTTGTTGG
 AAATATCACTCTCTCCATGTAATCAGAATTGACACACCCCTGCATGAGCCCATGTAACCTC
 TTTCTGGCCATGCTGCCATCACTGACCTGGCTCTCCTCCTCCACTCAACCTAAGATGTT
 25 GCCATATTCTGGTTTCATGCTCATGAGATTGAGATTGAGATTGACCATGCCTGCCTCATCCAGGTGTTCT
 TCATCCATGCCCTTTCTCTGTGGAGTCGGGGTGCTCATGGCTATGCCCTGGACTGCTAC
 GTGGCTACCTGCTTCCCACCTCCGACACTCTAGCATCCTGACCCATCGGCTGTGATCAAAC
 TGGGGACCATCGTGTGCTGAGAGGGCTGCTGTGGGTGAGCCCTCTGCTCATGGTGTC
 30 TAGGATGCCCTCTGCCAACACCAAGCCATTCCCCAGTCATACTGTGAGCACATGGCTGTG
 CTGAAGTTGGTGTGCTGATACAAGCATAAGTCGTGGGTATGGGCTCTTGTGGCCTTCT
 CTGTTGGCTGGCTTGTGATATGATTGTCATTGGTATGTCATACGTGATGATTGAGAGCTGT
 GCTTCAGTTGCCCTCAGGTGAAGCCGCCCTCAAAGCTTTAGCACACGTGCCTCCCATATC
 TGTGTCATCTGGCTCTTATATCCCAGCCCTTTCTTCTCCTCACCTACCGCTTGGCCAT
 35 GATGTGCCCGAGTTGACACATCCTGTTGCTAATCTCTACTGATACCTCCATGCT
 CAACCCCATCATTTATGGAGTTAGAACCAAACAGATGGGACAGGGTTATCCAAGGATG
 TTGTGGAAACATCCCTGA (SEQ ID NO: 342)

AOLFR186 sequences:

40 MSNASLVTAFILTGLPHAPGLDALLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNLS
 FIDMWFSVTVPKMLMTLVSPSGRAISFHSCVAQLYFFHFLGSTEFLYTVMSYDRYLAISYPL
 RYTSMMMSGSRCALLATGTWLSGSLHSAVQTILTFLPYCGPNQIQHYFCDAPPILKACADTS
 NVMVIFVDIGIVASGCFVLIVLSYVSIVCSILRIRTSDDRRRAFQTCASHCIVLCFFVPCVVTYLR
 PGSMIDAMDGVVAIFYTVLTPLLNPVYTLRNKEVKKAVLRLDKVAHPQRK (SEQ ID NO:
 343)

45 ATGTCCAACGCCAGCCTCGTACAGCATTCTACCTCACAGGCCCTCCCCATGCCCAAGGGC
 TGGACGCCCTCCTCTTGGATCTCCTGGTTACGTGCTCACTGTGCTGGGGAAACCT
 CCTCATCCTGCTGGTGTACAGGGCTTACACAGTCACTGCTCACCCACACCCCATGTACTACTTCTCA
 CCAACCTGTCCTCATGACATGTGGTCTCCACTGTCACGGTGCCAAAATGCTGATGAC
 50 CTTGGTGTCCCCAAGCGGCAGGGCTATCTCCTCCACAGCTGCGTGGCTCAGCTCTATT
 TCCACTTCCCTGGGAGCACCAGTGTGTTCTCTACACAGTCATGTCCTATGATCGCTACTTG
 GCCATCAGTACCCGCTCAGGTACACCAAGCATGATGAGTGGGAGCAGGGTGTGCCCTCTGG
 CCACCGGCACCTGGCTCAGTGGCTCTGCACTGCTGTCCAGACCAATTGACTTTCCAT
 TTGCCCTACTGTGGACCCAACCAGATCCAGCACTACTTCTGTGACGCACCGCCCATCCTGA
 55 AACTGGCCTGTGCAGACACCTCAGCCAACGTGATGGTATCTTGTGGACATGGGATAGT
 GGCCCTCAGGCTGCTTGTCTGATAGTGTGCTCATGTGTCCATCGTCTGTTCCATCCTGC

5 GGATCCGCACCTCAGATGGGAGGCAGAGCCTTCAGACCTGTGCCCTCCACTGTATTGT
 GGTCTTGTCTTGTGTCATTATCTGAGGCCAGGCTCATGGATGCCA
 TGGATGGAGTTGTGCCATTCTACACTGTGCTGACGCCCTCTCAACCTGTGTAC
 ACCCTGAGAAACAAGGAGGTGAAGAAAGCTGTGAAACTTAGAGACAAAGTAGCACAT
 CCTCAGAGGAATAA (SEQ ID NO: 344)

AOLFR187 sequences:

10 MAQVRALHKIMALFSANSIGAMNNSDTRIAGCFLTGIPGLEQLHILSIPFCIMYIAALEGNIL
 CVILSQAILHEPMYIFLSMLASADVLLSTTMMKPALANLWLGYSHISFDGCLTQKFFIHLFIHSA
 VLLAMAFDRYVAICSPRLYVTILTSKVIGKIVTATLSRSFIIMFPSIFLLEHLHYCQINIIAHTFCEH
 MGIAHLSCSDISINVWYGLAAALLSTGLDMLITVSYIHLQAVFRLSQDARSKALSTCGSHICV
 ILLFYVPALFSVFAYRGGRSIPCYVHILLASLYVVIPPMNPVIYGVRTKPILEGAKQMFSNLAK
 GSK (SEQ ID NO: 345)

15 ATGGCACAGGTGAGGGCGCTGCATAAAATCATGGCCCTTTCTGCTAACAGCATAAGGTG
 CTATGAACAACTCTGACACTCGCATAGCAGGCTGCTTCCTCACTGGCATCCCTGGCTGGA
 GCAACTACATACTGGCTGTCCATCCCCITCTGCATCATGTACATCGCTGCCCTGGAAAGGC
 AATGGCATCTAATTGTGTCATCCTCTCCAGGAATCCTGCATGAGCCCATGTACATAT
 TCTTATCTATGCTGCCAGTGTGATGTCITGCTCTCTACACACCACATGCCCTAAGGCCCTG
 20 GCCAATTGTGGCTAGGTTAGCCACATTCTTGTATGGCTGCCTCACTAAAAGTTCTT
 CATTCACTTCCTCTCATTCACTCTGCTGCTGGCCATGGCTTGTGACCGCTATGTGG
 CCATCTGCTCCCCCTGCGATATGTCACAATCCTACAAGCAAGGTATTGGGAAGATCGT
 CACTGCCACCCTGAGCCGCAGCTTCATCATTATGTTCCATCCATCTTCCTGAGCACC
 TGCACATTGCCAGATCAACATCATTGCACACACATTGTGAGCACATGGCATTGCCCA
 25 TCTGTCCTGTTCTGATATCTCCATCAATGTCGGTATGGGTTGGCAGCTGCTCTCTCCA
 CAGGCCTGGACATCATGCTTATTACTGTTCTACATCCACATCCTCCAAGCAGTCITCCGC
 CTCCCTTCTCAAGATGCCGCTCCAAGGCCCTGAGTACCTGTGGATCCCATCTGTGTCAT
 CCTACTCTCTATGTCCTGCCATTCTCCTGGCCAGCCTCACGTTGTCATTCTCCTATGCTCAAT
 30 TCCCATGCTATGTCATATTCTCCTGGGACTAAGCCAATACTGGAAAGGGCTAACAGATGTTTCA
 CCCGTTATTATGGAGTGAGGACTAACAGCAACTGGAAAGGGCTAACAGATGTTTCA
 AATCTTGCCAAAGGATCTAAATAA (SEQ ID NO: 346)

AOLFR188 sequences:

35 MFPSLCPVCVLLVQLPLMNEQMCFVFCSDSLLRMMVSRFIHPFVKMKRIVGGYSKHFFSN
 ELLCVRPWSGKTWSIRHHFDMELLTNLKFIDPFCVRLRHLSPPTSEEHMKKNNNVTEFILL
 GLTNPEGQKVLFVTFLLIYMTIMGNLLIVTIMASQSLGSPMYFFLASFIDTVYSTAFAPK
 MIVDLLSEKKTISFQGCMQLFMDHLFAGAEVILLVVMAYDRYMAICKPLHELITMRRVCVL
 MLLAAWIGGFLHSLVQFLFIYQLPFCGPVIDNFLCDLYPLLKLAECTNTYVTGLSMIANGGAIC
 AVTFFTILLSYGVILHSLKTQSLEGKRKAFTCASHVTVVLFFVPCIFLYARPNSTFPIDKSMTV
 40 VLTFTPMLNPLIYTLKNAEMKSAMRKLWSKKVSLAGKWLHYS (SEQ ID NO: 347)

45 ATGTCCTCCCTGTGTCATGTGTCCTTGTCAACTCCACTTATGAAAGAGACAT
 GCAGTGTGTTTGTGTTCTGTTGTGATAGTTGCTGAGAATGATGGTTCCCGCTTCATCC
 ATGTCCCATTGAAAAATGAAAAGGATAATTGTGGGAGGATATTCTAAACACTTCTTTC
 TAATGAGCTGCTGTGAGGCCCTGGTCAGGGAAAACGTGGTCGATAAGGCATCACAT
 TTTGACATGGAGCTCTGACAAATACTCAAATTATCACTGACCCCTTTGTTGTAGGC
 TCCGACACCTGAGTCCAACACCTTCAGAAGAACACATGAAAAATAAGAACAAATGTGACTG
 AATTTCCTCTAGGGCTCACACAGAACCCCTGAGGGGCAAAAGGTTTATTGTCACATT
 CTTACTAATCTACATGGTGACGATAATGGCAACCTGTTATCATAGTGACCATCATGGCC
 50 AGCCAGTCCCTGGGTTCCCCATGACTTTCTGGCTTATCATTCATAGATAACCGT
 CTATTCTACTGCATTGCTCCAAAATGATTGTTGACTTGCTCTGAGAAAAAGACCATTT
 CCTTCAGGGITGTATGGCTCAACTTTATGGATCATTTATTGCTGGTGTGAAGTCATT
 CTTCTGGTGGTAATGCCATGATCGATACATGGCCATCTGTAAGCCTCTCATGAATTGA
 TCACCATGAATCGTCGAGTCTGTGTTCTATGCTGTTGGCGGCCTGGATTGGAGGGCTTCT
 55 TCACTCATTGGTTCAATTCTCTTATTATCAGCTCCCTCTGTGGACCCAATGTCATTG
 ACAACTCCTGTGTGATTGTATCCCTATTGAAACTTGCTGCACCAATACCTATGTCACT

GGGCTTCTATGATAGCTAATGGAGGAGCGATTGTGCTGTCACCTCTTCACTATCCTGC
 5 TTTCTATGGGGTCATATTACACTCTCTTAAGACTCAGAGTTGAAAGGGAAACGAAAAGC
 TTTCTACACCTGTGCATCCCACGTCACTGTGGTCATTITATTCTTGTCCCCTGTATCTTCT
 GTATGCAAGGCCAATTCTACTTTCCATTGATAAAATCCATGACTGTAGTCTAACTTTA
 TAACCTCCATGCTGAACCCACTAATCTATACCCCTGAAGAATGCAGAAATGAAAAGTGCCAT
 GAGGAAACTTGGAGTAAAAAGTAAGCTAGCTGGAAATGGCTGTATCACTCATGA
 (SEQ ID NO: 348)

AOLFR189 sequences:

10 MQQNNSVPFILLGLTQDPLRKIVFVFLIFYMGTVVGNMLIIVTIKSSRTLGSPMYFFLFYLSF
 ADSCFSTSTAPRLIVDALSEKKIITYNECMQTQVFAHLFLFGCMEIFVLILMAVDRYVAICKPLRYP
 TIMSQQVCILIVLAWIGSLIHSTAQIILALRLPFCGPYLIDHYCCDLQPLLKACMDTYMINLLL
 VSNSGAICSSSFMLIISYIVILHSLRNHSAGKKKALSACTSHITVILFFGPCIFIYTRPPTTFPM
 KMVAVFYTIGTPFLNPLIYTSEECRSEKCHEK (SEQ ID NO: 349)

15 ATGCAGCAAAATAACAGTGTGCCCTGAATTCTACTGTTAGGATTAACACAGGATCCCTGA
 GGCAGAAAATAGTGTGTAACTCTCTTAATTCTATATGGAACTGTGGTGGGAATAT
 GCTCATTATTGTGACCATCAAGTCCAGCCGGACACTAGGAAGCCCCATGTAATTCTTCTA
 TTTATTGTCCATTGCCAGATTCTGCTTCAACTTCCACAGCCCCATGATTAATTGTGGA
 20 TGCTCTCTGTGAAAAGAAAATTATAACCTACAATGAGTGCATGACACAAGTCTTGCAC
 CATTATTGGCTGCATGGAGATCTTGCTCTCATCTCATGGCTGTTGATCGCTATGTGGC
 CATCTGTAAGCCCTTGCCTTACCCAACCACATGAGCCAGCAGGTCTGCATCATCTGATT
 GTTCTTGCCTGGATAAGGGCTTAAATACACTACAGCTCAGATTATCTGGCTTAAGATT
 25 GCCTTCTGTGGACCCATTGTGATTGATCATTATTGCTGTGATTGCAAGCCCTTGTGAAC
 TTGCTGCATGGACACTTACATGATCAACCTGCTGTTGGTCTAACAGTGGGCAATTG
 CTCAGTAGTTCATGATTGTATAATTCTATATTGTCATCTGCATTCACTGAGAAACC
 ACAGTGCCAAAGGGAAAGAAAAGGCTCTCCGCTTGCACGTCTCACATAATTGTAGTCAT
 CTTATTCTTGGCCATGTATATTCTATACACGCCCCCGACCACCTTCCCCATGGACA
 30 AGATGGTGGCAGTATTATACTATTGAAACACCCATTCTCAATCCACTCATCACATCT
 GAGGAATGCAGAAGTGAAAATGCCATGAGAAAG (SEQ ID NO: 350)

AOLFR190 sequences:

35 MQRSNHTVTEFILLGFTTDPMQLGLFVFLGVYCLTVVGSSTLIVLICNDSRLHTPMYFIGN
 LSFLDLWYSSVHTPKILVTCISEDKSISFAGCLCQFFSARLAYSECYLLAAMA YDHYVAISKPLL
 YAQTMPRLCICLVLYSYTGGFVNAILTSNTFTLDFCGDNVIDDFFCDVPLVKLACSVRESYQ
 AVLHFLLASNVISPTVLILASYLSIITLRIHSTQGRIKVFSTCSSHLISVTLYGSILYNSRPSSS
 YSLKRDKMVSTFYTMLFPMLNPMIYSLRSKDMKDALKFFKSA (SEQ ID NO: 351)

40 ATGCAGAGGAGCAATCACACAGTACTGAGTTCATCCTGCTGGGCTTCACCACAGATCCAG
 GGATGCAACTGGGCCTCTTGTGGTGTCTGGGTGTACTGTCTGACTGTGGTAGGAAG
 TAGCACCTCATCGTGTGATCTGTAATGACTCCCCCTACACACACCCATGTATTGTCA
 TTGGAAATCTGTCAATTCTGGATCTGTGATTCTCTGTCCACACCCAAAGATCCTAGTG
 ACCTGCATCTGTGAAGACAAAAGCATCTCTTGTGGCTGCCTGTGTCAGTTCTCTG
 CAGGCTGGCTATAGTGAGTGCACCTACTGGCTGCCATGGCTTATGACCAACTACGTGGCC
 45 ATCTCCAAGCCCTGCTTATGCTCAGACCATGCCAAGGAGATTGTGCATCTGTTGGTTT
 ATATTCTATACTGGGGTTTGTCAATGCAATAATATTAAACAGCAACACATTACATTG
 GATTTTGTTGTGACAATGTCATTGATGACTTTCTGTGATGTTCCACCCCTGTGAAGCT
 GGCATGCGAGTGTGAGAGAGAGTACCAAGGCTGTGCTGCACCTCCTCTGGCCTCCAATGTC
 ATCTCCCTACTGTGCTCATCCTGCCTTACCTCTCCATCATCACCACCATCTGAGGAT
 50 CCACTCTACCCAGGGCCGATCAAAGTCTCTCCACATGCTCCTCCACCTGATCTCCGTTA
 CCTTATACTATGGCTCCATTCTACAACACTCCCGCCAAGTCCAGCTACTCCCTCAAG
 AGGGACAAAATGGTTCTACCTTATACTATGCTGTTCCCATGTTGAAATCCCATGATCTA
 CAGTCTGAGGAGTAAAGACATGAAAGACGCTCTGAAAAAATTCTCAAGTCAGCATAA
 (SEQ ID NO: 352)

55

AOLFR191 sequences:

5 MTGGGNITEITYFILLGFSDFPRIKVLFTIFLVYITSLAWNLSLIVLIRMDSHLHTPMYFFLSNLS
 FIDVCYISSTVPKMLSNLQQEQQTITFVGCIQYFIFSTMGLSESCLMTAMAYDRYAAICNPLLYS
 SIMSPTLCVWMVLGAYMTGLTASLFQIGALLQLHFCGSNVRHFFCDMPQLLILSCTDTFFVQV
 5 MTAILTMFFGIASALVIMISYGYIGISIMKITSAKGSPKAFNTCASHLTAVSLFYSGIFVYLRSSS
 GGSSSFDRFASVFYTVVIPMLNPLIYSLRNKEIKDALKRLQKRKCC (SEQ ID NO: 353)

10 ATGACTGGGGGAGGAAATTACAGAAATCACCTATTCTACATCCTGCTGGGATTCTCAGATT
 TTCCCAGGATCATAAAAGTGCCTTCACTATATTCTGGTGTACATTACATCTCTGCC
 15 TGGAACCTCTCCCTCATGTTTAATAAGGATGGATTCCACCTCCATACACCCATGTATT
 CTTCTCAGTAACCTGCCTCATAGATGTCTGCTATATCAGCTCCACAGTCCCCAAGATGC
 TCTCCAACCTCTACAGGAACAGCAAACATCACCTTGTGTTGTATTATTCACTGACTTT
 ATCTTTCAACGATGGGACTGAGTGAGTCTGTCTCATGACAGCCATGGCTATGATCGTT
 ATGCTGCCATTGTAACCCCTGCTCTATTCACTCCATCATGTCACCCACCCCTGTGTTGG
 20 ATGGTACTGGGAGGCTACATGACTGGCCTCACTGCTCTTATTCAAATTGGTGTGTTGCT
 TCAACTCCACTCTGTGGGCTAATGTCATCAGACATTCTCTGTGACATGCCCAACTGT
 TAATCTTGTCCCTGTACTGACACTTCTTGTACAGGTATGACTGCTATATTAAACCATGTT
 TTTGGGATAGCAAGTGCCTAGTTATCATGATATCCTATGGCTATATTGGCATCTCCATCA
 TGAAGATCACTCAGCTAAAGGCAGTCCAAAGGCATTCAACACACTGTGCTCTCATCTAAC
 25 AGCTGTTCCCTCTTCTATACATCAGGAATTGGTCTATTGAGGTCCAGCTCTGGAGGTT
 CTTCAAGCTTGCATCTGTTCTACACTGTGGTCATCCATGTTAAAGAGGTTGCAAAGAGA
 TTGATTACAGTTGAGGAACAAAGAAATTAAAGATGCCTAAAGAGGTTGCAAAGAGA
 AAGTGCTGCTGA (SEQ ID NO: 354)

AOLFR192 sequences:

25 MENNTEVTEFILVGLTDDPELQIPLFIVFLFIYLITLVGNLGMIELILLDSCLHTPMYFFLSNLSLV
 DFGYSSAVTPKVMVGFLTGDKFILYNACATQFFFFVAFITAESFLASMAYDRYAAALCKPLHY
 TITMTTNVCACLAIGSYICGFLNASIHTGNTFRLSFRSNVVEHFFCDAPPLTLSCSDNYISEM
 30 VIFFVVGNDLFSILVILISYLFIFITIMKMRSPERQKAFTCASHLTAVSIFYGTGMYLRPNS
 HFMGTDKMASVFYAIVIPMLNPLVYSLRNKEVSAFKKTVGKAKASIGFIF (SEQ ID NO: 355)

35 ATGGAGAACACACAGAGGTGACTGAATTCATCCTTGTGGGTTAAGTGTGACCCAGAA
 CTGCAGATCCCACCTTCATAGTCTTCTTCACTCACCTCATCTGGTTGGGAAACCT
 GGGGATGATTGAATTGATTCTACTGGACTCCTGTCCACACCCCATGTACTCTTCTCA
 GTAACCTCTCCCTGGTGGACTTGGTATTCTCAGCTGTCACTCCCAAGGTGATGGTGG
 GTTCTCACAGGAGACAATTCAATTATAATGCTTGTGCCACACAATTCTTCTTCTTG
 TAGCCTTATCACTGCAGAAAGTTCTCTGGCATCAATGGCTATGACCGCTATGCAGC
 ATTGTGAAACCCCTGCAATTACACCAACCATGACAACAAATGTATGTGCTTGCCTGGCC
 ATAGGCTCCTACATCTGTGGTTCTGAATGCATCCATTCAACTGGAAACACTTCAAGGC
 40 TCTCCTCTGTAGATCCAATGTTGAGATGCTCTCTGAGATGGTATTGGTGGGATTCAATG
 CTCTCATGTTGAGACAACACTACATCAGTGAGATGGTATTGGTGGGATTCAATG
 ACCTCTTCTATCCTGGTAATCTGATCTCTACTTATTTATTTATCACCACATGAAG
 ATGCGCTCACCTGAAGGACGCCAGAAGGCCCTTCTACTTGTGCTTCCCACCTACTGCAG
 45 TTTCCATCTTATGGGACAGGAATCTTATGTACTTACGACCTAACCTCAGCCATTCAATG
 GGCACAGACAAATGGCATCTGTGTTCTATGCCATAGTCATTCCATGTTGAATCCACTGG
 TCTACAGCCTGAGGAACAAAGAGGTTAAGAGTGCCTTAAAAGACTGTAGGGAAGGCAA
 AGGCCTCTATAGGATTCAATTAA (SEQ ID NO: 356)

AOLFR193 sequences:

50 MENKTEVTQFILLGLTNDSLQVPLFITFPFIYIITLVGNLGIIVLIFWDSCLHNPMYFFLSNLSLV
 DFCYSSAVTPIVMAGFLIEDKVISYNACAAQMYIFVAFATVENYLASMAYDRYAAVCKPLHY
 TITMTTVCARLAIGSYLCGFLNASIHTGDTFSLSFCKSNEVHFFCDIPAVMVLSCSDRHISEL
 VLIYVVSFNIFIAALLVILISYTFIFITILKMHSAVYQKPLSTCASHFIAVGIFYGTIIFMYLQPSSSH
 SMDTDKMAPVFYTMVIPMLNPLVYSLRNKEVSAFKKVEKAKLSVGWSV (SEQ ID NO:
 55 357)

ATGGAAAATAAGACAGAAGTAACACAATTCAITCTCTAGGACTAACCAATGACTCAGAA
 CTGCAGGGTCCCTCTTATAACGTTCCCTCATCTATATTACTACTCTGGTGGAAACCT
 GGGAAATTATTGTATTGATATTCTGGGATTCCTGTCTCCACAATCCCATGTAACCTTTCTCA
 5 GTAACTTGTCTCTAGGGACTTTGCTACTCTCAGCTGCACTCCCATCGTCATGGCTGGA
 TTCCCTATAGAAGACAAAGGTCACTCTTACAATGCATGTGCTGCTCAAATGTATATCTTGT
 AGCTTTGCCACTGTGGAAAATTACCTCTGGCCTCAATGCCATGACCGCTATGCAGCA
 GTGTGCAAACCCCTACATTACACCACAACCATGACAACAACTGTGTGCTCGTCTGGCCA
 TAGGCTCCTACCTCTGTGGTTCTGAATGCCTCCACACTGGGGACACATTTAGTCTC
 10 TCTTCTGTAAAGTCCAATGAAGTCCATCACTTTCTGTGATATTCCAGCAGTCATGGTCT
 CTCTGCTCTGATAGACATATTAGCGAGCTTGTCTATTATGTTGAGCTTCATATCT
 TTATAGCTCCTGGTTATCTGATATCCTACACATTACATTTATCACCACCTAAAGATG
 CACTCAGCTTCAGTATACCAAGAAGCCTTGTCCACCTGTGCTCTCATTTCATTCAGTCGG
 CATCTCTATGGGACTATTATCTCATGTACTTACAACCCAGCTCCAGTCACTCCATGGACA
 15 CAGACAAAATGGCACCTGTGTTCTATACAATGGCATCCCCATGCTGAACCCCTCTGGCTA
 TAGTCTGAGGAACAAAGAAGTGAAGAGTCATTCAAGAAAGTTGTTGAGAAGGAAAATT
 GTCTGTAGGATGGTCAGTTAA (SEQ ID NO: 358)

AOLFR194 sequences:

MERQNQSCVVEFILLGFSNYPELQGQLFVAFLVIYLVTLIGNAIIIVSLDQSLHVPMYLFLLNL
 20 SVVDSLFSAVIMPEMLVVLSTEKTTISFGGCFAQMYFILLFGGAECFLLGAMAYDRFAAICHPL
 NYQMIMNKGVFMKLIIFSWALGFMGTQTSWVSSFPFCGLNEINHISCTPAVLELACADTFL
 FEIYAFGTFLIIIVPFLILLSYIRVLFAILKMPSTTGRQKAFSTCAAHLSVTLFYGTASMTYLQ
 PKSGYSPETKKVMSLSYSLLTPLNNLLIYSLRNSEMKRALMKLWRRRVVLHTI (SEQ ID NO:
 359)

25 ATGGAAAGACAAAATCAAAGCTGTGGTTGAATTCATCCTCTGGGCTTTCTAACTATC
 CTGAGCTCCAGGGCAGCTTGTGGCTTCTGGTAAATTATCTGGTGACCCCTGATAGG
 AAATGCCATTATTATAGTCATCGTCTCCCTAGACCAGAGCCTCCACGTTCCATGTACCTGT
 TTCTCCTGAACCTATCTGTGGTGGACCTGAGTTCACTGCAGTTATTATGCCTGAAATGCT
 30 GGTGGCTCTCTACTGAAAAAAACTACAATTCTTGGGGCTGTTGACAGATGTAT
 TTCACTCTCTTTGGTGGGGCTGAATGTTCTCTGGAGCAATGGCTATGACCGATT
 TGCTGCAATTGCCCCTCTCAACTACCAAAATGATTATGAATAAAAGAGTTTATGAAA
 TTAATTATATTTCATGGGCCTTAGGTTATGTTAGGTACTGTTCAAACATCATGGGTATC
 TAGTTTCCCTTTGTGGCCTTAATGAAATTAAACCATATATCTGTGAAACCCAGCAGTGT
 35 TAGAACTTGCATGTGCAGACACGTTTGTGAAATCTATGCATTACAGGCACCTTTG
 ATTATTGGTCCCTTCTGTGATACTCTGTCTTACATTGAGTTCTGTTGCCATCTG
 AAGATGCCATCAACCACTGGGAGACAAAGGCCTTCCACCTGTGCCGCTCACCTCACAT
 CTGTGACCCATTCTATGGCACAGCCAGTATGACTTATTACAACCCAAATCTGGCTACTC
 ACCGGAAACCAAGAAAGTGTGATGTCATTGCTTACTCACTCTGACACCACTGCTGAATCTG
 40 CTTATCTACAGTTGCAGAAATAGTGAGATGAAGAGGGTTGATGAAATTATGGCGAAGG
 CGAGTGGTTTACACACAACTGTA (SEQ ID NO: 360)

AOLFR195 sequences:

MIVQLICTVCLAVNTFVRSSFDLKADDMGEINQLVSEFLLGLSGYPKIEIVYFALILVMY
 45 LVILIGNGVLIASIFDSHFHTPMYFFLGNLSFLDICYTSVPLSTVSLISKRNISFSGCAVQMFF
 GFAMGSTECLLGMMMAFDRYVAICNPLRYPILSKVAYVLMASVWSLGGINSAVQTLLAMRL
 PFCGNNIINHFACEILAVKLACADISLNIIITMVISNMAFLVPLMVIFFSYMFILYTIQMNSATG
 RRKAFSTCSAHLTVVIFYTIFFMYAKPKSQDLIGEEKLQALDKLISLFYGVVTPMLNPILYSLR
 NKDVKAALKYLLNKKPIH (SEQ ID NO: 361)

50 ATGATTGTTCAGTTAATTGTACTGTTCTGGCAGTAAATACATTTCATGTTAGATC
 TTCTTGTATTCTGAAAGCAGATGACATGGGTGAGATTAACCAAGACACTTGTGTCAGAA
 TTTCTCTCTGGGTCTTCTGGATACCCAAAGATTGAGATTGTTACTTGTCTCATTCT
 AGTATGTACCTAGTGAATTCTAATTGGCAATGGTGTCTAATCATAGCCAGCATCTTGATT
 55 CTCATTTCACACACCAATGTACTCTCTGGCAACCTCTTCTGGATATCTGCTAT
 ACATCCTCTGTTCCCTCAACATTGGTGAGCTTAATCTCAAAGAAAACATTTCCCT

5 TCTCTGGATGTGCAGTGCAGATGTTCTTGGGTTGCAATGGGTCACAGAACATGTCTGCT
 TCTGGCATGATGGCATTGATCGTTATGTGGCCATCTGCAACCCACTGAGATACCCCATC
 ATCCTGAGCAAGGTGGCGTATGTATTGATGGCTCTGTGTCCCTGGCTGTCCGGTGGAAATAA
 ATTCACTGTGCAAACATTACTGCCATGAGACTGCCCTCTGTGGGAATAATATTATCAA
 10 5 TCATTCGCATGTGAAATATTAGCTGTCTCAAGCTGGCTGTGCTGATATATCCCTCAATA
 TTATCACCATGGTGATATCAAATATGGCCTCCTGGTTCTCCACTGATGGTCATTTTTC
 TCCTATATGTTCATCCTACACCATCTGCAAATGAATTAGCCACAGGAAGACGCAAGG
 CATTTCACGTGCTCACCTGACTGTGGTGATCATATTACGGTACCATCTTCTT
 ATGTATGCGAAACCGAAGTCTCAAGACCTGATTGGGAAGAAAAATTGCAAGCATTAGAC
 15 10 AAGCTCATTCTCTGTTTATGGGTAGTACACCCATGCTGAATCTATACTCTATAGCTT
 GAGAAATAAGGATGTAAAAGCTGCTGAAAATATTGCTGAACAAAAAACCAATTCACTA
 A (SEQ ID NO: 362)

20 **AOLFR196 sequences:**
 15 MLESNYTMPTEFLFVGFTDYLPLRVTLFLVFLVYTLTMVGNILLIILVNINSSLQIPMYYFLSNL
 SFLDISCSTAIPKMLANFLASRKSIISPYGCALQMFFFASFADAECILAAAMA YDRYAAICNPLL
 YTTLMSRRVCVCFIVAYFSGSTTSVLHVCLTFRLSFCGSNIVNHFCDIPPLLALSCDTDQINQL
 LLFALCSFIQTSTFVVFISYFCILITVLSIKSSGRSKTFSTCASHLIAVTLFYGALLFMYLQPTTS
 YSLDTDVKVAVFYTUVFPMFNPIYSFRNKDVKNAKKLERIGYSNEWYLNRLRIVNI (SEQ
 ID NO: 363)

25 ATGTTGGAGAGTAATTACACCATGCCAAGTGGCTTCTATTGTTGGATTACAGATTATC
 TACCTCTCAGACTCACACTGTCTGGTATTCTCTGGTATATACTAACATTAACATGGTCGGA
 AATAACTCTTAATAATTCTAGTTAATTTAATTCAAGCCTCAAATCCCATGTTATTATT
 TCTTAGCAACTTATCTTCTTAGACATCAGCTGTCTACAGCAATCACTCCTAAATGCTGG
 30 25 CAAACTCTGGCATCCAGAAAAGCATCTCTCCCTATGGGTGTGCACTACAAATGTTTT
 CTTCGCTTCTTGCTGATGCTGAGTGCCTATCTGGCAGCAATGGCTATGACCGCTATG
 CAGCCATCTGCAACCCACTGCTCTACTACACTGATGTCTAGGAGAGTCTGTCTGCTT
 CATTGTGTGGCATATTTCAGTGGAAAGTACAACATCACTGGTCCATGTGTGCCTCACATT
 35 30 AGGCTGTCACTTGTGGCTCCAATATCGTCAATCATTCTGTGATATCCCACCTCT
 GGCTTATCATGTACAGACACTCAGATCAACCAGCTCTGCTTTGCTTGAGCTTCA
 TCCAGACCAGCACTTGTGGTAATATTCTTACTCTGCATCCTCATACTGTGTTG
 AGCATCAAGTCCTCAGGTGGCAGAAGCAAAACATTCTCCACTTGTGCTTCCACCTCATAG
 CAGTCACCTTATTCTATGGAGCGCTCTGTTATGTTACAGCCCACCACTAGCTATTCC
 40 35 CTAGACACTGATAAGGTGGTGGCAGTGTATTTACTGTTGATTTCCATGTTAATCCAA
 TAATTATAGTTAGAAACAAGGATGTGAAAATGCTCTAAAAGCTATTAGAAAGAA
 TTGGATATTCAAATGAATGGTATTAAATGTTAAGAATAGTCAATATCTAA (SEQ ID NO:
 364)

45 **AOLFR197 sequences:**
 40 MCYLSQLCLSLGEHTLHMGMRHTNESNLAGFILLGFSDYPQLQKVLFVLILLYLLTILGNTTI
 ILVSRLEPKLHMPMYFFLSHLSFLYRCFTSSVIPQLLVLNWEPMKTIAYGGCLVHLYNSHALGS
 TECVLLALMSCDRYVAVCRPLHYTVLMHIHLCMALASMAWLSGIATTLVQSTLTLQPFCHH
 RQVDHFICEVPVLIKLACVGTTFNEAELFVASILFLIVPVSFILVSSGYIAAVLRIKSATRRQKAF
 GTCFSHLTVVTIFYGTIIFMYLQPAKSRSRDQGKFVSLFYTVVTRMLNPLIYTLRIKEVKGALKK
 VLAKALGVNIL (SEQ ID NO: 365)

50 ATGTGTTATCTTCTCAGCTATGCCCTAGCCTGGGAACACACACTTACATATGGGATGG
 TGAGACATACCAATGAGAGCAACCTAGCAGGTTCTACCTTTAGGGTTCTGATTATCC
 TCAGTTACAGAAAGGTCTATTGTGCTCATATTGATTCTGTATTACTAACATTTGGGA
 ATACCACCATCATTCTGGTTCTCGTCTGGAACCCAGCTTCATATGCCATGTATTCTC
 CTTCTCATCTCCTCCTGTACCGCTGCTCACAGCAGTGTATTCCCCAGCTCTGGT
 55 50 AAAACCTGTGGGAACCCATGAAAACATCGCCTATGGTGGCTGTTGGTTCACTTACAAC
 TCCCATGCCCTGGGATCCACTGAGTGCCTCTGGCTGATGTCTGTGACCGCTATGT
 GGCTGTCTGCCGTCTCCATTACACTGTCTTAATGCAATCCATCTGCATGCCCTGG
 CATCTATGGCATGGCTCAGTGGAAATAGCCACCAACCTGGTACAGTCCACCCCTCACCTGCA

5 GCTGCCCTCTGTGGCATGCCAAGTGGATCA TTTCATCTGGAGGGTCCCTGTGCTCATC
 AAGCTGGCTTGTGGCACCACTTAAAGGAGCTGAGCTTTGTGGCTAGTATCCTT
 TCCTTATAGTGCCTGCTCATTCATCCTGGCTCCTGGTACATTGCCACGCAGTGTG
 AGGATTAAGTCAGTACCAAGGAGACAGAAAGCATTGGGACCTGCTCTCCCACCTGACA
 10 GTGGTCACCATCTTATGGAACCATCATCTCATGTATCTGCAGCCAGCCAAGAGTAGAT
 CCAGGGACCAAGGGCAAGTTGTTCTCTTCTACACTGTGGTAACCCGCATGCTTAACCC
 TCTTATTTATACCTTGAGGATCAAGGAGGTGAAAGGGCATTAAAGAAAGTTCTAGCAA
 GGCTCTGGGAGTAAATATTATGA (SEQ ID NO: 366)

10 AOLFR198 sequences:

15 MENCTEVTKFILLGLTSVPELQIPLFILFTIYLLTLCGNLGMMLLIMDSDLHTPMYFFLSNLSL
 VDFGYSSAVTPKVMAGFLRGDKVISYNACAVQMFPFVALATVENYLLASMAYDRYAAVCKP
 LHYTTTMTASVGACLAALGSYVCGLNASFHIGGIFSLSFCKSNLVHHFFCDVPAVMALSCSDKH
 TSEVILVFMSFNIFVFLLVIFISYLFIFITILKMHSAKGHQKALSTCASHFTA VSVFYGTIVIYLQ
 PSSSHSMDTDKMASVFYAMIIPMLNPPVYSLRNREVQNAFKVLRQQFL (SEQ ID NO: 367)

20 ATGGAGAATTGTACGGAAGTGACAAAGTTCATTCTTAGGACTAACCAAGTGTCCCAGAAC
 TACAGATCCCCCTCTTATCTTGTACCTCATCACCTCCTCACTCTGTGTGGAACCTG
 GGGATGATGTTGCTGATCCTGATGGACTCTGTCTCCACACCCCATGTACTTTTCTCAG
 TAACCTGTCTCTGGTGGACTTGGATACTCCTCAGCTGTCACTCCAAAGGTATGGCTGGG
 TTCCCTAGAGGAGACAAGGTATCTCCTACAATGCATGTGTTGAGATGTTCTTGT
 AGCCTTGGCCACGGTGGAAAATTACTTGTGGCTCAATGCCATGACCGCTATGCAGCA
 GTGTGCAAACCCCTACACTACACCAACCCATGACGGCCAGTGTAGGGTGCCTGTGGCC
 TAGGCTCATATGTCGGCTTAAATGCCTCATTCCACATTGGGCAATTGGGGCATATTCA
 25 TCTTCTGTAAATCCAATCTGGTACATCACTTTCTGTGATGTTCCAGTCAGTCT
 GTCTGCTCTGATAAACACACTAGTGAGGTGATTCTGGTTTATGTCAGCAGTCAAGCT
 TTTTGTCTCTAGTTATCTTATCTCCTACTTGTGATATTCACTACCACTCTGAAGATGC
 ATTCACTAAGGGACACCAAAAGCATGTCCACCTGTGCTCTCACCTCACTGCAGTCTC
 CGTCTCTATGGGACAGTAATTCATCTACTTGAGCCAGCTCCAGCCACTCCATGGAC
 30 ACAGACAAAATGGCATCTGTGTTCTATGCTATGATCATCCCCATGCTGAACCCGTGGTCT
 ACAGCCTGAGGAACAGAGAAGTCCAGAATGCATTCAAGAAAGTGTGAGAAGGCAAAAT
 TTCTATAA (SEQ ID NO: 368)

AOLFR199 sequences:

35 MDTGNKTLQPQDFLLGFPGSQLQLSLFMLFLVMYILTVSGNVAILMLVSTSHQLHTPMYFFLS
 NLSFLEIWYTTAAVPKALAILGRSQTISFTSCLLQMYFVSLGCTEYFLAAMAYDRCLAICYP
 LHYGAIMSSLSAQLALGSWVCGFVAIAVPTALISGLSFCGPRAINHFFCDIAPWIALACTNTQA
 VELVAFVIAVVVILSSCLITFVSYVYIISTILRIPSASGRSKAFSTCSSHLTVVLIWYGSTVFLHVR
 TSIKDALDLIKA VHVLNTVVTVPVLNPFIYTLRNKEVRETLKKWKKGK (SEQ ID NO: 369)

40 ATGGACACAGGCAACAAACTCTGCCCAAGGACTTTCTCTTACTGGGCTTCTGGTCTC
 AAACTCTCAGCTCTCTCTTATGCTTTCTGGTGTACATCCTCACAGTTAGTGGT
 AATGTGGCTATCTGATGTTGGTGAGCACCTCCATCAGTTGCATACACCCATGTACTTCT
 TCTGAGCAACCTCTCTCTGGAGATTGGTATACCACAGCAGCAGTGCCTAACAGCACTG
 45 GCCATCCTACTGGGAGAAGTCAGACCATATCATTTACAAGCTGTCTTGTGAGATGTACT
 TTGTTTCTCATTAGGCTGCACAGAGTACTCCTCTGGCAGCCATGGCTTATGACCGCTGT
 CTTGCCATCTGCTATCCTTACACTACGGAGCCATCATGAGTAGCCTGCTCTCAGCGCAGC
 TGGCCCTGGGCTCTGGGTGTGGTTCTGTCGGCATTGAGTGCCTAACAGCCTCATCAG
 TGGCCTGTCCTCTGTGGCCCCCGTGCACATCAACCACTTCTGTGACATTGCACCCCTGGA
 50 TTGCCCTGGGCTGCACCAACACACAGGCAGTAGAGCTGTGGCTTGTGATTGCTGTTGT
 GGTTATCCTGAGTTCATGCCTCATCACCTTGTCTCTATGTGTACATCATCAGCACCAC
 TCAGGATCCCTCTGCCAGTGGCCGGAGCAAAGCCTCTCCACGTGCTCTCGCATCTCAC
 CGTGGTGCTCATTTGGTATGGGTCCACAGTTCTTACGTGCCACCTCTATCAAAGAT
 GCCTTGGATCTGATCAAAGCTGCCACGTCCATGAAACACTGTGGTGA CTCAGTTAAACC
 55 CCTTCATCTATACGCTCGTAATAAGGAAGTAAGAGAGACTCTGCTGAAGAAATGGAAGG
 GAAAATAA (SEQ ID NO: 370)

AOLFR200 sequences:

5 MTRKNYTSLEFVLLGLADTLELQIILFLFLVIYTLTVLGNLGMILLIRIDSQQLHTPMYFFLANL
 SFVDVCNSTTIPKMLADLLSEKKTISAGCFLQMYFFISLATTECILFGLMAYDRYAAICRPLL
 10 YSLIMSRTVYLKMAAGAFAAGLLNFMVNTSHVSSLSFCDSNVIHFFCDSPPLFKLSCSDTILKE
 SIISILAGVNIVGTLVLILSSYSYVLFISIFSMHSGEGRHRAFSTCASHLTAIIFLYATCIYTYLRPSS
 15 SYSLNQDKVASVFYTVVPIPMLNPLIYSLRSKEVKKALANVISRKRTSSFL (SEQ ID NO: 371)

10 ATGACCAGAAAAAAATTATACCTCACTGACTGAGTCGTCTATTGGGATTAGCAGACACGC
 TGGAGCTACAGATTATCCTCTTTGTGTTTCTGTGATTATACACTACAGTACTGGGA
 AATCTCGGGATGATCCTCTTAATCAGGATCGATTCCAGCTTCACACACCCATGTATTCTT
 CCTGGCTAACCTGTCCTTGACGTTGTAACCACTACCATCACCCAAAGATGCTG
 GCAGATTATTATCAGAGAAGAAAACCACATCTCTTGCTGGCTGCTCCTACAGATGTACT
 15 TCTTATCTCCCTGGCACAACCGAATGCATCCTCTTGCTGGGTTAATGGCCTATGACAGGTA
 TGCAGGCCATATGTCGCCCGCTGCTTACTCCTGATCATGTCAGGACCGTCTACCTAAAA
 ATGGCAGCCGGGCTTGCTGCAGGGTGCTGAACCTCATGGTCAACACAAGCCATGTCA
 GCAGCTTGTCAATTCTGTGACTCCAATGTCATCCATCACTCTCTGTGACAGTCCCCACCT
 TTCAAGCTCTCTGTTCTGACACAATCCTGAAAGAAAGCATAAGTCTATTTGGCTGGTG
 20 TGAATATTGTGGGGACTCTGCTTGTGATCCTCTCCTACTCCTACGTTCTCTCCATT
 TTTCTATGCATTGGGGAGGGGAGGCACAGAGCTTCTCCACGTGTGCCTCTCACCTGA
 CAGCCATAATTCTGTCTATGCCACCTGCATCTATACCTACCTGAGACCTAGTCCAGCTAC
 TCCCTGAATCAGGACAAAGTGGCTCTGTGTTACACAGTGGTGATTCCATGTTGAATC
 CTCTGATCTACAGCCTCAGGAGTAAGGAAGTAAAGAAGGCTTAGCGAATGTAATTAGCA
 25 GGAAAAGGACCTCTCCATTCTGTGA (SEQ ID NO: 372)

AOLFR201 sequences:

30 MEWENHTILVEFFLKGSLGHPRLELLFFVLIFIMYVILLGNGLLISILDPHLHTPMYFFLGNL
 SFLDICYYTSIPSTLVSLSERKTSLSGCAVQMFLGLAMGTTECVLLGMMAFDRYVAICNPLR
 YPIIMSKDAYVPMAAGSWIIGAVNSAVQSVFVQLPFCRNNIINHFTCEILAVMKLACADISDN
 EFIMLVATTLFILTPLLIIVSYTLLIISFKISSSEGRSKASSTCSAHLTVVIIYGTILFMYMKPKS
 KETLNSDDLDATDKIISMFYGVMPMMNPLIYSLRNKDVKAEVKHLLNRRFFSK (SEQ ID NO: 373)

35 ATGGAATGGGAAAACCACACCAATTCTGGTGAATTCTGAAGGGACTTCTGGTCACC
 CAAGACTTGAGTTACTCTTTGTGCTCATCTTCATAATGTATGTGGTCATCCTCTGGGG
 AATGGTACTCTCATTAAATCAGCATCTGGACCTCACCCTCACACCCCTATGTACTCTT
 TCTGGGAAACCTCTCCTCTGGACATCTGCTACACCACCCACTCTATTCCCTCACGCTAG
 TGAGCTTCTTCAGAAAGAACGACATTCCCTTCTGGCTGTGCAGTGCAGATGTTCT
 40 CGGCTTGGCCATGGGGACAAACAGAGTGTGCTCTGGCATGATGGCCTTGACCGCTAT
 GTGGCTATCTGCAACCTCTGAGATATCCATCATGAGTAAGGATGCCTATGTACCCA
 TGGCAGCTGGCTCTGGATCATAGGAGCTGTCAATTCTGCAGTACAATCAGTGTGTTGTT
 ACAATTGCTTCTGCAGGAATAACATCATCAATCATITCACCTGTGAAATTCTGGCTGTC
 ATGAAACTGGCCTGTGCTGACATCTCAGACAATGAGTTCATCATGCTTGTGCCCCACACAT
 45 TGTTCATATTGACACCTTGTATTAAATCATGTCTCTTACACGTTAATCATTGTGAGCATC
 TTCAAAATTAGCTCTCGAGGGAGAAGCAAAGCTTCTTACCTGTTCACTGCTTGTGACAT
 CTGTGGTCATAATTCTATGGGACCATCCTCTTACATGTACATGAAGCCCAAGTCTAAAGA
 GACACTTAATTGGATGACTGGATGCTACCGACAAAATTATATCCATGTTCTATGGGTG
 ATGACTCCCATGATGAATCCTTAATCTACAGTCTAGAAACAAGGATGTGAAAGAGGCA
 50 GTAAAACACCTACTGAACAGAAGGTTCTTAGCAAGTGA (SEQ ID NO: 374)

55 MEWENHTILVEFFLKGSLGHPRLELLFFVLIFIMYVILLGNGLLISILDPHLHTPMYFFLGNL
 SFLDICYYTSIPSTLVSLSERKTSLSGCAVQMFLSLAMGTTECVLLGVMAFDRYVAICNPLR
 YPIIMSKDAYVPMAAGSWIIGAVNSAVQTVFVQLPFCRNNIINHFTCEILAVMKLACADISGN
 EFILLVTTLFLLTPLLIIVSYTLLIISFKISSSEGRSKPSSTCSARLTVVITFCGTIFLMYMKPKSQ

ETLNSDDLDATDKLIFIFYRVMTPMMNPLIYSLRNKDVKEAVKHLRRKRNFK (SEQ ID NO: 375)

5 ATGGAATGGGAAAACCACACCATTCTGGTGGAACTTCTGAAGGGACTTCTGGTCACC
 CAAGACTTGAGTTACTCTTTGTGCTCATCTTCATAATGTATGTGGTCATCCCTCTGGGG
 AATGGTACTCTCATTTAATCAGCATCTGGACCCCTCACCTCACACCCCTATGTACTTCTT
 TCTGGGGAACCTCTCCTCTGGACATCTGCTACACCACCCACCTCTATTCCCTCACGCTAG
 TGAGCTTCCCTTCAGAAAGAACGACATTCCCTTCTGGCTGTGCAAGTCAGATGTTCTT
 CAGCTTGGCCATGGGACAACAGAGTGTGCTCTGGCGTGATGGCCTTGACCGCTAT
 10 GTGGCTATCTGCAACCTCTGAGATATCCCACATCATGAGTAAGGATGCCTATGTACCCA
 TGGCAGCTGGGTCTGGATCATAGGAGCTGTCAATTCTGCAGTACAAACAGTGTGTTGTGGT
 ACAATTGCCCTTCTGCAGGAATAACATCATCAATCATTCACCTGTGAAATTCTAGCTGTC
 ATGAAAATGGCCTGTGCTGACATCTCAGGCAATGAGTTCATCTGCTGTGACCAACAT
 15 TGTTCCTATTGACACCTTGTATTAAATTATTGTCTTACACGTTAATCATTTGAGCATT
 TTCAAAATTAGCTCTCGGAGGGAGAAGCAACACCTCCTACCTGCTCAGCTCGTCTGA
 CTGTGGTATAACATTCTGTGGGACCATCTTCATGTACATGAAGCCCAAGTCTCAAGA
 GACACTTAATTCAGATGACTTGGATGCCACTGACAAAACATTATTCATATTCTACAGGGTG
 ATGACTCCCAGTGAATCCTTAAATCTACAGTCTAGAAACAAAGGATGTGAAGGAGGCA
 20 GTAAAACACCTACTGAGAAGAAAAATTAAACAAGTAA (SEQ ID NO: 376)

AOLFR203 sequences:

25 MKRQNQSCVVEFILLGFSNFPQVQLFGVFLVYVVTLMGNAITVIISLNQSLHVPMLFLLN
 LSVVEVSFSAVTPLEMVVLSTEKTMSFVGCFQMYFILLFGTECFLLGAMA YDRFAAICHPL
 NYPVIMNRGVMKLVIFSWISGIMVATVQTTWVFSFPFCGPNEINHLFCETPPVLELVCADTF
 EIYAFGTILIVMVPFLILLSYIRVLFAILKMPSTTGRQKAFSTCASHLTSVLFYGTANMTYLQ
 PKSGYSPETKKLISLAYLLTPLLNPLIYSLRNSEMKRTLKLWRRKVILHTF (SEQ ID NO: 377)

30 ATGAAAAGACAAAATCAAAGCTGTGTTGAATTCATCCTCCTGGGCTTTCTAACCTTC
 CTGAGCTCCAGGTGCAGCTCTGGGTTTCCTAGTTATTATGTGGTGACCCCTGATGGG
 AAATGCCATCATTACAGTCATCATCTCCTAAACCAAGAGCCTCCACGTTCCATGTACCTGT
 TCCTCCTGAACCTATCTGTGGTGGAGGTGAGTTCACTGCAGTCATTACGCTGAAATGCT
 GGTGGTGCCTCTACTGAGAAAACATATGATTCTTGTGGCTGTTGCACAGATGTAT
 TTCATCCTCTTTGGTGGGACTGAATGTTCTCCTGGGAGCGATGGCTATGACCGATT
 TGCTGCAATTGCCATCCTCTGAACACTACCCAGTGAATTATGAACAGAGGGTTTATGAAA
 35 TTAGTAATATTCTCATGGATCTCAGGGATCATGGTGGCTACTGTGCAGACCACTGGGTAT
 TTAGTTTCCATTGTGGCCCCAATGAAATTAAATCATCTCTGTGAGACTCCCCGGTA
 CTAGAGCTGTGTGCGAGACACCTCTATTGAAATCTATGCCTCACAGGCACCATTT
 GATTGTTATGGTTCCTTCTTGTGATCCTCTGTCTACATTCGAGTTCTGTTGCCATCCT
 40 GAAGATGCCATCAACTACTGGGAGACAAAAGCCTTCCACCTGTGCTCTCACCTCACA
 TCTGTGACCCCTGTCTATGGCACAGCCAATATGACTTATTACAACCCAAATCTGGCTACTC
 ACCCGAAACCAAGAAACTGATCTCATTGGCTTACACGTTGCTTACCCCTGCTCAATCCG
 CTCATCTATAGCTTACGAAACAGTGAAGATGAAGAGGACTTGTATAAAACTATGGCGAAGA
 AAAGTGATTTCACACACATTCTGA (SEQ ID NO: 378)

AOLFR204 sequences:

45 MEKKNVTEFILIGLTQNPIKEVTFVVFLVLYMITLSGNLLIVVTITTSQALSSPMYFFLTHSL
 IDTVYSSSSAPKLVDSFQEKIISNGCMAQAYAEHIFGATEIILLTVMACDCYVAICKPLNYTT
 50 IMSHSLCILLVAVAIVVGGFLHATIQILFTVWLPFCGPNVIGHFMCDLYPLLKLVCIDHTLGLFV
 AVNSGFICLLNFLILVVSYVIILRSKNNNSLEGRCALKSTCISHTVVVLFFVPCIFVYLSVTTLPI
 DKAVALVFYTMVVPMLNPVYTLRNAEVKSAIRKLWRRKVTSDND (SEQ ID NO: 379)

55 ATGGAGAAGAAAAAGAATGTGACTGAATTCAATTAAATAGGTCTTACACAGAACCCATA
 ATGGAGAAGTCACGTTGTAGTATTGGTTCTTACATGATAACACTTCAGGCAACC
 TGCTCATTGTGGTTACCAATTACCAACCAAGCCAGGCTCTGAGCTCCCCATGACTTCTCCTG
 ACCCACCTTCTTGATAGACACAGTTATTCTCTTCACTGCTCTAACGTTGATTGTGGA
 TTCCCTTCAAGAGAAGAAAATCATCTCCTTAATGGGTGATGGCTCAAGCCTATGCAGAA

5 CACATTTGGTGCTACTGAGATCATCCTGCTGACAGTGATGGCTGTGACTGCTATGTGG
 CCATCTGCAAACCTCTGAACACTACACAACCATTATGAGCCACAGCCTGTGCATTCTCTGGT
 GGCAGTGGCTGGTGGGAGGATTCTCATGCAACTATTCAAGATTCTCTTACAGTATGG
 CTGCCCTCTGTGGCCCCAATGTCATAGGCCACTTCATGTGACTTGTACCCATTGTTAAA
 10 ACTTGTCTGCATAGACACTCATACCCCTGGCTCTTGTGCTGTGAAACAGTGGGTTATCT
 GCTTATTAAACTCCCTATCTTGGTGGTATCCTATGTGATCATCTTGAGATCTTAAAGAAC
 AATAGCTTGGAGGGAGGTGAAAGCCCTCTCCACCTGTATTCTCACATCATAGTAGTTG
 TCTTATTCTTGTGCCCTGTATATTGTGATCTGCGCTCAGTGACCACTCTGCCATTGAT
 AAAGCTGTGCTGTATTATACTATGGTGGCCAATGTTAAATCCGTGGTCTACACAC
 15 TCAGAAATGCTGAGGTAAGTGCAATAAGGAAGCTTGGAGAAAAAAAGTGACTTCAG
 ATAATGATTAA (SEQ ID NO: 380)

AOLFR205 sequences:

15 MESENRTVIREFILLGLTQSQDIQLLVFVLVLIFYFIIILPGNLIIFTIKSDPGLTAPLYFFLGNL AFL
 DASYSFTVAPRMLVDFLSAKKIISYRCITQLFFLHFLLGGGEGLLLVMAFDRYIAICRPLHYPT
 VMNPRTCYAMMLALWLGGFVHSIIQVVLRLPFCGPQLDNFFCDVPQVIKLA CDTFVVEL
 LMVFNSGLMTLLCFLGLLASYAVILCIRGSSEAKNKAMSTCITHIVIFFMFGPGIYTRPFRA
 FPADKVVSFLHTVIFPPLLNPVIYTLRNQEVKASMKVFNKHIA (SEQ ID NO: 381)

20 ATGGAAAGCGAGAACAGAACAGTGATAAGAGAACATTATCCTCCTGGTCTGACCCAGTCT
 CAAGATATTCAAGCTCCTGGTCTTGTGCTAGTTTAATATTCACTTCATCATCCTCCCTGG
 AAATTCTCATTATTTCACCATAAAGTCAGACCCCTGGTCTCACAGCCCCCTCTATTCT
 TTCTGGCAACTTGGCCTCCTGGATGCATCCTACTCCTCACTGTGGCTCCCCGGATGTG
 25 GTGGACTTCCTCTGCAGAAGAGATAATCTCCTACAGAGGCTGCATCACTCAGCTCTTT
 TCTGCACCTCCTTGAGGAGGGAGGGATTACTCCTGTGATGGCCTTGACCGCTA
 CATCGCCATCTGCCGCCCTGCACTATCCTACTGTCA TGAAACCTAGAACCTGCTATGCA
 ATGATGTTGGCTCTGGCTGGCTGGGGTTTGTCCACTCCATTATCCAGGTGGCTCATCCT
 CCGCTTGCCCTTTGTGGCCAAACAGCTGGACAACTCTCTGTGATGGCTCTCAACAGTGGCC
 30 ATCAAGCTGGCCTGCACCGACACATTGTGGTGGAGCTCTGTGATGGCTCTCAACAGTGGCC
 TGATGACACTCCTGTCTTCTGGGCTCTGGCCTCTGGCCTCATGCACTTCTGTGCGATA
 CGAGGGTCTCTCTGAGGCAAAAACAGGCCATGTCCACGTGCATCACCCATATCATTG
 TTATATTCTCATGTTGGACCTGGCATCTCATCACCGGCCCTTCAGGGCTTCCCA
 GCTGACAAGGTGGTTCTCTTCCACACAGTGATTTCTGTGAATCCTGTCAATT
 35 TACCCCTCGCAACCAGGAAGTGAAAGCTCCATGAAAAAGGTGTTAATAAGCACATAGC
 CTGA (SEQ ID NO: 382)

AOLFR206 sequences:

40 MANRNNVTEFILLGLTENPKMQKIIFFVFSVYINAMIGNVLIVVTTASPSLRSRSPMYFFFLAYLSFI
 DACYSSVNTPKLITDSLYENKTILFNGCMTQVFGEHFFRGVEVILLTVMA YDHYVAICKPLHYT
 TIMKQHVCSSLVGVSWVGGFLHATIQILFICQLPFCGPVIDHFMCDLYTLINLACTNTHTLGLF
 IAANSGFICLLNCLLLVLSCVVLILYSLKTHSLEARHEALSTCVSHITVVLISFIPCIFVYMRPPATL
 PIDKAVAVFTYTMITSMLNPLIYTLRNAQMKNAIRKLCRKAISSVK (SEQ ID NO: 383)

45 ATGGCGAATAGAAACAATGTGACAGAGTTATTCTATTGGGCTTACAGAGAACCTAAAA
 ATGCAGAAAATCATATTGTGTTCTGTCACTACATCAACGCCATGATAGGAAATG
 TGCTCATTGGTCACCACACTGCCAGCCATCACTGAGATCCCCATGTACTTTCTG
 GCCTATCTCTCCTTATTGATGCCGTCTTCACTACCCCTAACGCTGATCACAGA
 TTCACTCTATGAAAACAAGACTATCTTATTCAATGGATGTATGACTCAAGTCTTGGAGAA
 CATTTCAGAGGTGGTGGAGGTCTACCTACTGTAATGGCTATGACCACTATGTGG
 50 CCATCTGCAAGCCCTGCACATACCAACATCATGAAGCAGCATGTTGTAGCCTGCTAGT
 GGGAGTGTCTGGTAGGAGGCTTCTCATGCAACCCATACAGATCCTCTCATCTGTCAA
 TTACCTTCTGTGGTCTTAATGTCATAGATCACTTATGTGATCTCTACACTTGATCAA
 TCTTGCTGCACAAACCCACACTCTAGGACTCTCATGCTGCCAACAGTGGGTCATAT
 GCCTGTTAAACTGTCTTGTCTGGTCTCCTGCGTGGTCATACTGTACTCCTTAAAGACC
 55 CACAGCTTAGAGGCAAGGCATGAAGCCCTCTCACCTGTGCTCCACATCACAGTTGTCA
 TCTTATCCTTATACCCCTGCATATTGTGATCATGAGACCTCCAGCTACTTACCCATTGAT

AAAGCAGTTGCTTATTCTACACTATGATAACTTCTATGTTAAACCCCTTAATCTACACCTT
GAGGAATGCTCAAATGAAAATGCCATTAGGAAATTGTGTAGTAGGAAAGCTATTCAG
TGTCAAATAA (SEQ ID NO: 384)

5 **AOLFR207 sequences:**

MERTNDSTSTEFFLVGLSAHPKLQTVFFVLILWMLYMLLNGNGVLISVIIFDSHLHTPMYFFLCN
LSFLDV CYTSSSVPLILASFLAVKKKVSFGCMVQMFISFAMGATECMILGTMALDRYVAICYP
LRYPVIMSKGAYVAMAAGSWVTGLVDSVVQTAFA MQLPFCANNVIKFVCEILAILKLACADI
10 SINVISMTGSNLIVLVIPLLVISISYIFIVATILRIPSTEKGHKAFSTCSAHLTVVIFYGTIFFMYAKP
ESKASVDSGNEDIIAEALISLFYGVMTPLNPLIYSLRNKDVKAAVKNILCRKNFSDGK (SEQ ID
NO: 385)

15 ATGGAAAGGACCAACGATTCCACGTCGACAGAATTCTCTGGTAGGGCTTCTGCCACC
CAAAGCTCCAGACAGTTTCTCGTCTAATTCTGTGGATGTACCTGATGATCCTGCTTGG
AATGGAGTCCTTATCTCAGTTATCATCTTGATTCTCACCTGACACCCCCATGTATTCTT
CCTCTGTAATCTTCCTCCTCGACGTTGCTACACAAGTTCTCTGTCCCCTAATTCTT
20 CCAGCTTCTGGCAGTAAAGAAAAAGGTTCTCTGGGTGTATGGTCAAATGTATT
TTCTTTGCATGGGGCCACGGAGTGCATGATCTAGGCACGATGGCACTGGACCGCTAT
GTGGCCATCTGCTACCCACTGAGATACCCGTATCATGAGCAAGGGTGCCTATGTGGCA
TGGCAGCTGGGTCTGGTCACTGGGCTTGTGGACTCAGTAGTGCAGACAGCTTGCAT
GCAGTTACCAATTCTGTGCTAATAATGTCATTAACATTTGTCTGTGAAATTCTGGCTATCT
TGAAACTGGCCTGTGCTGATATTCAATCAATGTGATTAGTATGACAGGGTCGAATCTGAT
25 TGTTCTGGTTATTCCATTGTTAGTAATTCCATCTCTTACATATTATTGTGCACTATTCT
GAGGATTCTCCACTGAAGGAAAACATAAGGCCCTCTCACCTGCTCAGCCCACCTGACA
GTGGTATTATATTCTATGGAACCCTCTCTCATGTACGCAAAGCCTGAGTCTAAAGCCT
CTGTTGATTCAAGTAATGAAGACATCATTGAGGCCCTCATCTCCCTTTCTATGGAGTGAT
GACTCCCCTGCTTAATCCTCTCATCTATAGTCTGCGAAACAAGGATGTAAGGCTGCTGTC
30 AAAAACATACTGTGTAGGAAAAACTTCTGATGGAAAATGA (SEQ ID NO: 386)

30 **AOLFR208 sequences:**

MFPANWTSVKVFFFLGFFHYPKVQVIIFAVCLLMLYLITLLGNIFLISITLDSHLHTPMYLFLSNL
SFLDIWYSSSALSPMLANFVSGRNTISFSGCATQMYLISLAMGSTEVCVLLPMMAYDRYVAICNP
LRYPVIMNRRTCVQIAAGSWMTGCLTAMVEMMSVPLSLCGNSIINHFTCEILAILKLVCVDT
35 LVQLIMLVISVLLPMPMLLICISYAFILASLRISSVEGRSKAFSTCTAHLMVVVLFYGTALSMH
LKPSAVDSQEIDKFMALVYAGQTPMLNPIYSLRNKEVKVALKKLIRNHFNTAFISILK (SEQ
ID NO: 387)

40 ATGTTCCCGCAAATTGGACATCTGAAAAGTATTCTCTGGATTTCTCACTACCC
CAAAGTTAGGTATCATATTGCGGTGCTGCTGATGTACCTGATCACCTGCTGGG
AACATTCTGATCTCCATCACCATTCTAGATTCCCACCTGCACACCCCTATGTACCTCTT
CCTCAGCAATCTCTCCCTCTGGACATCTGGTACTCTCTCTCTGCCCTCTCTCCAATGCTGG
CAAACTTGTTAGGGAGAAACACTATTCAATTCTCAGGGTGCGCCACTCAGATGTACCT
45 CTCCCTGCCATGGGCTCACTGAGTGTGTGCTCTGCCATGATGGCATATGACCGGTAT
GTGGCCATCTGCAACCCCTGAGGATACCCGTATCATGAATAGGAGAACCTGTCAGA
TTGCAGCTGGCTCTGGATGACAGGCTGTCCTGCCATGGAAATGATGTCTGTGCT
GCCACTGTCCTCTGGTAATAGCATCATCAATCATTTCACTGTGAAATTCTGGCCATCT
TGAAAATTGGTTGTGGACACCTCCCTGGTCAGTTAATCATGCTGGTGTACAGTGTACT
TCTTCTCCCCATGCCAATGCTACTCATTTGATCTCTTATGCATTATCCTGCCAGTATCC
50 TGAGAATCAGCTCAGTGGAAAGGTCGAAGTAAAGCCTTTCAACGTGCACAGCCCACCTGA
TGGGGTAGTTTGTCTATGGGACGGCTCTCCATGCACCTGAAGGCCCTCCGCTGAGA
TTCACAGGAAATAGACAAATTATGGCTTGGTGTATGCCGGACAAACCCCCATGTTGAAT
CCTATCATCTATAGTCTACGGAACAAAGAGGTGAAAGTGGCCTGAAAAAAATTGCTGATTA
GAAATCATTTAATACTGCCITCATTTCCATCCTCAAATAA (SEQ ID NO: 388)

AOLFR209 sequences:

MDKINQTFVREFILLGLSGYPKLEIIFALILVMYVVLIGNGVLIASIIDSRLHMPMYFFLGMLS
 5 FLDICYTTSSIPSTLVSLSIKKRNISFSGCAVQMFFGFMAGSTECFLGMMAFDRYVAICNPLRY
 PIIMNKVVYVLLTSVLSGGINSTVQTSLAMRWPFCGNNINHFLCEILAVLKLACSDISVNIV
 TLAVSNIAFLVLPPLLIVFFSYMFLYTILRTNSATGRHKAFSTCSAHLTVVIFYGTIFFMYAKPKS
 QDLLGKDNLQATEGLVSMFYGVVTPMLNPITYSLRNKDVKAAIKYLLSRKAINQ (SEQ ID NO:
 389)

10 ATGGACAAGATAAACAGACATTGTGAGAGAATTCAATTCTCTGGACTCTCTGGTACCC
 CCAAACATTGAGATCATTCTTGCTCTGATTCTAGTACGTAGTGTGATTCTAATTGGC
 AATGGTGTCTGATCATAGCAAGCATCTGGATTCTCGTCTCACATGCCATGTACTCTT
 CCTGGCAACCTCTTCTGGATATCTGCTATACAACCTCCATTCCCTAACACTGG
 TGAGCTTAATCTCAAAGAAAAGAACATTCTCTGGATGTGCAGTGCAGATGTTCT
 15 TGGGTTGCAATGGGGTCAACAGAATGTTCTCTGGCATGATGGCATTTGATCGTTAT
 GTGCCATCTGTAACCCCTCTGAGATACCCATCATCATGAACAAGGTGGTATGTACTGC
 TGACTTCTGTATCATGGCTTCTGGTGAATCAATTCAACTGTGCAAACATCACTGCCAT
 GCGATGCCCTTCTGTGGAAACAATTATTAAATCATTCTTATGCGAGATCTAGCTGTCC
 TAAAATTAGCTTGTGATATACTGCAATTGTTACCTAGCAGTGTCAAATATTGCT
 20 TTCCTAGTTCTCCTCTGCTCGTATTCTCTATATGTCATCCTACACCATCTG
 CGAACGAACTCGGCCACAGGAAGACACAAGGCATTCTACATGCTCAGCTCACCTGACTG
 TGGTGTATCATATTATGGTACCATCTCTTATGTCATGCAAACACCTAAGTCCCAGGACCT
 CTTGGAAAGACAACCTGCAAGCTACAGAGGGCTTGTCCATGTTTATGGGGTGTGA
 25 CCCCATGTTAAACCCCATAATCTATAGCTTGTGAGAAATAAGATGTAAGCTGCTATAAA
 ATATTGCTGAGCAGGAAAGCTATTACCAGTAA (SEQ ID NO: 390)

AOLFR210 sequences:

MMGRRNDTNVADFLTGLSDSEEVQMALFMLFLLYLITMLGNVGMLIIRLDLQLHTPMYFFL
 30 THLSFIDLSYSTVVTPKTLANLLTSNYISFTGCFQMFCFVFLGTAECYLLSSMAYDRYAAICSP
 LHYTVIMPKRLCLALITGPYVIGFMDSFVNVSMSRLHFCDSNIIHHFFCDTSPILALSCTDTDN
 TEMLIFIAGSTLMVSЛИTISASYVSILSTILKINSTSGKQAFSTCVSHLLGVTIFYGTMIFTYLKP
 RKSYSLGRDQVAPVFYTIVIPMLNPLIYSLRNREVKNALIRVMQRQDSR (SEQ ID NO: 391)

ATGATGGGTAGAAGGAATGACACAAATGTGGCTGACTTCATCCTACGGGACTGTCAGAC
 35 TCTGAAGAGGTCCAGATGGCTCTGTTATGCTATTCTCCTCATATACTAACCTAATTACTATGCT
 GGGGAATGTGGGATGCTATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTAT
 TTTTCTTACTCACCTGTCTTATTGACCTCAGTTACTCAACTGTGTCACACCTAAAC
 CTAGCGAACTTACTGACTTCAACTATATTCCCTCACGGCTGCTTGCCTACAGATGTTCT
 GTTTGTCTCTGGTACTGCTGAATGTTATCTCTCTCTCAATGCCCTATGATGCTAT
 40 GCAGCGACTGCACTGCAGTCCTCTACACTACACAGTTATTATGCCAAAGGCTCTGCCTCGCTC
 TCATCACTGGCCTTATGTGATTGGCTTATGGACTCCTTGTCAATGTGGTTCCATGAGC
 AGATTGCAATTCTGTGACTCAAACATAATTCACTTTCTGTGACACTCCCCAATT
 AGCTCTGCTCTGCAGACACAGACAACACTGAAATGCTGATATTCAATTATGCTGGTCC
 45 ACCCTGATGGTGTCCCTATCACAATATCTGCATCTATGTGCTTCTCATTAGCTCTCACCACCT
 GAAAATTAAATTCCACTTCAGGAAAGCAGAAAGCTTCTCTACTTGCGTCTCTCATCTCTG
 GGAGTCACCATCTCTATGGAACATGATTTTACTTAAAGCCAAGAAAGTCTTATT
 CCTTGGGAAGAGATCAAGTGGCTCTGTGTTTATACTATTGTGATTCCATGCTGAATCC
 ACTCATTATAGTCTTAGAAACAGAGAAGTAAAAATGCTCTCATTAGAGTCATGCAGAG
 AAGACAGGACTCCAGGTAG (SEQ ID NO: 392)

50

AOLFR211 sequences:

MMGRRNNNTNVADFLMGLTLSEEIQMALFMLFLLYLITMLGNVGMLIIRLDLQLHTPMYFFL
 THLSFIDLSYSTVVTPKTLANLLTSNYISFTGCFQMFFAFLGTAECYLLSSMAYDRYAAICSP
 LHYTVIMSKRLCLALITGPYVIGFIDSFVNVSMSRLHFYDSNVIHHFFCDTSPILALSCTDTYNT
 55 EILIFIIVGSTMVSLFTISASYVFLFTILKINSTSGKQAFSTCVSHLLGVTIFYSTLIFTYLKPRK
 SYSLGRDQVASFYTIIVPVLNPLIYSLRNKEVNAIRVMQRQDSR (SEQ ID NO: 393)

ATGATGGGTAGAAGGAATAACACAAATGTGGCTGACTTCATCCTTATGGGACTGACACTT
 CTGAAGAGATCCAGATGGCTCTGTTATGCTATTCTCCTGATATACTAATTACTATGCTG
 GGGATGTGGGGATGATATTGATAATCCGCCTGGACCTCCAGCTCACACTCCATGTATT
 5 TTTCCCTACTCACCTGTCATTATTGACCTCAGTTACTCAACTGTGTCACACCTAAAACC
 TTAGCGAACCTACTGACTTCAACTATATTCCCTTACGGGCTGCTTGCCTCAGATGTTCTT
 TTTGCCTCTGGGACTGCTGAATGTTACCTCTCCTCAATGGCCCATGATCGCTATG
 CAGCGATCTGCAGTCCCTACACTACACAGTTATTATGTCAAAAGGCTCTGCCTCGCTCT
 10 CATCACTGGGCCTATGTGATTGGTTATAGACTCCTTGTCAACGTGGTTCCATGAGCA
 GATTGCATTCTACGACTCAAACGTAATTCACTCACTTTCTGTGACAGTCCCCAATTAA
 GCTCTGTCTGCAGTACATACAAACACCGAAATCCTGATATTCAATTGTGGTCCAC
 CCTGATGGTGTCCCTTTCACAATATCTGCATCCTATGTGTTCTTACCATCCTGA
 15 AAATTAACTTCAACTCAGGAAAGCAGAAAGCTTCTACTTGCCTCTCATCTCTGGG
 AGTCACCATCTTATAGCACTCTGATTTTACTTATTAAACCAAGAAAGTCTTATTCCCT
 TGGGAAGAGATCAAGTGGCTCTGTTTTACTTATTGTGATTCCCGTCTGAATCCACT
 CATTATAGTCTAGAAACAAAGAGGTGAAAATGCTGTCAAGAGTCATGCAGAGAAAG
 ACAGGACTCCAGGTAA (SEQ ID NO: 394)

AOLFR212 sequences:

20 MAGNNFTEVTVFILSGFANHPELQVSLFLMFLFIYLTFLGNLGLITLIRMDSQLHTPMYFFLSN
 LAFIDIFYSSVTVPKALVNQSNRRSISFVGCFVQMYFFVGLVCECFLLGSMAYNRYIAICNPL
 LYSVVMQSQVSNWLGVMPYVIGFTSSLISVWVISSLAFCDSSINHFFCDTTALLALSCVDTFGT
 EMVSFVLAGFTLSSLLIITVTYIIISAILRIQSAAGRQKAFSTCASHLMAVTIFYGSLIFTYLQPD
 NTSSLTQAQVASVFTIVIPMLNPLIYSLRNKDVKNALLRVIHRKLFP (SEQ ID NO: 395)

25 ATGGCTGGCAACAATTCACTGAGGTTACCGTCTTCATCCTCTGGATTGCAAATCACC
 CTGAATTACAAGTCAGTCTTCTGATGTTCTCTCATTATCTATTCACTGTTGGGA
 AACCTGGGACTGATCACGTTAACAGAATGGATTCTCAGCTCACACCCCTATGACTTT
 30 TCCTGAGCAATTAGCATTTATTGACATATTACTCCTACTGTAACACCTAAGGCATG
 GTGAATTCCAATCCAATCGGAGATCCATCCTCTGGCTGTTGTTCAAATGTACTT
 TTTGTTGGATTGGTGTGAGTGTGTTCTGGATCAATGGCTACAATCGCTACA
 TAGCAATCTGCAATCCTTACTGTATTCACTGAGTGTCCAAAAAGTGTCCAACGGCT
 GGGAGTAATGCCATATGTGATAGGCTCACAAGCTCGTGTATCTGCTGGGTGATAAGC
 AGTTTGGCGTTCTGTGATTCCAGCATCAATCATTGTTGTGACACCACAGCTCTTACG
 35 ACTCTCCTGTGAGATACATTGGCACAGAAATGGTAGCTTGTCTAGCTGGATTCACT
 CTTCTAGCTCTCCTTATCATCACAGTCACTTATCATCATCTCAGCCATCCTGAG
 GATCCAGTCAGCAGCAGGCAGGAGAAGGCCTCTCCACCTCGCATCCCACCTCATGGCT
 GTAACATCTTTATGGGTCTCTGATTTCACCTATTGCAACCTGATAACACATCATCGCT
 40 GACCCAGGCGCAGGTGGCATCTGTATTCTATACGATTGCACTTCCATGCTGAATCCACTC
 ATCTACAGTCTGAGGAACAAAGATGTGAAAATGCTCTGAGAGTCATACATAGAAAA
 CTTTTCCATGA (SEQ ID NO: 396)

AOLFR213 sequences:

45 MNSLGKLVSMILSAHVFCYSKFNCFGTHSIPALGADPPGMGLGNESSLMDFILLGFSDHPR
 EAFLVFVLFYLLTLVGNFTIIISYLDPPHTPMYFFLSNLSLLDICFTSLAPQTLVNLQRPKK
 TITYGGCVAQLYISLALGSTECLLADMALDRYIAVCKPLHYVVIMNPRLCQQLASISWLSGLA
 SSLIHATFTLQLPLCGNHRLDHFICEVPALLKACVDTTVNELVLFVVSVLFVIPPALISISYGFI
 TQAVLRIKSVEARHKAFSTCSSHLTVVIIYGTIIYVYLQPSDSYAQDQGKFISLFYTMVPTLNP
 IIYTLRNKDMKEALRKLLSGKL (SEQ ID NO: 397)

50 ATGAATAGTTGGGAAAGTGGCTCCATGATCCTCTCAGCTCATGTGTTCTGTTATTCTAA
 ATTTAATTGTTGGATGTACCCATTCCATTCCCTGCCTTAGGTGCGGATCCCCCTGGAGGG
 ATGGGATTGGCAATGAGAGTCCCTAATGGATTCTCATCCTCTAGGCTCTCAGACACC
 CTCGTCTGGAGGCTGTTCTCTTGTATTGTCCTTCTACCTCCTGACCCCTGTGGGA
 55 AACCTCACCATAATCATCATCTCATATCTGGATCCCCCTCTCATAACCCCAATGTACTTTT
 TCTCAGCAACCTCTTTACTGGACATCTGCTTCACTACTAGCCTGCTCTCAGACCTTAG

TTAACTTGCCTAAAGACCAAAGAACGATCACTTACGGTGGTGTGGCGCAACTCTATAT
 TTCTCTGGCACTGGGCTCCACTGAATGTATCCTCTGGCTGACATGCCCTGGATCGGTAC
 ATTGCTGTCTGCAAACCCCTCCACTATGTAGTCATCATGAACCCACGGCTTGCCAACAGC
 TGGCATCTATCTCCTGGCTCAGTGGTTGGCTAGTCCCTAATCCATGCAACTTTACCTG
 5 CAATTGCCCTCTGTGGCAACCATAGGCTGGACCATTATTTGCGAAGTACCAAGCTCTTCT
 CAAGTGGCTTGTGGACACCACGTCAATGAATTGGTCTTTTGTGTTAGTGTCTGT
 TTGTTGTCATTCCACCGACTCATCTCCATCTCTATGGCTTCATAACTCAAGCTGTGCTG
 AGGATCAAATCAGTAGAGGCAAGGCATAAGGCCCTCAGCACCTGCTCCCTCCACCTACAG
 TGGTGTGATTATATTCTATGGCACCATAACTACGTGTACCTGCAACCTAGTGACAGCTATGC
 10 CCAGGACCAAGGGAAGTTATCTCCCTCTACACCATGGTGAACCCCCACTTAAATCCT
 ATCATCTATACCTTAAGGAACAAGGATATGAAAGAGGCTCTGAGGAAACTTCTCTCGGGA
 AAATTGTGA (SEQ ID NO: 398)

AOLFR214 sequences:

15 MDKSNSVVSEFVLLGLCSSQKLQLFYFCFFSVLYTVIVLGNLLIILTVTSDSLHSPMYFLLGN
 LSFVDICQASFATPKMIAFLSAHETISFSGCIAQIFFIHLFTGEMVLLVSMAYDRYVAICKPLY
 YVVIMSRRTCTVLVMSIWAVSLVHTLSQLSFTVNLPFCGPNVVDSFFCDLPRVTKLACLDSYII
 ILIVVNSGILSLSTFSLLVSSYIILVTWLKSSAAMAKFSTLASHIAVVILFFGPCIYVWPFTIS
 PLDKFLAIFYTVFTPVLNPITYTLRNRMKAARVKAIVNHYLRPRRISEMSLVVRTSFH (SEQ ID
 20 NO: 399)

25 ATGGATAAGTCCAATTCTTCAGTGGTGTCTGAATTGTACTGTTGGACTCTGTAGTTCTC
 AAAAACTCAGCTTCTATTCTCACAGTGACTCTGATACCGCTGCACCTCCCTATGTACTTTCT
 CTTGGAAACCTTCTTGTGACATTGTCAGGCTCTTGTCTACCCCTAAAATGATTG
 CAGATTTCTGAGTGACACGAGACCATATCTTCAGTGGCTGCATAGCCAAATTCTTCTT
 ATTACACCTTTACTGGAGGGAGATGGTGTACTGTTCGATGGCTATGACAGGTATG
 TAGCCATATGCAAACCCCTATACTATGTGGTCATCATGAGCGAAGGACATGCACTGTCTT
 30 GGTAAATGATCTCCTGGCTGTGAGCTGGTGCACACATTAAGCCAGTTATCATTACTGTG
 AACCTGCCTTTGTGGACCTAATGTAGTAGACAGCTTTGTGATCTCCTCGAGTCAC
 CAAACTGCCTGCCTGGACTCTACATCATTGAAATACTAATTGTGGTCAATAGGAAATT
 CTTCCCTAAGCACTTCTCTCTGGTCAGCTCTACATCATTATTCTTGTACAGTTG
 GCTCAAGTCTCAGCTGCAATGGCAAAGGCATTCTACGCTGGCTCCATATTGAGTA
 35 GTAATATTATTCTTGGACCTTGATCTCATCTATGTGTGGCCCTTACCATCTCCTT
 GGATAAAATTCTTGCATATTTCACCTGTTTACCCCCGCTAAACCCCAATTATATA
 CACTAAGGAATAGGGATATGAAGGCTGCCGTAAAGAAAATTGTGAACCATTACGTGAGGC
 CAAGGAGAATTCTGAAATGTCACTAGTAGTGAGAACTCCTTCTTACCTAA (SEQ ID NO:
 400)

AOLFR215 sequences:

40 MAHTNESMVSEFVLLSNSWGLQLFFFAIFSIVYVTSVLGNVLIVIISFDSHLNSPMYFLLSNL
 SFIDICQSNFATPKMLVDFFIERKTISFEGCMAQIFVLSFVGSEMLLVAMAYDRFIAICKPLH
 YSTIMNRRLCVIFVSISWAVGVLHSVSHLAFTVDPFCGPNEVDSFFCDLPLVIELACMDTYEM
 EIMLTNSGLISLSCFLALIISYTIILIGVRCRSSSGSSKALSTLTAHITVVILFFGPCIYFYIWPFSRL
 45 PVDKFLSVFYTVCTPLNPIIYSLRNEDVKAAMWKLRNHHVNSWKN (SEQ ID NO: 401)

50 ATGGCTCACACAAATGAATCGATGGTGTCTGAGTTGTACTTTGGGACTCTCTAATTCT
 GGGGACTTCAACTTTCTTCTGCCATCTCTCTATAGTCATGTGACATCAGTGTAGGC
 AATGTCTTAATTATTGTCTTCTGACTCCATTGAACTCTCCTATGTACTCTG
 CTCAGTAATCTTCTTCTGATATCTGTCACTGCTAATTGCCCACCCCCAAGATGCTTGT
 AGACTTTTATGAGCGCAAGACTATCTCTTGAGGGTGTGATGGCCCAGATATTG
 CTTCACAGTTTGTGGAGTGTGAGATGATGTTGCTGTAGCTATGGCATATGACAGATT
 TAGCCATATGTAAGCCTCTGCACTACAGTACAATTATGAACCGGAGGCTGTGTAATT
 TGTTGCTATTCTCTGGCGGTGGCGTCTTCATTCTGTGAGGCCACTTGGCTTTACAGTGG
 55 ACCTGCCATTCTGTGGTCCCAATGAGGTGGATAGCTTCTTGTGACCTTCCCTGGTGATA
 GAGCTGGCTGATGGATAACATGAAATGAAATTATGACCCCTAACGAACAGTGGCCTG

5 ATATCATTGAGCTGTTCTGGCTTAATTATTTCTACACCATCATTTGATCGGTGTCCG
 ATGCAGGTCTCCAGTGGGTCACTAAAGGCTTTCTACATTAACGCCACATCACAGTG
 GTCATTCTTCTTCTGGGCTTGCATTATTCATATGGCCTTTAGCAGACTTCCTGT
 GGACAAATTCTTCTGTGTTCTACACTGTTGACTCCCTGTTGAACCCATCATCTACT
 CTTGAGGAATGAAGATGITAAGCAGCCATGTGAAGAAACCATCATGTGAACCT
 CCTGGAAAAACTAG (SEQ ID NO: 402)

AOLFR216 sequences:

10 MDVGNKSTMSEFVLLGLSNSWELQMFFMVFSLLYVATMVGNSLIVITVIVDPHLHSPMYFLL
 TNLSIDMSLASFATPKMITDYLTHKTISFDGCLTQIFLHLFTGTEIILMAMSFDRYIAICKPL
 HYASVISPQVCVALVVASWIMGVMHSMSQVIFALTLPCGPYEVDSFFCDLPVVFQLACVDTY
 VLGLFMISTSGIIALSCFIVLFNSYVIVLVTVKHHSSRGSSKALSTCTAHFIVVFLFFGPCIFIYMW
 PLSSFLTDKILSVFYTIFTPTLNPIYTLRNQEVKIARMRKLKNRFLNFNKAMPS (SEQ ID NO: 403)

15 ATGGATGTGGGCAATAAGTCTACCATGTCTGAATTGTTTGCTGGGGCTCTCTAATTCT
 GGGAACTACAGATGTTTCTTATGGTGTTCATTGCTTATGTGCAACAATGGTGGG
 TAACAGCCTCATAGTCATCACAGTTATAGTGGACCCCTCACCTACACTCTCTATGTATTCTC
 TGCTTACCAATCTTCAATCATTGATATGTCTCTGCTTCCGCCACCCAAAGATGATT
 ACAGATTACCTAACAGGTACAAAACCATCTCTTGTATGGCTGCCTACCCAGATATTCT
 20 TTCTCCACCTTTCACTGGAACATGAGATCATCTTACTCATGGCCATGCTTGTGATAGGTAT
 ATTGCAATATGCAAGCCCCTGCACTATGCTTCTGTCATTAGTCCCAGGTGTGTTGCTCT
 CGTGGTGGCCTCCTGGATTATGGGAGTTATGCAATGAGTCAGGTCAATATTGCCCTC
 ACGTTACCATTCGTGGTCCCTATGAGGTAGACAGCTTTCTGTGACCTTCCGTGGTGT
 CCAGTTGGCCTGTGGATACTTATGTTCTGGCCTTTATGATCTAACAGTGGCATA
 25 ATTGCGTTGCTCTGTTTATTGTTTATTAACTCATATGTTATTGTCCTGGTTACTGTGAA
 GCATCATTCTCCAGAGGATCATCTAACGGCTTCTACTTGTACAGCTCATTCATTGTTG
 TCTTCTGTTCTGGCCATGCATCTCATCTACATGTGGCCACTAACAGCTTCTCACA
 GACAAGATTCTGCTGTGTTTATACCATCTTACTCCACTCTGAACCCAATAATCTATAC
 30 TTTGAGGAATCAAGAAGTAAAGATAGCCATGAGGAAACTGAAAAATAGGTTCTAAATT
 TAATAAGGCAATGCCTCATAG (SEQ ID NO: 404)

AOLFR217 sequences:

35 MLESFQKSEQMAWSNQSAVTEFILRGLSSLELQIFYFLFFSIVYAAATVLGNLLIVVTIASEPHLH
 SPTYFLLGNLSFIDMSLASFATPKMIADFLREHKAISFEGCMQMFFLHLGGAEIVLLISMSFD
 RYVAICKPLHYLTIMSRMCVGLVILSWIVGIFHALSQLAFTVNLPCGPNEVDSFFCDLPLVIK
 LACVDTYILGVFMISTSGMIALVCFILLVISYIILVTVRQRSSGGSSKALSTCSAHFTVVTLLFFGP
 CTFIYVWPFTNFPIDKVLVSFYTIYTPLLNPVIYTVRNKDVKYSMRKLSSHIFKSRKTDHTP
 (SEQ ID NO: 405)

40 ATGCTAGAGTCCTCCAGAAATCAGAGCAAATGGCCTGGAGCAATCAGTCTGGTAACC
 GAATTCTACTACGGGGTCTGTCAGTTAGAAACTCCAGATTCTACTTCCTGTTTT
 CTCCATAGTCATGCAGCCACTGTGCTGGGAACCTCTTATTGTCACCATTCATCA
 GAGCCACACCTTCATTCCCTACGTACTTCTGCTGGCAATCTCTCTTATTGACATGTC
 CCTGGCCTCATTCACCCAAAATGATTGCAAGACTCCTTAGAGAACACAAAGCCATC
 45 TCTTTGAAGGCTGCATGACCCAGATGTTCTCTACATCTTCTAGGGGTGCTGAGATTG
 TACTGCTGATCTCCATGTCCTTGATAGGTACGTGGCTATCTGTAAGGCTCTACATTACCTA
 ACAATCATGAGCCGAAGAATGTGTTGGCTTGATACCTTCTGGATTGTCGGCATCT
 TCCATGCTCTGAGTCAGTTAGCATTTACAGTGAATCTGCCCTCTGTGGACCCAATGAAGT
 AGACAGTTCTTGTGACCTCCCTTGGTATTAAACTTGTGCTGTCGACACATATATT
 50 TGGGGGTGTTCATGATCTCAACCAAGTGGCATGATTGCCCTGGTGTGCTTCATCCTCTTGGT
 GATCTCTTACACTATCATCCTGGTCACGGTCTGGCAGCGTTCTCTGGTGGATCCTCCAAA
 GCCCTCTCCACGTGCAAGTGGCCACTTACTGTTGACCCCTTCTTGGCCATGCACTT
 CATTATGTGTTGGCCTTCACAAATTCCCAATAGACAAAGTACTCTCAGTATTATACCA
 TATACACTCCCCTTGAATCCAGTGAATACCGTTAGGAATAAGATGTCAAGTATT
 55 CATGAGGAAACTAAGCAGCCATATCTTAAATCTAGGAAGACTGATCATACTCCTTAA
 (SEQ ID NO: 406)

AOLFR218 sequences:

5 METANYTKVTEFVLTGLSQTREVQLVLFVIFLSFYLFILPGNLIICITIRLDPHLTSPMYFLLANLA
 LLDIWYSSITAPKMLIDFFVERKIIISFGGCIAQLFFLFVGASEMFLLIVMAYDRYAAICRPLHYA
 10 TIMNRRLCILVALSWMGGFIHSIIQVALIVRLPFCGPNELDSYFCIDTQVVRACANTFPEELVM
 ICSSGLISVVCFIALLMSYAFLLALLKKHSGSDENTNRAMSTCYSHITIVLMFGPSIYIYARPF
 SFSLDKVVSVFHTVIFPLLNPIIYTLRNKEVKAAMRKVVTKYILCEEK (SEQ ID NO: 407)

15 ATGGAAACTGCAAATTACACCAAGGTGACAGAAATTGTTCTCACTGGCTATCCCAGACTC
 GGGAGGTCCAACACTAGCCTATTGTTATTTCTATCCTCTATTGTTCATCCTACCAAGGA
 AATATCCTTATCATTGCACCATCAGGCTAGACCCCTCATCTGACTTCTCCTATGTATTCT
 GTGGCTAATCTGGCCCTCCTGATATTGGTACTCTCCATTACAGCCCTAAAATGCTCA
 TAGACTTCTTGTGGAGAGGAAGATAATTCCCTTGGTGGATGCATTGACAGCTCTT
 CTTACACTTGTGGGGCTTCGGAGATGTTCTGCTCATAGTGTGGCTATGACCGCTAT
 GCTGCTATCTGCCGACCCCTCCACTATGCTACCATCATGAATCGACGGTCTCTGCTGTATCCT
 GGTGGCTCTCTCCTGGATGGGGGCTCATTCTATAATACAGGTGGCTCTCATTGTT
 CGACTTCCTTCTGTGGGCCAAAGGGTACTCTGTGACATCACACAGGTG
 TCCGGATTGCCGTGCCAACACCTCCAGAGGGAGTTAGTGTGATCTGTAGTAGTGGTCT
 GATCTCTGTGGTGTGTTCTGCTCTGTTAATGCTCTGCTATGCCTATGCCCTCTGGCCTTGCTCA
 20 AGAAAACATTAGGCTCAGATGAGAATACCAACAGGGCCATGTCACCTGCTATTCCCACAT
 TACCAATTGTTGGTGTAAATGTTGGCCATCCATCATTATGCTCGCCATTGACTCAT
 TTTCCCTAGATAAAAGTGGTGTCTGTGTTCTAATGTAATTCCCTTACTTAATCCCATT
 ATTACACATTGAGAAAACAAGGAAGTAAAGGCAGCCATGAGGAAGGTGGTACCAAATAT
 25 ATTGTTGTGAAGAGAAGTGA (SEQ ID NO: 408).

AOLFR219 sequences:

30 MLTSLTDLCFSPIQVAEIKSLPKSMNETNHSRVTEFVLLGLSSRELQPFLFLTFSLLYLAILGNF
 LIILTVDSDRLHTPMYFLLANLSFIDVCVASFATPKMIADFLVERKTISFDACLAQIFFVHLFTGS
 EMVLLVSMAYDRYVAICKPLHYMTVMSRRVCVVLVLISWFGFIHTTSQLAFTVNLPCGP
 KVDSFFCDLPLVTKLACIDTYVVSLLIVADSGFLSLSFLLVSVTIVLTVRNRSSASMAKAR
 STLTAHITVVTLLFFGPCIFIYVWPSSYVDKVLAVFYTIITLILNPVIYTLRNKEVKAAMSKLKS
 RYLKPSQSVVSVIRNVLFLETK (SEQ ID NO: 409).

35 ATGCTCACCTCATTAACTGATCTCTGTTCTCCTATTAGGTAGCTGAAATTAGTCCT
 TCCAAAATCGATGAATGAGACAAATCATTCTCGGGTGACAGAAATTGTTGCTGGACTG
 TCTAGTTCAAGGGAGCTCAACCTTCTGTTCTACATTTCACACTTATCTAGCAAT
 TCTGTTGGCAACTTCTCATCATCCTCACTGTGACCTCAGATTCCGCCCTCACACCCCCA
 TGTACTTTCTGCTGCAAACCTGTCAATTAGACGTATGTGTTGCTCTTTGCTACCCCT
 40 AAAATGATTGAGACTTTCTGTTGAGCGCAAGACTATTCTTGTGATGCTGCCTGGCC
 AGATTTCCTTGTTCATCTCTCACTGGCAGTGAAATGGTGTCTCTAGTTCCATGGCCTAT
 GACCGTTATGTTGCTATATGCAAACCTCTCCACTACATGACAGTCATGAGCCGTCGTGAT
 GTGTTGTGCTCGTCTCATTTCTGTTGCTGTTGCTCATCCACTACAGCCAGTTGGCA
 TTCACTGTTAATCTGCCATTGTGCTTAATAAGGTAGACAGTTCTGTGACCTTCC
 TCTAGTGACCAAGTTAGCCTGCATAGACACTTATGTTGCTAGCTTACTAATAGTTGAGAT
 45 AGTGGCTTCTCTGAGTTCTCTGTTCTCTGTTGCTCTACACTGTAATACTTGT
 ACAGITAGGAATCGCTCTGCAAGCATGGCGAAGGCCGCTCCACATTGACTGCTACA
 TCACTGTGGTCACTTATTCTTGGACCATGCATTCTCATCTATGTTGCTGCCCTCAGCAGT
 TACTCAGTTGACAAAGTCTGTGTTCTACACCATCTTCAGCTTATTAAACCCCTGT
 AATCTACACGCTAAGAAACAAGTAAGGCAAGCTATGTCAGCTAAACTGAAGAGTCGGTA
 50 TCTGAAGCCTAGTCAGGTTCTGTAGTCATAAGAAATGTTCTTCTAGAAACAAAGTAA
 (SEQ ID NO: 410).

AOLFR220 sequences:

55 MKQYSVGNQHSNRSLLFPFLCSQMTQLTASGNQTMVTEFLFSMFPHARGGLLFFIPLLLIYG
 FILTGNLIMFIVIQVGMALHTPLYFFISVLSFELCYTTTIPKMLSCLISEQKSISVAGCQLQMYFF
 HSLGITESCVLTAMAIDRYIAICNPLRYPTIMPKLCIQLTVGSCFCGFLVLPEIAWISTLPFCGS

NQIHQIFCDFTPVLSLACTDTFLVVIVDAIHAEEIVASFLVIALSYIRIIVILGMHSAEGHHKAFST
CAAHLAVFLLFFGSVAVMYLRFSAATYSVFWDTAIAVTFVILAPFFNPIYSLKNKDMKEAIGRLF
HYQKRAGWAGK (SEQ ID NO: 411).

5 ATGAAGCAATATTCACTGGGTAAATCAACATTCCAATTATAAGGAGTCTCTGTTCCCTTCT
GTGTTCACAGATGACACAGTTGACGGCCAGTGGGAATCAGACAATGGTACTGAGTCCT
CTTCTCTATGTTCCCGCATGCCACAGAGGTGGCCTCTTATTCTTATTCCCTGCTTCTCA
TCTACGGATTATCCTAACTGAAACCTAATAATGTTATTGTCTTCAGTGCATCCAGGTGGCAGTGGC
CCTGCACACCCCTTGATTCTTATCAGTGCCTCTCCTGGAGATCTGCTATACCA
10 CAACCACCATCCCCAAGATGCTGTCCTGCCTAATCAGTGCAGAGAAGACATTCCGTGGC
TGGCTGCCTCCTGCAGATGTTCTTCACTCAGTGCAGAGAAGCTGTGCT
ACAGCAATGGCCATTGACAGGTACATAGCTATCTGCAATCCTCCAGTACCCACCATCA
TGATTCCCAAACCTTGATCCAGTGCACAGTTGGATCCTGCTTTGTGGCTTCCCTGTG
CTTCCTGAGATTGCATGGATTCCACCTGTGCTGAGCTTGGCAGAGATCCACAGAT
15 ATTCTGTGATTTCACACCTGTGCTGAGCTTGGCCTGCAAGATACTCCTAGTGGTCA
TTGGATGCCATCCATGCAGCGAAATTGTAAGCCTCTTCTGGTCAATTGCTCTAC
TCCGGATTATTATAGTGAATTCTGGGAATGCACTCAGCTGAAGGTACATCACAAGGCCTTTC
CACCTGTGCTGCTCACCTTGCTGTGTTCTGCTATTGTCAGTGTGGCTGT
TGAGATTCTCAGCCACCTACTCAGTGTGGACACAGCAATTGCTGTCACTTGT
20 CTTGCTCCCTTTTCAACCCCCATCATCTATAGCCTGAAAAACAAGGACATGAAAGAGGCTA
TTGGAAGGCTTCCACTATCAGAAGAGGGCTGGTTGGGCTGGAAATAG (SEQ ID NO:
412).

AOLFR221 sequences:

25 MRNLSGGHVEEFVLVGFPTTPPLQLLLFVLFIAIYLTLLENALIVFTIWLAPSLHRPMYFFLGH
LSFLELWYINVTPRLLAFLTQDGRVSYVGCMQYFFIALACTECVLLAVMAYDRYLAICGP
LLYPSLMPSSLATRLAAASWGSFFSSMMKLLFISQLSYCGPNIIHFFCDISPLLNLTCSDEQA
ELVDFLALVMILLPLAVVSSYTAIIAIIIRIPTSRGRHKAFSTCAAHЛАVVIYSSTLFTYAR
PRAMYTFNHNKIISVLYTIIVPFFNPAYCLRNEVKEAFRKTVMGRCHYPRDVQD (SEQ ID
30 NO: 413).

ATGAGAAATTGAGTGGAGGCCATGTCGAGGAGTTGTCTGGTGGGTTCCCTACCACGC
CTCCCTCCAGCTGCTCCTCTTGTCTTGTCAATTACCTCTGACATTGTTGGAGA
ATGCACITATTGTCTTCACAATTGGCTGCTCAAGCCTCATCGTCCATGTACTTTTC
35 CTTGGCCATCTCTTCTGGAGCTATGGTACATCAATGTCACCATCCTCGGCTTGGC
AGCCTTCTTACCCAGGATGGTAGAGTCTCCTACGTAGGTTGCATGACCCAACTGACTTC
TTTATTGCCTTAGCCTGTACTGAATGTGTGCTGTTGGCAGTTATGGCCTATGATCGTAC
GCCATCTGTGGACCCCTCTTACCTAGTCTCATGCCCTCCAGTCTGGCCACTCGCCTG
CTGCTGCCTCTTGGGGCAGTGGCTCTTCAGCTCCATGATGAAGCTTCTTTTATTCCCAA
40 TTGTCTACTGTGGACCCAACTATTCAACACTTTCTGTGATATTCCCCACTACTCAA
CCTCACCTGCTCTGACAAGGAGCAAGCAGAGCTAGTAGACTCTCTGGCCCTGGTATG
ATTCTACTCCCTCTATTGGCTGTGGTTCATCATACTGCCATATTGCGACCCATCCTGAG
GATCCCTACGTCCAGGGACGCCACAAAGCCTTCCACTGTGCGCTCATGGCAGTG
GTTGTTATCTACTACTCCTCCACTCTCTCACCTATGCACGGCCGGGAGTGTACAC
45 CAACCACAAAGATTATCTCTGTGCTACACTATCATTGACCATCTTCAACCCAGCCA
TCTACTGCCTGAGGAACAAGGAGGTGAAGGAGGCCAGTGAAGACAGTGTGATGGGAGAT
GTCACTATCCTAGGGATGTTAGGACTGA (SEQ ID NO: 414).

AOLFR222 sequences:

50 MGQTNVTWRDFVFLGFSSSGELQLLLFALFLSLYLVTLTSNVFIILAIRLDSHLHTPMYLFSL
SFSETCYTGLIIPRMLSGLAGGDQAISYVGCAAAQMFSASWACTNCFLAAAMGFDRYVAICAPL
HYASHMNPTLCAQLVITSFLTGYLFLGMLTVIFHLSFCSSHEIQHFFCDTPPVLSLACGDTGPS
ELRIFILSLLVLLVSFFFITISYAYIILAIIIRIPTSAEGQKKAFTCAHLSLTVIIHYGCASFVYLRPK
ASYSLERDQLIAMTYVVTPLLNPIVYSLRTRAIQTLRNAFRGRLLGKG (SEQ ID NO: 415).

ATGGGGCAGACCAACGTAACCTCCTGGAGGGATTGGCTTCCTGGGCTTCTCCAGTTCTG
 5 GGGAGTTGCAAGCTCCTCTTGCCTGTCCTCTGTATCTAGTCACTGACCAGC
 AATGTCTTCATTATCATAGCCATCAGGCTGGATAGCCATCTGCACACCCCCATGTACCTCT
 CTTTCCCTCCTATCCTCTGTAGACCTGCTACACTTGGCATCATCCCTAGAATGCTCT
 CTGGCCTGGCTGGGGGACAGGCTATCTCCTATGTGGCTGTGCCAGATGTTCTT
 TTCTGCCTCATGGGCCTGTACTAACTGCTCCTCTGGCTGCCATGGCTTGAAGATATG
 10 TGGCCATCTGTGCTCCACTCCACTATGCCAGCCACATGAATCCTACCCCTGTGCCAGCT
 GGTCACTACTCCTCTGTAGACGGACCTCTTGGACTGGAAATGACACTAGTTATTTC
 ACCTCTCATTCTGCAGCTCCCATGAAATCCAGCACTTTTGACACGCCACCTGTGCTG
 AGCCTAGCCTGTGGAGATAACAGGCCAGTGAGCTGAGGATCTTTATCCTCAGTCTTGG
 TCCTCTGGTCTCCTCTTCTCATCACCATCTCCTACGCCACATCTGGCAGCAAACTG
 AGGATCCCCCTGTGCTGAGGGCAGAAGAAGGCCCTCTCCACTTGTGCCTGCACCTTACAG
 TGGTCATTATTCAATTATGGCTGTGCTTCTCGTACCTGAGGCCAAAGCCAGCTACTCT
 15 CTTGAGAGAGATCAGCTTATTGCCATGACCTATACTGTAGTGACCCCCCTCCTTAATCCA
 TTGTTATAGTCTAAGGACTAGGGCTATACAGACAGCTTGAGGAATGCTTCAGAGGGAG
 ATTGCTGGTAAAGGATGA (SEQ ID NO: 416).

AOLFR223 sequences:

MEAANESSEGISFVLLGLTSPGQQRPLFVLFLYYVASLLNGNGLIVAAIQASPAHLAPMYFILLA
 20 HLSFADLCFASVTVPKMLANLLAHDHSISLAGCLTQMYFFFALGVTDSCLLAAMA YDCYVAIR
 HPLPYATRMSRAMCAALVGMAWLVSHVHSLLYILLMARLSCASHQVPHFFCDHQPLRLSC
 SDTHIQLLIFTEGAAVVTPFLILASYGAIAAVLQLPSASGRLRAVSTCGSHLAVVSLFYGT
 VIAVYFQATSRREAEWGRVATVMYTVVTPMLNPIYSLWNRDVQGALRALLIGRRISASDS
 (SEQ ID NO: 417).

25 ATGGAGGCTGCCAATGAGTCTTCAGAGGGAACTCTATTGGACTGACAACAA
 GTCCCTGGACAGCAGCCGCTCTCTTGTGCTGTTCTGTATGTGGCCAGCCTCTG
 GGTAAATGGACTCATTGTGGCTGCCATCAGGCCAGTCCAGGCCCTCATGCACCCATGTACT
 30 TCCCTGCTGGCCCACCTGTCTTGTGACCTCTGTTGCCCTCGTCACTGTGCCCAAGATG
 TTGGCCAACCTGTGCTGCCATGACCACTCCATCTCGCTGGCTGGCTGCCTGACCCAAATGT
 ACTTCTCTTGTGCCCTGGGGTAACTGTAGCTGCTCTGGCGGCCATGGCCTATGACTG
 CTAGTGGCCATCCGGCACCCCTCCCTATGCCACGAGGATGTCCCGGCCATGTGCGCA
 GCCCTGGGGAAATGGCATGGCTGGTGTCCCACGTCCACTCCCTCTGTATATCCTGCTCA
 TGGCTCGCTTGTGCTTGTGCTTCCCACCAAGTGCCCACTTCTGTGACCAACCAGCCT
 35 CTCTTAAGGCTCTGTGCTCTGACACCCACCACATCCAGCTGCTCATCTCACCGAGGGCG
 CCGCAGTGGTGGTCACTCCCTCCTGCTCATCTCGCCTCATGGGCCATCGCAGCTGC
 CGTGCCTCAGCTGCCCTCAGCCTCTGGGAGGCTCCGGCTGTGTCACCTGTGGCTCCAC
 CTGGCTGTGGTGAGCCTCTTCTATGGGACAGTCATTGAGCTACTTCCAGGCCACATCCC
 40 GACGCGAGGGCAGAGTGGGCCGTGTGCCACTGTACACTGTAGTCACCCCCATGC
 TGAACCCCATCATCTACAGCCTCTGGAATCGCAGTACAGGGGGCACTCGAGGCCCTCT
 CATTGGCGAAGGATCTCAGCTAGTGACTCCTGA (SEQ ID NO: 418).

AOLFR224 sequences:

45 MGSFNTSFEDGFILVGFSDWPKLEPILFVIFIFYSLTIFGNIIIALSWLDLRLHTPMYFFLHLSL
 LDLCFTTSTVPQLLNLGVDRITRGGCVAQLFIYLALGSTECLVVMAFDRYAAVCRPLHY
 MAIMPHLQLCQLIAISWGAGFVNLSIQTGLAMAMPLCGHRLNHFFCEMPVFLKLACADTEGT
 EAKMFVARVIVVAVPAALILGSYVHIAHVLRVKSTAGRRAFGTCGSHLLVFLFYGSAIYT
 YLQSIHNSEREKGKVALFYTIITPILNPLIYTLRNKDVKLGALWKVLWRGRDSG (SEQ ID NO:
 419).

50 ATGGGAAGTTCAACACCAAGTTGAAGATGGCTTCATTTGGGGATTCTCAGATTGGC
 CGCAACTGGAGCCCATCCTGTTGTCTTATTCTACTCCCTAACCTCTTGGC
 AACACCATCATCATCGCTCTCCCTGGCTAGACCTTCGGCTGCACACACCTATGTACTCTT
 TCTCTCTCATCTGTCCCTCCTGGACCTCTGCTTACCCACCGAGCACCCTGGCCAGCTCCTGA
 55 TCAACCTTGCAGGGTGGACCGCACCACCAACCGTGGAGGGTGTGGCTCAGCTCTTCA
 CTACCTAGCCCTGGCTCCACAGAGTGTGCTCTGGTGTGGCATGGCCTTGACCGCTAT

5 GCTGCTGTCTGTCGTCCACTCCACTACATGGCCATCATGCACCCCCATCTCTGCCAGACCCCT
 GGCTATGCCTCCTGGGTGCGGGTTCTGTGAACCTCTGATCCAGACAGGTCTCGCAATG
 GCCATGCCTCTGTGGCCATCGACTGAATCACTTCTCTGTGAGATGCCTGTATTCCTGAA
 GTTGGCTTGTGCGGACACAGAAGGAACAGAGGCCAAGATGTTGTGGCCGAGTCATAGT
 10 CGTGGCTTGTCTGCAGCACTTATTCTAGGCTCTATGTGACATTCGCTATGCAGTGCTG
 AGGGTGAAGTCAACGGCTGGCGCAGAAAGGCTTGGACTTGTGGTCCCACCTCTA
 GTAGTTTCTTTTATGGCTCAGCCATCTACACATATCTCAATCCACAAATTATTC
 TGAGCGTGAGGGAAAATTGTTGCCCTTTTATACTATAATTACCCCCATTCTCAATCTC
 TCATTTATACTAAAGAAACAAGGACGTGAAGGGGCTCTGTGAAAGTACTATGGAGGG
 GCAGGGACTCAGGGTAG (SEQ ID NO: 420).

AOLFR225 sequences:

15 MENYNQTSTDFILLGLFPPSIIDLFFFILIVFIFLMALIGNLSMILLIFLDTHLHTPMYFLLSQLSLID
 LNYISTIVPKMASDFLHGNKSISFTGCGIQSFFFALGGAEALLASMAYDRYIAICFPLHYLIRM
 SKRVCVLMITGSWIIGSINACAHVYVLHIPYCRSRAINHFFCDVPAMVTLACMDTWVYEGTV
 FLSATIFLVFPFIGISCSYGVLFAYHMKSAEGRKAYLTCSTHLTVVTFYYAPFVYTYLRPRS
 LRSPTEDKVLAVFYTILTPMLNPIIYSLRNKEVMGALTRVSQRICSVKM (SEQ ID NO: 421).

20 ATGGAAAATTACAATCAAACATCAACTGATTCTATTTCTTATGGGGCTTCCACCATCAA
 TAATTGACCTTTCTTCTCATTCATTGTTCTCATTTCTGATGGCTCTAATTGGAAACC
 TGTCATGATTCTTCTCATCTCTGACACCCATCTCCACACACCCATGTATTCTACTG
 AGTCAGCTCCCTCATTGACCTAAATTACATCTCCACCATGTTCTAAGATGGCATCTGA
 TTTCTGCATGAAACAAGTCTATCTCCCTACTGGCATCTATGGCTATGATCGTTACATTGC
 25 TGGCATTAGGAGGTGCAGAACGACTACTTGGCATCTATGGCTATGAGCAAAGAGTGTGTGCTGATGATA
 ACAGGGTCTTGGATCATAGGCTCGATCAATGCTTGTGCTCACACTGTATATGTACTCCATA
 TTCCATTGCGATCCAGGGCCATCAATCATTTCTCTGTGATGTCCAGCAATGGTACT
 CTGGCCTGCATGGACACCTGGCTATGAGGGCACAGTGTGAGTGCCACCATTTTC
 30 TCGTGTTCCTCTTGTGATTCATGTTCTATGGCCAGGTCTTGTGCTGCTGCTACAC
 ATGAAATCTGCAGAAGGGAGGAAGAAAGCTATTGACCTGCAGCACCCACCTCACTGTA
 GTAACTTCTACTATGCACCTTGTCTACACTTACACGCTTGTGCTCACCTGCAAGATCCCTGCGATCTCC
 AACAGAGGACAAGGTTCTGGCTGCTTCTACACCATCCTCACCCCAATGCTCAACCCCCATC
 ATCTATAGCCTGAGGAACAAGGAGGTGATGGGGCCCTGACACGAGTGTGAGTCAGAGAATC
 TGCTGTGAAAATGTAG (SEQ ID NO: 422).

35

AOLFR226 sequences:

40 MEWRNHSGRVSEFVLLGFPAPAPLQVLLFALLLAYVLVLTENTLIIMAIRNHSTLHKPMYFFL
 ANMSFLEIYWVTVTIPKMLAGFVGSKQDHGQLISFEGCMTQLYFFLGLGCTECVLLAVMAYD
 RYMAICYPLHYPVIVSGRLCVQMAAGSWAGGFGISMVKVFLISGLSYCGPNIINHFFCDVSPLL
 NLSCTDMSTAELTDFILAIFILLGPLSVTGAASYVAITGAVMHISSAAGRYKAFSTCASHLTVVIF
 YAASIFTYARPKALSAFDTNKLVSVLYAVIVPLNPIIYCLRNQEVKRALCTLHLYQHQDPDP
 KKASRNV (SEQ ID NO: 423).

45 ATGGAGTGGCGGAACCATAGTGGGAGAGTGAGTGAGTTGTGTTGCTGGCTCCCTGCT
 CCTGCGCCACTACAGGTACTATTGTTGCCCTTGCTGCTGGCCTATGTGTTGGTGTGAC
 TGAGAACACACTCATATTGGCAATTAGGAACCATTCTACCCCTCCACAAACCCATGTAC
 TTTCTAGCTAATATGTCCTTCTGGAGATCTGGTATGTCACTGTCACTATTCCCAAGAT
 GCTGCTGGCTTGTTGGATCCAAACAGGATCATGGACAGCTAATCTCCTTGAGGGATGC
 ATGACACAGCTCTACTTTCTGGCTGGCTGCACTGAGTGTGCTTCTCGCTGTAT
 50 GGCCTATGATCGCTATATGCCATCTGCTATCCTCTCCACTACCCAGTCATTGTCAGTGGCC
 GGCTGTGTGCGAGATGGCTGCTGGCTTGGAGGTTGGCATCTCCATGGTCAA
 AGTTTTCTATTCTGGCCTCTTACTGTGGCCCAACATCATCAACCACTTTCTGTG
 ATGTCTCTCATTGCTCACCTCTCATGCACTGATATGTCACAGCAGAGCTACAGATTTC
 ATCCTGGCCATTCTTATTCTTAGGGCCACTCTGTCACTGGGGCCCTATGTGGCCAT
 55 TACTGGTGTGTGATGCACATATCTCGCTGCTGGACGCTATAAGGCCTTCCACCTGT
 GCCTCTCATCTCACTGTTGTGATAATCTCTATGCAGCCAGTATCTCATATGCTCGGCC

AAAGGCACCTCTCAGCTTTGACACCAACAAGTTGGTCTCTGTACTGTATGCTGTCAATTGTA
 CCATTGCTCAATCCCATCTTACTGCCTGCGCAATCAAGAGGTCAAGAGAGGCCCTATGCT
 GTACTCTGCACCTGTACCAGCACCAGGATCCTGACCCCAAGAAAGCTAGCAGAAATGTATA
 G (SEQ ID NO: 424).

5

AOLFR227 sequences:

MEPQNTSTVTNFQLGFQNLLWEQALLFVIFLLIYCLTIIGNVVIITVVSQGLRLHSPMYMFLQH
 LSFLEVWYTSTTVPLLNLSSWQQAISFSACMAQLYFFVFLGATECFLLAFMAYDRYLAICSP
 LRYPFLMHRGLCARLVVSVWCTGVSTGFLHSMMISRLDFCGRNQINHFFCDLPLMQLSCSRV
 10 YTEVTIFILSIAVLCICFFLTGLPYVFIVSSILRIPSTGRRKTGSTCGSHLA⁵VTLYYGTMISMV
 CPSPHLLPEINKIISVFYTVVTPLLNPVIYSLRNKDFKEAVRKVMRRKGILWSTSKRKF
 LY (SEQ ID NO: 425).

15 ATGGAGCCCCAAAATACCTCCACTGTGACTAACCTTCAGCTGTAGGATTCCAGAACCTTC
 TTGAATGGCAGGCCCTGCTCTTGTCAATTTCCTGCTCATCTACTGCCTGACCATTATAGGG
 AATGTTGTCACTCATCACCGTGGTGAGCCAGGGCCTGCGACTGCACCTCCCTATGTACATGT
 20 TCCTCCAGCATCTCTCCTTCTGGAGGTCTGGTACACGTCCACCACTGTGCCCTCTCCTA
 GCCAACCTGCTGTCTGGGCCAACGCCATCTCCTCTGCCTGCATGGCACAGCTACT
 TCTTCGATTCTCTCGGCCACCGAGTGCCTTCTCCTGGCCTCATGGCCTATGACCGTTAC
 CTGGCCATCTGCAGGCCACTCCGCTACCCCTTCTCATGCATCGTGGCTATGTGCCAGGTT
 25 GGTGGTGGTCTCATGGTCACAGGGTCAGCACAGGCTTCTGCATTCCATGATGATTCC
 AGGTTGGACTTCTGTGGCGCAATCAGATTAACCATTCTCTGCACCTCCGCCACTCA
 TGCAGCTCCTGTTCCAGAGTTATATCACCGAGGTGACCATCTCATCCTGTCATTGCC
 GTGCTGTGCATTGTTTTCTGACACTGGGCCCTATGTTTCTATTGTGTCCTCCATATT
 30 GAGAATCCCTCCACCTCTGCCGGAGAAAGACCTTTCCACATGTGGCTCCACCTGGCT
 GTTGTCACTCTACTACGGGACCATGATCTCATGTATGTGTCCTCCAGTCCCCACCTGTT
 GCCTGAAATCAACAAGATCATTCTGTCITCTACACTGTGGTCACACCACTGCTGAACCCA
 GTTATCTACAGCTGAGGAACAAAGACTTCAAAGAAGACTGTTAGAAAGGTGATGAGAAGG
 AAATGTGGTATTCTATGGAGTACAAGTAAAAGGAAGTTCTTTATTAG (SEQ ID NO: 426).

30

AOLFR229 sequences:

MFVNQIPFQLYHISFVYPTELWSRAIIPCMPTLSFWVCSATPVSPGFFALILLVFVTSIASNVVK
 IIIHIDSRLHTPMYFLSQLSLRDILYISTIVPKMLVDQVMSQRAISFAGCTAQHFLYLTLAGAE
 35 FFLGLMSCDRYVAICNPLHYPDLMRKRICWLIVAAA WLGGSIDGFLLTPVTMQFPFCASREIN
 HFCCEVPALLKLSCTDTSAyetAMYVCCIMMLIIPFSVISGSYTRILITVYRMSEAEGRRAVAT
 CSSHMVVVSLFYGAAMYTYVLPHSYHTPEQDKAVSAFYTILTPMLNPLIYSLRNKDVTGALQK
 VVGRCVSSGKVTTF (SEQ ID NO: 427).

40 ATGTTTATGTAAATCAGATACCTTCCAACTTATCATATCTCTTCGTGTACCCCTACAGA
 GCTATGGAGCAGAGCAATTATCCGTGTATGCCGACTTTATCCTCTGGTTTGTTCAGCA
 ACGCCCGTTTCCCCTGGCTCTTGCCTCATCCACATAGACTCCGCCCTCCACACCCCCATGTACTTC
 CAACGTGGTCAAGATCATTCTCATCCACATAGACTCCGCCCTCCACACCCCCATGTACTTC
 45 CTGCTCAGCCAGCTCCCTCAGGGACATCCTGTATAATTCCACCATTTGTGCCCTTGTGGATGCACTGCCAACACTTC
 GGTGCGACCAGGTGATGAGCCAGAGGCCATTCCCTTGTGGATGCACTGCCAACACTTC
 CTCTACTTGACCTTAGCAGGGCTGAGTTCTCCTCCTAGGACTCATGTCCTGTGATCGCTA
 CGTAGCCATCTGCAACCTCTGCACTATCCTGACCTCATGAGCCGCAAGATCTGCTGGTTG
 ATTGTGGCGGCAGCTGGCTGGAGGGTCTATCGATGGTTCTGCTCACCCCCGTACCA
 TGAGCTTCCCTCTGTGCTCTCGGGAGATCAACCATCTCTGCGAGGTGCCTGCCCT
 50 CTGAAGCTCTCTGCACGGACACATCAGCCTACGAGAGACAGCCATGTATGTGCTGTATTA
 TGATGCTCCTCATCCCTTCTGTGATCTGGGCTTACACAAGAATTCTCATTACTGTT
 TATAGGATGAGCGAGGCAGAGGGAGGGCAAAGGCTGTGGCCACCTGCTCCTCACACATG
 GTGGTTGTCAGCCTCTTCTATGGGCTGCCATGTACACATACGTGCTGCCTCATTCTTACCA
 55 CACCCCTGAGCAGGACAAAGCTGTATCTGCTTACACCATCCTCACTCCCATGCTCAAT
 CCACTATTACAGCCTAGGAACAAGGATGTACACGGGGCCCTACAGAAGGTTGTTGGG
 AGGTGTGTGTCCTCAGGAAGGTAACCACCTTCTAA (SEQ ID NO: 428).

AOLFR230 sequences:

5 MGMEGLLQNSTNFVLTGLITHPAFPGLLFAIVFSIFVVAITANLVMILLIHMDSLRHTPMYFLLS
 QLSIMDTIYICITVPKMLQDLSKDKTISFLGCAVQIFLYLTLLIGEFFLLGLMAYDRYVAVCNP
 LRYPLLMNRRVCLFMVVGWSVGGSLDFMLTPVTMSFPFCRSREINHFFCEIPAVLKLSCDTS
 LYETLMLYACCVLMLIPLSVISVSYTHILLTVHRMNSAEGRRKAFATCSSHIMVSVFYGAAFY
 TNVLPHSYHTPEKDKVVSAYTILTPMLNPLIYSLRNKDVAALRKVLGRGSSQSIRVATVIR
 KG (SEQ ID NO: 429).

10 ATGGGCATGGAGGGCTTCTCCAGAACTCCACTAACTCGCCTCACAGGCCTCATCACCC
 ATCCTGCCTTCCCCGGGCTTCTCTTGCAATAGTCTCTCCATCTTGTTGTTGGCTATAACA
 GCCAACCTGGTCATGATTCTGTCATCCACATGGACTCCGCCACACACCCATGTACTT
 CTTGCTCAGCCAGCTCCATCATGGATACCATCTACATCTGTATCACTGTCCCCAAGATGC
 TCCAGGACCTCTGTCAGGACAAGACCAATTCTCTCTGGGCTGTGCAGTTAGATCTT
 CCTCTACCTGACCCGATTGGAGGGATTCTCTCTGCTGGGTCTCATGGCCTATGACCGC
 15 TATGTGGCTGTGCAACCCCTACGGTACCCCTCTCCTCATGAACCGCAGGGTTGCTTATT
 CATGGTGGTCGGCTCTGGGTTGGTGGCTTGATGGGTTCATGCTGACTCTGTCACT
 ATGAGTTCCCTCTGTAGATCCCAGAGAGATCAATCACTTTCTGTGAGATCCCAGCCGT
 GCTGAAGTTGTCTTGACAGACACGTCACTCTATGAGACCTGATGTATGCCTGCTGCGTG
 CTGATGCTGCTTATCCCTATCTGTACACGACATCCTCTGACTGT
 20 CCACAGGATGAACTCTGCTGAGGGCCGGCGAAAGCCTTGCTACGTGTTCCCTCCACATT
 ATGGTGGTGAGCGTTTCTACGGGGCAGCCTCTACACCAACGTGCTGCCCACTCCTACC
 ACACCTCCAGAGAAAGATAAAGTGGTGTCTGCCTTCTACACCATCCTACCCCCATGCTCAA
 CCCACTCATCTACAGCTGAGGAATAAAGATGTGGCTGAGCTGACTGAGGAAGTAGACTAGG
 25 GAGATGTGGTCTCCAGAGCATCAGGGTGGCACTGTGATCAGGAAGGGCTAG (SEQ ID
 NO: 430).

AOLFR231 sequences:

30 MERANHSVSEFILLGLSKSQNLQILFFLGSVVFVGIVLGNLLILVTVTFDSSLHTPMYFLLSNL
 SCIDMILASFATPKMIVDFLRLERKTISWWGCVSQMFFMHLLGGSEMLLVAMAIDRYVAICKP
 LHYMTIMSPRVLTGLLSSYAVGFVHSSSQAFAFMLTPFCGPVIDSFFCDLPLVIKLACKDTYI
 LQLLVIADSGLLSLVCFLLLVSYGVIIFSVRYRAASRSSKAFSTLSAHTVVTLLFFAPCVFIYVW
 PFSRYSVVDKILSVFYTIFTPLLNPIYTLRNQEVKAAIKKRLCI (SEQ ID NO: 431).

35 ATGGAAAGAGCAAACCATTCACTAGTGGTATCGGAATTATTGTTGGGACTTCAAATCTC
 AAAATCTCAGATTATTCTCTGGGATTCTCTGTGGTCTCGTGGGATTGTGTTAGGA
 AACCTGCTCATCTGGTACTGTGACCTTGATTGATATGATCCTGGCTTCTTGTACACACCAATGTATTCT
 GCTTAGCAACCTCTCCTGCATTGATATGATCCTGGCTTCTTGTACCCCTAAGATGATTG
 TAGATTCTCCGAGAACGTAAGACCATCTCATGGTGGGGATGTTATTCCAGATGTTCTT
 TATGCACCTCTGGTGGGAGTGAGATGATGTTGCTGTGACCATGGCAATAGACAGGTAT
 40 GTGCCATATGCAAACCCCTCCATTACATGACCATCATGAGCCCACGGGTGCTCACTGGC
 TACTGTTATCCTCTATGCACTGGATTGTGCACTCATCTAGTCAAATGGCTTCTATGTTG
 ACTTTGCCCTCTGTGGTCCCAGTGTATAGACAGCTTCTGTGACCTTCCCTGTGAT
 TAAACTGCTGCAAGGAACACCTACATCCTACAGCTCCTGGTATTGCTGACAGTGGGCTC
 CTGTCAGTGGCTGCTTCCTCTTGTCTCTTGTGCTTCTCAAGGCTTCTCCACTCTCAGCTCACATCACAGTTG
 45 GTACCGTGTCTAGTCGATCCTCTAAGGCTTCTCCACTCTCAGCTCACATCACAGTTG
 TGACTCTGTTCTTGCTCCGTGTGTTATCTACGTCTGGCCCTCAGCAGATACTCGGTA
 GATAAAATTCTTCTGTGTTTACACAATTTCACACCTCTCTAAATCCTATTATTTATAC
 ATTAAGAAATCAAGAGGTAAAGCAGCCATTAAAAAGACTCTGCATATAA (SEQ ID NO:
 432).

50

AOLFR232 sequences:

55 MDNITWMASHTGWSDFILMGLFRQSKHPMANITWMANHTGWSDFILLGLFRQSKHPALLCV
 VIFVVFLMALSGNAVILLIHCDAHLHTPMYFFISQLMDMAYISVTVPKMLLDQVMGVNKIS
 APECGMQMFFYVTLAGSEFFLLATMAYDRYVAICHPLRYPVLMNHRVCLFLSSGCWFLGSVD
 GFTFTPITMTPFRGSREIHFFCEVPAVLNLSCSDTSLYEIFMYLCCVLMLLIPVVISSSYLLILL

TIHGMNSAERKKAFA^TCSSHL^TV^VILFY^GA^IY^TY^MLPSSY^HT^PE^KD^MM^VS^VF^YT^IL^TP^VV^NP^Y
LIYSLRNKDVMGALKMLTVEPAFQKAME (SEQ ID NO: 433).

5 ATGGACAACATCACCTGGATGGCCAGCCACACTGGATGGTCGGATTTCATCCTGATGGGAC
TCTTCAGACAATCCAAACATCCAATGGCCAATATCACCTGGATGGCAACCACACTGGATG
GTCGGATTCATCCTGGACTCTTCAGACAATCCAAACATCCAGCACTACTTTGTGTG
GTCATTTGTGGTTTCCTGATGGCGTTGCTGGAAATGCTGCTGTATCCCTGATACA
CTGTGACGCCACCTCCACACCCCCATGTACTTTCATCAGTCAATTGCTCTCATGGACA
TGGCGTACATTCTGTCAGTGTGCCAAGATGCTCCTGGACCAGGTATGGGTGTGAATAA
10 GATCTCAGCCCCCTGAGTGTGGGATGCAGATGTTCTTACAGTGCACACTAGCAGGTTCAGAA
TTTTCCCTCTAGCCACCATGGCCTATGACCGCTACGTGGCCATCTGCCATCCTCTCCGTTA
CCCTGTCCTCATGAACCATAGGGTGTGTCTTCTGTATCAGGCTGCTGGTCTGGGCT
CAGTGGATGGCTTCACATTCACTCCCACCATGACCTCCCTCCGTGGATCCGGGA
GATTCA^TCATTTCTGTGAAGTTCTGTGTATTGAATCTCCTGCTCAGACACCTCAC
15 TCTATGAGATTTCATGTA^TCTGTGTGTCTCATGCTCCTCATCCCTGTGGTATCATT
TCAAGCTCCTATTACTCATCCTCCTCACCATCCACGGGATGAAC^TCAGCAGAGGGCCGGAA
AAAAGGCTTTGCCACCTGCTCCTCCACCTGACTGTGGTCATCCTCTATGGGGCTGCC
ATCTACACCTACATGCTCCCAGCTCCTACCACACCCCTGAGAAGGACATGATGGTATCTG
TCTTCTATACCATCCTACTCCAGTGGTGAACCCCTTAATCTATAGTCTAGGAATAAGGAT
20 GTCATGGGGCTCTGAAGAAATGTTAACAGTGGAACCTGCCTTCAAAAGCTATGGAG
TAG (SEQ ID NO: 434).

AOLFR233 sequences:

25 MANITRMANHTGKLD^TFILMGLFRSKHPALLSVVIFVVFLKALSGNAVLILLIHCDAHLHSPMY
FFISQLSLMDMAYISVTPKMLLDQVMGVNKVS^APECGMQMFLYLTLAGSEFFLLATMAYDR
YVAICHPLRYPVLMNHRVCLFLASGCWFLGSVDGFMLTPITMSFPFCRSWEIHHFFCEVPAVTI
LSCSDTSLYETL^TMYLCCVLM^TLIPV^TI^ISSSYLL^TLLTVH^TRMNSAERKKAFA^TCSSHL^TV^VILFY
GA^AYYTYMLPSSY^HT^PE^KD^MM^VS^VF^YT^IL^TP^VLNPLIYSLRNKDVMGALKMLTVRFVL
(SEQ ID NO: 435).

30 ATGGCCAACATCACCAAGGATGGCCAACCACACTGGAAAGTGGATTTCATCCTCATGGGAC
TCTTCAGACGATCCAAACATCCAGCTACTTAGTGTGGTCATCTTGTGGTTTCCTGAAG
GCGTTGTCTGGAAATGCTGCTGTATCCTCTGATACACTGTGACGCCACCTCCACAGCC
CCATGTACTTTTCATCAGTCAATTGTCTCATGGACATGGCGTACATTCTGTCAGTGTG
35 CCCAAGATGCTCCTGGACCAGGTATGGGTGTGAATAAGGTC^TCAGCCCTGAGTGTGGG
ATGCAGATGTTCTCTATCTGACACTAGCAGGTTCGGAATTTCCTCTAGCCACCATGGC
CTATGACCCTACGTGGCCATCTGCCATCCTCTCCGTTACCC^TGCTCTCATGAACCATAGG
GTCTGTCTTCTGGCATGGC^TTGGCTGCTGGTCTGGCTCAGTGGATGGCTCATGCTCAC
TCCCACCATGAGCTCCCCTCTGAGATCCTGGGAGATT^TCATCATTCTCTGTGAAG
40 TCCCTGCTGTAACGATCCTGTCTGCTCAGACACCTCACTCTATGAGACCC^TCATGTACCTA
TGCTGTCTCTATGCTCCTCATCCCTGTGACGATCATTTCAAGCTCCTATTACTCATCCT
CCTCACCGTCCACAGGATGAAC^TCAGCAGAGGGCCGGAAAAGGCC^TTGCCACCTGCTC
CTCCCACCTGACTGTGGCATCCTCTATGGGGCTGCC^TTACACCTACATGCTCCCCA
GCTCCTACCACACCCCTGAGAAGGACATGATGGTATCTGCTCTATACCACCTCACTCC
45 GGTGCTGAACCCCTTAATCTATAGTCTAGGAATAAGGATGT^TCATGGGGCTCTGAAGAAA
ATGTTAACTGTGAGATCGTCCCTTAG (SEQ ID NO: 436).

AOLFR234 sequences:

50 MPNSTTVM^TEFLLMRFS^TVWTLQILHSASFFMLYLV^TLMGNILIVTV^TCDSSLHMPMYFFLRN
LSILDACYISVTP^TPTSCVNLLD^TSTISKAGCVAQVFLVVFFVYVELLFLTIMAHD^TRYVAVCQPL
HYPVIVNSRICQMTLASLLSGLVYAGMHTGSTFQLPFCRSNVIHQFFCDIPSLLKLSCSDTFSNE
VMIIVSALGVGGGCFIFI^TRSYIHF^TSTVLGFPRGADRTKA^TSTC^TPHLVVS^TFLSSCSSVYL^TRPP
AIPAA^TQDL^TLISGFYSIMPLFN^TPIYSLRNKQIKVAIKKIMKR^TYSENV (SEQ ID NO: 437).

55 ATGCCAATTCAACCACCGT^TGATGGAAATTCTCCTCATGAGGTTCTGATGTGTGGACAC
TACAGATTTCATCATTCTG^TCATCCTCTTATGTTGTATTGGTA^TCTAATGGGAAACATC

CTCATTGTGACCGTCACCACCTGTGACAGCAGCCTTCACATGCCCATGTACTTCTCCTCAG
 GAATCTGTCTATCTGGATGCCTGCTACATTCTGTTACAGTCCTACCTCATGTGTCAATT
 CCCTACTGGACAGCACCACCATTTCTAAGGGGGATGTGTAGCTCAGGTCTCCTCGTGGT
 TTTTTTGTATATGTGGAGCTCTGTTCTCACCATATTGGCTCATGACCGCTATGTGGCTG
 5 TCTGCCAGCCACTTCACTACCCGTGATCGTAACCTCGAATCTGCATCCAGATGACACT
 GGCCCTCCACTCAGTGGCTTGTCTATGCAGGCATGCACACTGGCAGCACATTCCAGCTG
 CCCTCTGTGGTCCAACGTTATCATCAATTCTCTGTGACATCCCCTCTGCTGAAGCT
 CTCTGCTCTGACACCTCAGCAATGAGGTATGATTGTCTCTGCTCTGGGGTAGGT
 GGCCTGTTCATCTTATCATCAGGCTTACATTCACATCTTGCACCGTGCTCGGGTT
 10 TCCAAGAGGAGCAGACAGAACAAAGGCCCTTCCACCTGCATCCCTCACATCCTGGTGGTG
 TCAGTCCTCCTCAGTTCATGCTCTCTGTGTAACCTCAGGCCACCTGCGATACCTGCAGCCAC
 CCAGGATCTGATCCTTCTGGTTTATTCCATAATGCCTCCCTCTTAAACCTATTATTA
 CAGTCTTAGAATAAGCAAATAAGGTGCCATCAAGAAAATCATGAAGAGAATTTTA
 TTCAGAAAATGTGTAA (SEQ ID NO: 438).

15

AOLFR235 sequences:

MDGVNDSSLQGFVLMGIDSHPQLEMIFFIAILFSYLLTLLGNSTIILSRLEARLHTPMYFFLSNL
 SSLDLAFATSSVPQMLNWLWPGPKTISYGGCITQLYVFLWLGATECILLVVMAFDRLYVAVCRPL
 20 RYTAIMNPQLCWLLAVIACLGGLGNSVIQSTFTLQLPLCGHRRVEGFLCEVPAMIKLACGDTSL
 NQAVLNGVCTFFTAVPLSIVISYCLIAQAVLKIRSAEGRRAFNTCLSHLLVVFLFYGSASYGY
 LLPAKNSKQDQGKFISLFYSLVTPMVNPLIYTLRNMEVKGALRLLGKGREVG (SEQ ID NO:
 439).

25

ATGGACGGGGTGAATGATAGCTCCTGCAGGGCTTGTCTGATGGCATATCAGACCATC
 CCCAGCTGGAGATGATCTTTTATAGCCATCCTCTCTCTTCTCTTCTGACCCACTTGGG
 AACTCAACCACATCATCTGCTTCCGCCCTGGAGGGCCGGCTCCATACACCCATGTACTTCTT
 CCTCAGCAACCTCTCTCTTCTGGACCTGCTTCTGCTACTAGTTAGTCCAGTCCCCAAATGCTGA
 TCAATTATGGGGACCAGGCAAGACCATCAGCTATGGTGGCTGCATAACCCAGCTATGT
 CTTCTTGGCTGGGGCCACCGAGTGCATCCTGCTGGTGGTATGGCATTGACCGCTAC
 30 GTGGCAGTGTGCCGGCCCTCCGCTACACCGCCATCATGAACCCCCAGCTCTGCTGGCTGC
 TGGCTGTATTGCCCTGGGCTGGGCAACTCTGTGATCCAGTCACATTCACTCT
 GCAGCTCCATTGTGTGGGACCGGAGGGGGATTCCCTCTGCGAGGTGCCAT
 GATCAAACCTGGCTGTGGCACAAGCTCAACCAGGCTGTGCTCAATGGTGTCTGCACC
 TTCTCACTGCAGTCCCACTAAGCATCATCGTATCTCTACTGCCTATTGCTCAGGAGT
 35 GCTGAAAATCCGCTCTGCAGAGGGGAGGCAGAAGGCCTCAATACGTGCCTCTCCCATCT
 GCTGGTGGTGTCTCTTCTATGGCTAGCCAGCTATGGGTATCTGCTTCCGGCCAAGAAC
 AGCAAACAGGACCAGGGCAAGTCAATTCCCTGTTACTCGTGGTCACACCCATGGTGA
 ATCCCTCATCTACACGCTGCCAACATGGAAGTGAAGGGCGACTGAGGAGGTTGCTGG
 GGAAAGGAAGAGAAGTTGGCTGA (SEQ ID NO: 440).

40

AOLFR236 sequences:

MTSQERDTAIFIYSINVSVAKGMTSRVCEKMTMTENPNQTVVSHFFLEGLRYTAKHSSLFL
 LFLLIYSITVAGNLLLTVGSDSHLSLPMYHFLGHSFLDACLSTVTVPKVMAGLLTLDGKVIS
 45 FEGCAVQLYCFHFLASTECFLYTVMAYDRYLAICQPLHYPVAMNRRMCAEMAGITWAIGATH
 AAIHTSLTFRLLYCGPCHIAYFFCDIPPVLKLAETDTTINELVMLASIGIVAAGCLILIVISYIFIVA
 AVLRIRTAQGRQRRAFPCTAQLTVLYYYYVPPVCIYLQPRSSEAGAGAPAVFYTIVTPMLNPFTY
 TLRNKEVKHALQRLCSSFRESTAGSPPP (SEQ ID NO: 441).

50

ATGACATCTCAGGAAAGGGATACAGCTATTTATTCATTAATGTCAGTTGTGCAAAGG
 GGATGACTAGCCGCTCTGTGTGAGAAGATGACCATGACAACGGAGAACCCCAACCAGA
 CTGTGGTGAGCCACTCTTCCCTGGAGGGTTGAGGTACACCGCTAACATTCTAGCCTCTT
 CTTCCTCCTCTCCTCATCTACAGCATCACTGTGGCTGGAAATCTCCTCATCCTCCTAA
 CTGTGGCTCTGACTCTCACCTCAGCTACCCATGTACCAACTCTGGGGCACCTCTCCTTC
 CTGGATGCCCTGTTGTCTACAGTGACAGTGCCCAAGGTATGGCAGGCCCTGCTGACTCTGG
 55 ATGGGAAGGTGATCTCTTGGGGCTGTGCCGTACAGCTTATTGCTTCCACTTCTGGC
 CAGCACTGAGTGCTTCTGTACACAGTCATGCCATGACCGCTATCTGGCTATCTGTCAA

5 CCCCTGCACTACCCAGTGGCCATGAACAGAAGGATGTGAGAAATGGCTGGAATCACC
TGGGCCATAGGTGCCACGCACGCTGCAATCCACACCTCCCTCACCTCCGCCTGCTCTACT
GTGGGCCTTGCACATTGCCTACTTCTCTGCGACATACCCCTGTCCTAAAGCTCGCCTGT
ACAGACACCACCAATTAAATGAGCTAGTCATGCTTGCAGCATGGGCATCGTGGCTGCAGGCT
10 GCCTCATCCTCATCGTTATTCTACATCTCATCGTGGCAGCTGTGTTGCGCATCCGCACA
GCCAGGGCCGGCAGCGGGCCTCTCCCCCTGCAC TGCCCAGCTCAGTGGGTGCTCCTGT
ACTACGTGCCACCTGTCTGTATCTACCTGCAGCCTCGCTCCAGTGAGGCAGGAGCTGGGC
CCCTGCTGTCTCTACACAATCGTAACCCAATGCTCAACCCATTCAATTACACTTGGGA
ACAAGGAGGTGAAGCATGCTCTGCAAAGGCTTGTGCAGCAGCTCCGAGAGTCTACAG
CAGGCAGCCCACCCCCATAG (SEQ ID NO: 442).

AOLFR237 sequences:

15 MDQRNYTRVKEFTFLGITQSRELSQVLFFLVYMTTLMGNFLIMVTVTCESHLHTPMYFLL
RNLSILDICFSSITAPKVLIDLLSETKTISFSGCVTQMFFFHLLGGADVFSLSVMAFDRYIAISKPL
HYMTIMSRGRCTGLIVFLGGGLVHSIAQISLLLPLPVCVPNVLDTFYCDVPQVLKLA
LELMISNNGLVSWFVFFFLLISYTVILMMLRSHTGEGRRAISTCTSHITVVTLHFVPCIVYA
RPFTALPTDTAISVTFTVISPLNPIIYTLRNQEMKLMRKLRRLGQSERILIQ (SEQ ID NO:
443).

20 ATGGATCAGAGAAATTACACCAAGAGTGAAAGAAATTACCTTCCGGAAATTACTCAGTCCC
GAGAACTGAGCCAGGTCTTATTACCTTCCGTGTTGGTGTACATGACAACCTAATGGG
AAACTCCTCATCATGGTACAGTTACCTGTGAATCTCACCTCATACGCCATGTACTTCC
TGCTCCGCAACCTGTCTATTCTGACATCTGCTTTCCATCACAGCTCTAAGGTCTG
25 ATAGATCTCTATCAGAGACAAAAACCATCTCCTCAGTGGCTGTGACTCAAATGTCT
TCTTCCACCTCTGGGGGAGCAGACGTTCTCTCTGTGATGGCGTTGACCGCTAT
ATAGCCATCTCCAAGCCCCCTGCACTATATGACCATCATGAGTAGGGGGCGATGCACAGGCC
TCATCGTGGCTTCTGGTGGACCAATGTTCTGACACTTCTACTGCGATGTCCCCCAGGTCC
30 TCAAACTTGCCTGCACTGACACCTCACTCTGGAGCTCTGTGATGTTCAAATAATGGGTT
AGTCAGTTGGTTGTATTCTCTTCTCCTCATATCTTACACGGTCATTTGATGATGCTGA
GGTCTCACACTGGGAAGGCAGGAGGAAAGCCATCTCCACCTGCACCTCCCACATCACCG
TGGTGACCCCTGCATTCTGTCACCTCAGTCATCTCCCTTGCTCAATCCTATAATTAA
35 CACGCTGAGGAATCAGGAATGAAGTTGGCATGAGGAACACTGAAGAGACGGCTAGGAC
AATCAGAAAGGATTAAATTCAATAA (SEQ ID NO: 444).

AOLFR238 sequences:

40 MAPENFTRVTEFILTVSSCPELQIPLFLVFLVLYVLT MAGNLGIITLTSVDSRLQTPMYFFLRHL
AIINLGNSTVIAPKMLMNFLVKKKTTSFYECATQLGGFLFFFIVSEVMMALAVMAYDRYVAICNP
LLYMMVVSSRLCLLLVLVSLTYLYGFSTAIVVSPCIFSVSYCSSNIINHFYCDIAPLLALSCSDTYIPE
TIVFISAATNLFFSMITLVSYFNIVLSILRIRSPEGRKAFSTCASHMIAVTVFYGTMLFMYLQP
QTNHSLDTDKMASVFYTLVIPMLNPLIYSLRNNNDVNVALKKFMENPCYSFKSM (SEQ ID NO:
445).

45 ATGGCTCCTGAAAATTCAACCAGGGTCACTGAGTTATTCTCACAGGTGTCTAGCTGTC
CAGAGCTCCAGATTCCCTCTTCCGTCTCTAGTGTCTATGTGCTGACCATGGCAGG
GAACCTGGGCATCATCACCCCTCACCAGTGTGACTCTGACATCTCAAACCCCCATGTACTTT
50 TCCTGAGACATCTAGCTATCATCAATCTTGCACACTCTACTGTCATCTGCCCCCTAAATGCTG
ATGAACCTTTAGTAAAGAAGAAAACCTACCTCATTCTATGAATGTGCCACCCAACTGGGAG
GGTTCTTGTCTTATTGTATCGGAGGTAATGATGCTGGCTGTGATGGCCTATGACCGCTA
TGTGGCCATTGTAAACCTCTGCTCTACATGGTGGTGGTGTCTCGCCGGCTCTGCCTCTGC
55 TGGTGTCCCTCACGTACCTCTATGGCTTCTACAGCTATTGTGGTTTCACCTTGTATATTC
TCTGTGTCTTATTGCTCTCTAATATAATCAATCATTTTACTGTGATATTGCACCTCTGTT
AGCATTATCTGCTCTGATAACTACATACCAAGAAACAATAGTCTTATATCTGAGCAACA
AATTGTTTTTCCATGATTACAGTTCTAGTATCTTCAATATTGTTTGCCATTCTA
AGGATACGTTACCAAGAAGGAAAAAGCCCTTCCACCTGCGCTTCGATATGATA

GCAGTCACGGTTTCTATGGGACAATGCTATTATGTATTGCAGCCCCAAACCAACCAACT
CACTGGATACTGATAAGATGGCTCTGTGTTTACACATTGGTATTCCATGCTGAATCC
CTTGATCTACAGCCTGAGGAATAATGATGTAAATGTTGCCTAAAGAAATTCAATGGAAAAT
CCATGTTACTCCTTAAATCAATGTAA (SEQ ID NO: 446).

5

AOLFR239 sequences:

MDPQNYSLVSEFVLHGLCTSRLQNFNFIFFFGVVVAIMLGNLILVTVISDPCLHSSPMYFLLG
NLAFLDMWLASFATPKMIRDQLSDQKLISFGGCMAQIFFLHFVGAEMVLLVSMAYDRYVAIC
KPLHYMTLMSWQTCIRVLASWVVGFGVHSISQVAFTVNLPCGPNEVDSFFCDLPLVIKLCM
10 DTYVLGIIIMSDSGLLSCFLLLISYTVILLAIRQRAAGSTSALSTCSAHIIVVTLFFGPCIIV
YVRPFSRFSVDKLLSVFYTIFTPLLNPIIYTLRNEEMKAAMKKLQNRRVTFQ (SEQ ID NO: 447).

15 ATGGACCCACAGAACTATTCCCTGGTGTCAAGAATTGTGTTGCATGGACTCTGCACCTCAC
GACATCTTCAAAATTTCCTTATATTTCCTGGGGCTATGTGCCATTATGCTGGGT
AACCTTCTCATTTGGTCACTGTAATTCTGATCCCTGCCCTGCACTCCTCCCTATGTACTT
CCTGCTGGGAACCTAGCTTCCCTGGACATGTGGCTGGCCTCATTGCCACTCCAAGATG
ATCAGGGATTCCCTAGTGTATCAAAAACCTATCTCCTTGGAGGATGTATGGCTAAATCT
TCTTCTGCACTTACTGGTGGGGCTGAGATGGTGTCTGGTTCCATGGCCTATGACAG
ATATGTGGCCATATGCAAACCCCTGCATTACATGACTTGTAGAGTTGGCAGACTTGCATC
20 AGGCTGGTGTGGCTTCACTGGGCTGGATTGTGCACTCCATCAGTCAGTCAGTGGCTTCA
CTGTAATTTCCTTACTGTGGCCCCAATGAGGTAGACAGCAGCTTCTGTGACCTCCCTG
GTGATCAAACATTGCCTGCACTGGACACCTATGTCTGGGTATAATTATGATCTCAGACAGTG
GGTGTCTTCCCTGAGCTGTTCTGCTCCTCCTGATCTCCTACACCGTGTACCTCCCTCGCT
25 ATCAGACAGCGTGTGGCGTAGCACATCCAAAGCAGCTTCCACTTGCTCTGCAACATATCA
TGGTAGTGAACGCTGTCTTGGCCCTTGCAATTGTGTTATGTGCGGGCTTCACTGAGGTTC
TCTGTGGACAAGCTGCTGTCTGTTTATACCATTTTACTCCACTCCTGAACCCATTAT
CTACACATTGAGAAATGAGGAAGATGAAAGCAGCTATGAAGAAACTGCAAAACCGACGGGT
GACTTTCAATGA (SEQ ID NO: 448).

30 **AOLFR240 sequences:**

MAGENHTTLPEFLLLGFSDLKALQGPLFWVVLVYLVTLGNSLIILLTQVSPALHSPMYFFLR
QLSVVLFYTTDIVPRTLNLGSPHPQAISFQGCAAQMYFIVLGISECCLLTAMAYDRYVAIC
QPLRYSTLLSPRACLAMVGSSWLTGIIATTHASLIFSLPFRSHPIPHFLCDILPVLRLASAGKHR
35 SEISVMTATIVFIMIPFSLIVTSYIRILGAILAMASTQSRRKVFPSTCSSHLLVVSLLFFGTASITYIRPQ
AGSSVTTDRVLSLFYTVITPMNLNPPIYTLRNKDVRRALRHLVKRQRPSP (SEQ ID NO: 449).

40 ATGGCTGGGGAAAACCATACTACACTGCCCTGAATTCCCTCTGGGATTCTCTGACCTCA
AGGCCCTGCAGGGCCCCCTGTTCTGGGTTGGCTCTGGTCTACCTGGCACCTGCTGGG
TAACCTCCCTGATCATCCTCCTCACACAGGTCAGCCCTGCCCTGCACTCCCCCATGTACTTCT
TCCCTGCCAACTCTCAGTGGTGGAGCTCTACACCACTGACATCGTCCCCAGGACCC
GCCCAATCTGGGCTCCCCGCATCCCCAGGCCATCTCTTCCAGGGCTGTGCAGCCCAGATG
TACGTCTTCAATTGTCTGGCATCTGGAGTGTCTGCTCACGCCATGGCTATGACC
GATATGTTGCCATCTGCCAGCCCCTACGCTATTCCACCCCTTGTAGGCCACGGGCTGCTT
GCCATGGTGGGGCTCTCCTGGCTCACAGGCATCATCACGCCACCCATGCCCTCC
45 ATCTTCTCTACCTTTCTGCAGCCACCGATCATCCGCACCTTCTCTGTGACATCCCTGCC
AGTACTGAGGCTGGCAAGTGCTGGGAAGCAGCAGGAGCGAGATCTCCGTATGACAGCCAC
CATAGTCTCATTATGATCCCCCTCTCTGATTGTGACCTCTTACATCCGCATCTGGGTG
50 CCATCCTAGCAATGCCCTCACCCAGAGGCCCGCAAGGTCTTCTCCACCTGCTCCCTCCA
TCTGCTCGTGGTCTCTCTTGGAACAGCCAGCATCACCTACATCCGCCAGGCA
GGCTCCTCTGTTACACAGACCGCGTCTCAGTCTTCTACACAGTCATCACACCCATGCT
CAACCCCATCATCACACCCCTCGAACAAAGGACGTGAGGAGGGCCCTGCGACACTTGGT
GAAGAGGCAGCGCCCCCTCACCCCTGA (SEQ ID NO: 450).

AOLFR241 sequences:

55 MPQILIFTYLNMFYFFPPLQILAENLTMVTEFLLGFSSLGEIQLALFVVFLFLYLVILSGNVTIIS
VIHLDKSLHTPMYFFLGILSTSETFYTFVILPKMLINLLSVARTISFNCCALQMFFLGFAITNCLL

LGVMGYDRYAAICPLHYPTLMSWQVCGKLAACAAIGGFLASLTVVNLVFSLPFCSANKVNHYFCDISAVILLACTNTDVNEFVIFICGVVLVVPFLICVSYLCILRTILKIPSAEGRKAFSTCASHLSVVIVHYGCASFYLRPTANYVSNKDRLVTVTYTIVTPLLNPMVYSLRNKDVLQLAIRKVLGKKGSALKYN (SEQ ID NO: 451).

5

ATGCCCAAATTCTTATTCACATACCTGAATATGTTTACTCTTCCCCCTTGAGATCTTGGCAGAAAACCTCACCATGGTACCGAATTCCTGTTGCTGGGTTTCCAGCCTGGTGAATTCACTGGCCCTTTGTAGTTTCTGTATCTAGTCATTCTAGTGGCAAAGTCACCATTATCAGTGTACCCACCTGGATAAAAGCCTCACACACCAATGTACTCTCC TTGGCATTCTCTCAACATCTGAGACCTCTACACCTTGTCAATTCTACCCAAAGATGCTCATCAATCTACTTCTGTGGCCAGGACAATCTCCTCACTGTTGTCTTCAAATGTTCTTCTCCTGGTTTGCATTACCAACTGCCTGCTATTGGGTGTGATGGGTATGATCGCTATGCTGCCATTGTCAACCCTGCATTACCCACTCTTATGAGCTGGCAGGGTGTGGAAAAGTGCAGCTGTGCAATTGGTGGCTCTTGGCCTCTTACAGTAGTAAATTAGTTAGTTCAAGCTCCCTTTGTAGCGCCAACAAAGTCACATTACTCTGTGACATCTCAGCAGTCATTCTCTGGCCTGTACCAACACAGATGTTAACGAATTGTGATATTCAATTGTGGAGTTCTGTACTTGTGGTCCCTTCTGTATTCTGTCTTATCTGTGCTTCTTACTCTGCAATTCTGAGGACTATCCTGAAGATTCCCTCAGCTGAGGGCAGACGGAAAGCGTTTCCACCTGCGCTCTCACCTCAGTGTGTTATTGTTCATTATGGCTGTGCTTCCTCATCTACCTGAGGCCAACAGCAAACATATGTGTGCAACAAAGACAGGCTGGTGACGGTACACAGATTGTCACTCCATTACTAAACCCCATGGTTCTCTAAACTATATAATTGA (SEQ ID NO: 452).

AOLFR242 sequences:

25 MNTTLFHPYSFLLGIPGLESMHLWVGFPFFAVFLTAVLGNITILFVIQTDSSLHHPMFYFLAILS SIDPGLSTSTIPKMLGTFWFTLREISFEGCLTQMFFIHLCTGMESAVLVAMA YDCYVAICDPLCY TLVLTNKVVSVMALAIFRPLVVFIPVLFILRLPFCGHQIIPHTYGEHMGIAIRLSCASIRVNIYGLCAISILVFDIIAIVISYVQILCAVFLSSHDARLKAFTCGSHVCVMLTFYMPAFFSFMTHRFGRNIPHFIHILLANFYVVVPPALNSVIYGVRTKQIRAQVLKMFNFN (SEQ ID NO: 453).

30

ATGAATACCACTCTATTCTACCTTACTCTTCTGGAAATCCTGGCTGGAAAGTATGCATCTCTGGGTTGGTTTCTTCTTCTGCTGTTGCTTCCTGACAGCTGTCTGGAAATATCACCATCCTTGTGATTCACTGACAGTAGTCTCCATCATCCCATGTTCTACTCCTGGCAGCTCTGGTTTACCTGAGAGAAAATCTCTTGAAGGATGCCCTACCCAGATGTTCTCATCCACCTGTGCACTGGCATGGAATCAGCTGTGCTTGTGGCCATGCCCTATGATTGCTATGTGGCCTACTGTGACCCCTTTGCTACACGTTGGTGCTGACAAACAAGGTGGTGTCAAGTATGGCACTGGCCATCTTCTGAGACCCTAGTCTTGTCAACCCCTTGTCTATTATCTAAGGCTTCCATTGTGGACACCAAATTATCCTCATACTTATGGTGAGCACATGGCATTGCCCTGCTGCTGAGCATCAGGGTTAACATCATCTATGGCTTATGTGCCATCTCTATCCTGGCTTGTGACATCATAGCAATTGTCTTCTTCTATGTACAGATCCTTGTGCTGTATTCTACTCTTCACATGATGCACGACTCAAGGCATTGACCCATGTGGCTCTCATGTGTGTGTCATGTTGACTTCTATATGCCTGCATTCTCATGACCCATAGGTTGGTGGAAATATACCTCCTTATCCACATTCTCTGGCTAATTCTATGTAGTCATTCCACCTGCTCTCAACTCTGATTATGGTGTGAGAACACAGATTAGAGCACAAGTGTGAAATGTTTCAATAAAATAA (SEQ ID NO: 454).

AOLFR243 sequences:

50 MEQVNKTVVREFVVLGFSSLARLQQLLFVFLYLFTLGTNAIIISTIVLDRALHTPMYFFLAISSCSEICYTFVIVPKMLVDLSQLKKTISFLGCAIQMFSLFFGSSHSFLAAMGYDRYMAICNPLRYSVLMGHGVCMGLMAAACACGFTVSLVTTSLVFHLPFHSSNQLHHFFCDISPVLKLASQHSGFSQLVIFMLGVFALVPIPLLILVSYIRIISAILKIPSSVGRYKTFSTCASHLIVVTVHYSCASFYLRPKTNYTSSQDTLISVSYTILTPLFNPMIYSLRNKEFKSALRRTIGQTFYPLS (SEQ ID NO: 455).

55

ATGGAGCAAGTCATAAGACTGTGGTGAGAGAGTTCGTCGTCCTCGGCTCTCATCCCTGGCCAGGCTGCAGCAGCTCTTGTATCTCCTGCTCCTACCTGTTACTCTGGCACC

5 AATGCAATCATATTCCACCATTGTGCTGGACAGAGCCCTCATACTCCCAGTACTTCTT
 CCTGCCATCCTTCTGCTGAGATTGCTATACCTTGCTATTGACCCAGATGCTGG
 TTGACCTGCTGCTCCAGAAGAAGACCATTTCTTCTGGCTGCCCCATCCAAATGTTTCC
 TTCTCTTCTGGCTCTCACTCCTCTGCTGGCAGCCATGGGCTATGATCGCTATAT
 10 GCCATCTGTAACCCACTGCCTACTCAGTGCTCATGGGACATGGGGTGTATGGGACTA
 ATGGCTGCTGCCTGTGCCTGTGGCTTCACTGTCCTCCCTGGTCACCACCTCCCTAGTATTTCA
 TCTGCCCTTCCACTCCTCCAACCAGCTCCATCACTTCTGTGACATCTCCCCTGTCTTA
 AACTGGCATCTCAGCACTCCGGCTTCAGTCAGCTGGTCATATTGCTGGTGTATTG
 15 CTGGTCATTCCTCTGCTACTTATCCTAGTCTCCTACATCCGCATCATCTGCCATTCTAA
 AAATCCCTCCCTGGAAAGATACAAGACCTCTCCACCTGTGCCTGCCATCTCATTG
 GTAAGTTCACTACAGTTGTGCCTCTTCATCTACTTAAGGCCAAGACTAATTACACTTC
 AAGCCAAGACACCCCTAATATCTGTGTCATACACCATCCTACCCATTGTTCAATCCAATG
 ATTATAGTCTGAGAAATAAGGAATTCAAATCAGCCCTACGAAGAACAAATCGGCCAAACT
 TTCTATCCTCTTAGTTAA (SEQ ID NO: 456).

15 **AOLFR244 sequences:**

MWQEYYYFLNVFFPLKVCCLTINSHVILLPWECYHLIWLPYIGTTVGSMEYNTSSTDFTF
 MGLFNRKETSGLIFAIISIIFTALMANGVMIFIQTDLRLHTPMFLLSHLSIDMMYIISTIVPKM
 20 LVNYLLDQRTISFVGCTAQHFLYLTVAEFFLGLMAYDRYVAICNPLRYPVLMSSRVCWMI
 IAGSWFGGSLDGFLTPITMSFFPCNSREINHFFCEAPAVLKLACADTALEYTVMYVCCVLMILL
 IPFSVVLASYARILTTVQCMSSVEGRKKAFATCSSHMTVVSFYGAAMYTYMLPHSYHKPAQ
 DKVLSVFYTIITPMLNPLIYSLRNKDVTGALKRALGRFKGPQRVSGGVF (SEQ ID NO: 457).

25 ATGTGGCAAGAATACTATTTAAATGTTCTTCCACTTTAAAAGTTGCTGCCAAC
 AATTAATTACATGTTGTTATTTACTGCCCTGGGAATGCTATCATCTTATTTGAAGATAT
 TACCTTATATCGGCACAACGTAGGATCAATGGAAGAGTACAACACATCCTCTACAGACTT
 CACITTCATGGGGCTTCAACAGAAAGAAACCTCAGGTCTTATTTGCCATCATCTCT
 ATCATCTTCTTCACCGCACTGATGCCAATGGGGTTATGATCTCCTGATCCAACAGATT
 30 TGCGCCTTCATACACCCATGTTACCTCTCAGCCACCTTCTTAATTGACATGATGTAT
 ATTCCACTATTGCTCTAACAGATGCTGGTAATTACCTGCTGGATCAAAGGACCATTCTCTT
 TGTTGGGTGACAGCTAACACTTCTTACCTTACCCCTGTGGGAGCTGAATTCTCCTG
 CTGGGCCTCATGGCTATGACCGCTATGTGGCCATTGCAACCCCTCTGAGATACCCCTGTCC
 TCATGAGCCGCCGGGCTGTGGATGATTATAGCAGGGTCTGGTTGGGGCTTTGG
 35 TGGCTTCTCTTAACCCCCATCACCATGAGCTTCCCTCTGCAATTCCCGGGAGATTAAAC
 ACTCTCTGTGAGGCCAGCAGCAGTGAAGTGGCATGTGCAGACACAGCCCTACGA
 GACAGTGATGTATGTGCTGTGTTGATGCTGCTGATTCTTCTCTGATGCTCTGCTT
 CCTATGCCGAATCTGACTACAGTTCACTGAGCTCAGTGGAGGGCAGGAAGAAGG
 CATTGCCACTGCTCATCCCACATGACTGTGGTGTCTTCTGACGGGCTGCCATGTAC
 40 ACCTACATGCTGCCACATTCTTACCAAGCCAGCCCAGGACAAAGTCTCTGTGTTT
 ACACCATTCTCACACCCATGCTGAACCCCTCATCTACAGCTTAGAAACAAGGATGTGAC
 TGGAGCTCTGAAGAGGGCTTGGGGAGGTTCAAGGGCTCTAAAGGGTGTAGGAGGTGT
 CTTTGA (SEQ ID NO: 458).

50 **AOLFR245 sequences:**

45 MDLKNGSLVTEFILLGFFGRWELQIFFVTSLSIYGATVMGNILIMVTVCRLSPLYFLLGN
 LSFLDMCLSTATTPKMIIDLLTDHKTISVWCVTQMFFMHFFGGAEMTLLIIMAFDRYVAICKP
 LHYRTIMSHKLLKGFAILSWIIGFLHSISQIVLTMNLPFCGHNVINNIFCDLPLVIKLA
 CIEITYTLELFVIADSGLLSFTCFILLVSYIVLVSVPKKSSHGLSKALSTLSAII
 VVTLLFGPCIFIYVWPSSLASNKTLAVFYTVITPLNPSIYTLRNKKMQEAIRK
 LRFQYVSSAQNF (SEQ ID NO: 459).

55 ATGGATCTTAAAATGGATCTCTAGTGACCGAGTTTATTTACTAGGATTTGGACGAT
 GGGAACTTCAAATTCTCTTGTGACATTTCCTGATCTACGGTGTACTGTGATGGGA
 AACATTCTCAATTGGTCACAGTGACATGTAGGTCAACCTCTCATTCTCCCTGTACTTTCT
 CCTGGAAATCTCTTTGGACATGTGTCCTCCACTGCCACAAACACCAAGATGATCA
 TAGATTGCTCACTGACCCACAAGACCATCTCTGTGAGATGACTCTGATAATCATGCC
 60 TTGACAGGGT
 CATGCACTCTTGGGGTGCTGAGATGACTCTGATAATCATGCCATTGACAGGGT

5 GTAGCCATATGTAACCCCTGCACTATAGGACAATCATGAGCCACAAGCTGCTAAAGGGG
 TTTGCGATACTTTCATGGATAATTGGTTTTACACTCCATAAGCCAGATAGTTTAACAAT
 GAACCTGCCTTCTGGCCACAATGTCATAAAACAACATATTGTGATCTCCCTTGTGA
 TCAAGCTTGCTTGCATTGAAACATACACCCCTGGAATTATTGTCAATTGCTGACAGCGGGCT
 10 GCTCTTTCACCTGTTCATCCTCTGCTTGTTCATACATTGTCATCCTGGTCAGTGTACC
 AAAAAAAATCATCACATGGGCTCTCAAGGCCTGTCCACATTGTCCTGCCACATCATTGTG
 GTCACTCTGTTCTGGACCTGTATTTTATCTATGTTGCCATTCACTAGTAGTTGGCAAG
 CAATAAAACTCTGCCGTATTATACAGTTACACACCCCTACTGAATCCGAGTATTATA
 CCCTGAGAAAATAAGAAAATGCAAGAGGCCATAAGAAAATTACGGTTCAATATGTTAGTT
 CTGCACAGAATTCTAG (SEQ ID NO: 460).

AOLFR246 sequences:

15 MSPENQSSVSEFLLLGLPPEQQAVFFTLFLGMYLTTVLGNLLIMLLIQLDSHLHTPMYFFLSH
 LALTDISFSSVTVPKMLMDMRTKYKSILYEECISQMYFFIFFTDLDLSFLITSMAYDRYVAICHPL
 HYTVIMREELCVFLVAVSWILSCASSLSHTLLLRLSFCAANTIPHVFCDLAALLKLSCSDIFLNE
 LVMFIVGVVVVITLPPMCILVSYGYIGATILRVPSTKGHIKALSTCGSHLSVVSLYYGSIFGQYLF
 PTVSSSIDKDVIVALMYTVVTPMLNPFIYSLRNNDMKEALGKLFSRATFFSW (SEQ ID NO:
 461).

20 ATGAGCCCTGAGAACCAAGAGCAGCGTGTCCGAGTTCCCTCTGGGCCCTCCCCATCCGGC
 CAGAGCAGCAGGCTGTGTTCTCACCTGTTCTGGCATGTACCTGACCACGGTGCTGGG
 25 GAACCTGCTCATCATGCTGCTCATCCAGCTGGACTCTCACCTCACACACCCCATGTACTCT
 TCCTCAGCCACTTGCTCTCACTGACATCTCCTTTCATCTGTCACTGTCCCTAAGATGCTG
 ATGGACATGCGGACTAAGTACAATCGATCCTCATGAGGAATGCAATTCTCAGATGTATT
 30 TTTTATAATTTTACTGACCTGGACAGCTCCTTATTACATCAATGGCATATGACCGATAT
 GTGCCATATGTCACCCCTCTCACTACACTGTCATCATGAGGGAAAGAGCTCTGTGCTTCTT
 AGTGGCTGTATCTGGATTCTGTCTTGCCAGCTCCCTCTCACACCCCTCTGACCC
 35 GGCTGTCTTCTGTGCTGCAACACATCCCCATGTCCTGTGACCTTGCTGCCCTGCTC
 AAGCTGTCTGCTCAGATATCTCCTCAATGAGCTGGTCATGTTCACAGTAGGGGTGGTGG
 TCATTACCCGCCATTATGTTATCCTGGTATCATGGTACATTGGCTACATTGGGCCACCATCTG
 AGGGTCCCTCAACCAAAGGGATCCACAAAGCATGGCCACATGTGGCTCCATCTCTG
 TGGTGTCTCTATTATGGGCAATATTGGCAGTACCTTCTCCGACTGTAAGCAGTTCT
 ATTGACAAGGATGTCATTGTGGCTCTCATGTACACGGTGGTCACACCCATGTTGAACCCCT
 TTATCTACAGCCTAGGAACAGGGACATGAAAGARGCCCTGGAAACTCTCAGTAGAG
 CAACATTCTCCTGGTACATCTGACTTTAAAAAATTAG (SEQ ID NO: 462).

AOLFR247 sequences:

40 MGQHNLTVLTEFILMELTRRPELQIPLFGVFLVIYLITVVGNLTMILTKLDSHLHTPMYFSIRHL
 ASVDLGNSTVICPKVLANFVVDRNTISYYACAAQLAFFLMISEFFILSAMAYDRYVAICNPLL
 YYVIMSQRQLCHVLVGQYLYSTFQALMFTIKIFLTFCGSNVISHFYCDDVPLPMLCSNAQEIE
 LLSILFSVFNLISSFLIVLVSYMLLLAICQMHSAEGRKKAFTCGSHLTVVVVFYGSLLFMYMQ
 PNSTHFFDTDKMASVFYTLVPMNPLIYSLRNNEEVKNAFYKLFEN (SEQ ID NO: 463).

45 ATGGGCCAACACAATCTAACAGTCTAACTGAATTCTGATGGAACTCACAAGGGCGC
 CTGAGCTGCAGATTCCCTTTGGAGTCCTCGTCATCTACCTAACAGTGGTGGGC
 AACCTAACTATGATCATTGACCAAACCTGGACTCCCACCTACATACACCTATGTACTTT
 TATCAGACATTGGCTCTGTTGATCTGGTAATTCTACTGTCATTGTCCTCAAGGTGCTGG
 CAAATTGTTGATGAAACTATTCTCATGATGTGCTGCACAGCTGGCATT
 50 TTCCTTATGTTCAATTATCAGTGAATTCTCATCCTGTCAGCATGGCTATGACCGCTATGT
 GGCATTGTAACCCCTGCTTATTATGTTATTATGTCAGCGACTGTGTCATGTACTGG
 TGGCATTCAATATCTACAGCACATTTCAGGCTCTGATGTTCACTATTAAAGATTTACA
 TTGACCTTCTGTGGCTTAATGTCATCAGTCATTACTGTGATGATGTTCTTGTAC
 TATGCTTGTCAAATGCAACAGGAAATAGAATTGTTGAGCATACTATTCTGTATTAAATT
 TGATCTCCCTCTGATAGTCATTAGTGTCTACATGTTGATTGTTAGCTATATGTCAA
 55 ATGCATTCTGCAGAGGGCAGGAAAAAGCTTCTCCACATGTGGTCCCATITGACAGTGG
 TGGTTGTGTTCTATGGGTCTACTCTCATGTACATGCAGCCAACTCACTCTT

GATACTGATAAAATGGCTCTGTGTTTACACTTAGTAATCCCCATGCTAACCCCTTGAT
TTACAGCTTAAGAACGAAGAGGTGAAAAATGCCITCTATAAGCTCTTGAGAATTGA
(SEQ ID NO: 464).

5 **AOLFR248 sequences:**

MPCMPCALPTGGLPHPQHTMMEIANVSSPEVFVLLGFSTRPSLETVLFIVVLSFYMVSILNGNI
IILVSHTDVHLHPTMVFYFLANLPFLDMSFTTSIVPQLLANLWGPQKTISYGGCVVQFYISHWLG
ATECVLLATMSYDRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTSMVGSTLTMLLPLCG
10 NNCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVVLPLGLILVSYGHIIARAVLKIRSAEGR
RKAFTNCSSHVAVVSFLYGSIIIFMYLQPAKSTSHEQKFIALFYTVVTPALNPYIYTLRNEVKS
ALRHMVLENCCGSAGKLAQI (SEQ ID NO: 465).

15 ATGCCCTGTATGCCCTGTGCTCTTCCCACAGGTGCCCTTGGCCCCACAGCATAACAT
GATGGAAATAGCCAATGTGAGTTCTCCAGAAGTCTTGTCTCCTGGGCTTCTCCACACGA
CCCTCACTAGAAACTGTCCCTCTCATAGTTGTCTGAGTTTACATGGTATCGATCTTGG
CAATGGCATCATCATTCTGGCTCTCCATACAGATGTGACCTCCACACACCTATGTA
20 CCTTGTCCAACCTCCCCCTCCTGGACATGAGCTTACCAACAGCAGCATTGTCCCACAGCTCCTG
GCTAACCTCTGGGGACCAACAGAAAACCATAACGCTATGGAGGGTGTGGTCCAGTTCTAT
ATCTCCCATTGGCTGGGGCAACCGAGTGTGTCTGCTGGCCACCATGTCCTATGACCGCT
ACGCTGCCATCTGCAGGCCACTCATTACACTGTCTTATGCATCCACAGCTTGCCTTGG
GCTAGCTTGGCCTCTGGCTGGGGCTGACCAACAGCATGGTGGGCTCCACGCTCACC
ATGCTCCTACCGCTGTGGAAACAATTGCATCGACCACTCTTGTGCGAGATGCCCTCA
25 TTATGCAACTGGCTGTGTGGATACCAGCCTCAATGAGATGGAGATGTACCTGGCCAGCCT
TGTCTTGTGTCTGCCTCTGGGCTCATCTGGTCTCTACGGCCACATTGCCCGGGCCG
TGTGAAGATCAGGTCAAGCAGAAGGGGGAGAAAGGCATCAACACCTGTTCTCCCACG
TGGCTGTGGTGTCTGTGTTTACGGGAGCATCATCTCATGTATCTCCAGCCAGCAAGAG
CACCTCCCATGAGCAGGGCAAGTTCATAGCTCTACACCGTAGTCACTCTGCGCTG
AACCCACTTATTACACCCTGAGGAACACGGAGGTGAAGAGCGCCCTCCGGACATGGTA
30 TTAGAGAACTGCTGTGGCTCTGCAGGCAAGCTGGCGCAAATTAG (SEQ ID NO: 466).

30 **AOLFR249 sequences:**

MKSQIEKSDLKYRAILQLKVTRMFLLFWVLLLVLRSLLVVMGRGNSTEVTEFHLLGFGVQHEF
QHVLFIVLLIYVTSIGNIGMILLIKTDSRLQTPMVFYFLPQHLAFVDICYTSAITPKMLQSFTEEN
35 NLITFRGCVIQFLVYATFATSDCYLLAIMAMDCYVAICKPLRYPMIMSQTVYIQLVAGSYIIGSI
NASVHTGFTFSLSFCKSNKINHFCDFGLPILALSCSNIDINILDVVFVGFDFLMFTELVIFSYIYIM
VTLKMSSTAGRKKSFSTCASHLTAVTIFYGTLSYMYLQPQSNNSQENMKVASIFYGTVIPMLN
PLIYSLRNKEGK (SEQ ID NO: 467).

40 ATGAAAAGTCAAATTGAAAAAGTGAATTAAATAGAGCCATTATTGCAAAAGTC
ACAAGGATGTTCTGTTCTGGGTCTTCTCTGGTCTTCTAGACTTTGGTAGTCAT
GGTCGAGGAAACAGCACTGAAGTGAATTCATCTGGGATTGGTAGTCAACAC
GAATTTCAGCATGTCCTTTCATTGTACTCTTCTATCTATGTGACCTCCCTGATAGGAAA
TATTGGAATGATCTTACTCATCAAGACCGATTCCAGACTCAAAACACCCATGTACTTTTC
45 CACAACATTGGCTTTGTGATATCTGTTACTCTGCTATCACTCCAAAGATGCTCAA
AGCTTCACAGAAGAAAATAATTGATAACATTGGGGCTGTGTGATACAATTCTAGTT
ATGCAACATTGCAACCAGTGAATGTTACCTCTAGCTATTATGCAATGGATTGTTATGT
TGCATCTGTAAGCCCCCTCGCTATCCATGATCATGTCCTAACAGTCTACATCCAACCTCG
TAGCTGGCTCATATATTAGGCTAATAAAATGCCCTGTACATACAGGTTTACATTTC
50 CTGCTCTCTGCAAGTCTAATAAAATCAATCACTTTCTGTAATGGCTCCCAATTCTGC
CCTTCATGCTCCAACATTGACATCAACATCAATTCTAGATGTTGTCTTGAGGATTGACT
TGATGTTCACTGAGTTGGTCATCATCTTCTACATCTACATTATGGTCACCATCCTGAAG
ATGCTCTACTGCTGGGAGGAAAAATCCTCTCCACATGTGCTCCCACCTGACAGCAG
TAACCATTTCATGGGACACTCTTACATGTACTTACAGCCTCAGTCTAATAATTCTCAG
GAGAATATGAAAGTAGCCTCTATTATGGCACTGTTATTCCATGTTGAATCCTTAAT
55 CTATAGCTTGAGAAATAAGGAAGGAAATA (SEQ ID NO: 468).

AOLFR250 sequences:

5 MENQSSISEFFLRGISAPPEQQQLFGIFLCMYLVTLTGNLLIILAIGSDLHLHTPMYFFLANLSFV
 DMGLTSSTVTKMLVNIQTRHTISYTGCCTQMYFFLMFGDLSFFLAAMAYDRYVAICHPLCY
 STVMRPQVCALMLALCWVLTNIVALTHFLMARLSFCVTGEIAHFFCDITPVLKLSCSDTHINE
 MMVFVLGGTVLIVPFLCIVTSYIHVPAILRVRTRGGVGKAFSTCSSHLCVVCVFYGTLFSAYLC
 PPSIASEEKDIAAAAMYTIVTPMLNPFYSLRNKDMKGALKRLFSHRSIVSS (SEQ ID NO: 469).

10 ATGGAAAACCAATCCAGCATTCTGAATTTCCTCCGAGGAATATCAGCGCCTCCAGAGC
 AACAGCAGTCCCTCTCGGAATTTCCTGTATGTATCTGTACCTTGACTGGAACCTG
 CTCATCATCCTGGCATTGGCTCTGACCTGCACCTCCACACCCCCATGTACTTTTCTTGGC
 CAACCTGTCTTTGTTGACATGGGTTAACGTCTCCACAGTACCAAGATGCTGGTGAAT
 ATACAGACTCGGCATCACACCATCTCTATACGGGTTGCCACAGCAAATGTATTCTTCT
 GATGTTGGTGTACTAGACAGCTTCTTCTGGCTGCCATGGCGTATGCCGATGTGGCC
 ATTGCCACCCCTCTGCTACTCCACAGTCATGAGGCCCCAAGTCTGCCCCAATGCTTGC
 15 ATTGTGCTGGTCCTCACCACATTCGAGGCCCCAAGTCTGCCCCAATGCTTGC
 CTTCTGTGTGACTGGGAAATTGTCACCTTCTGTGACATCACCTCTGTCTGAAGCTG
 TCATGTTCTGACACCCACATCAACGAGATGATGTTCTGTCTGGGAGGGACCGTACTCA
 TCGTCCCCCTTATGCAATTGTCACCTCTACATCCACATTGTGCCAGCTATCTGAGGGTC
 CGAACCCGTGGTGGGTGGCAAGGCCCTTCCACCTGCAGTTCCCACCTCTGCGTTGTT
 20 GTGTGTTCTATGGGACCTCTCAGTGCCTACCTGTGCTCCCTCCATTGCCTCTGAAGAG
 AAGGACATTGCAGCAGCTGCAATGTACACCATACTGACTCCCCTGTTGAACCCCTTATCT
 ATAGCCTAAGGAACAAGGACATGAAGGGGCCCTAAAGAGGCTCTCAGTCACAGGAGTA
 TTGTTCTCTTAG (SEQ ID NO: 470).

AOLFR251 sequences:

25 MEGNKTWITDITLPRFQVGPALIELLCGLFSAFYTLTLLNGNGVIFGIICLDCKLHTPMYFFLSHLA
 IVDISYASNYVPKMLTNLMNQESTISFFPCIMQTFLYLAFAHVECLLIVVMSYDRYADICHPLRY
 NILMSWRVCTVLAVASWVFSFLLALVPLVLRLPFCGPHEINHCEILSVKLACADTWLNQV
 VIFAACVFLVGPLCLVLVSYLRILAAILRIQSGEGRKAFSTCSSHLCVVGFLFFSAIVTYMAPK
 30 SRHPEEQKVLSLFYSLFNPMLNPLIYSLRNAEVKGALRRALRKERLT (SEQ ID NO: 471).

35 ATGGAAGGCAACAAGACATGGATCACAGACATCACCTGCCCGATTCCAGGTTGGTCCA
 GCACTGGAGATTCTCCTCTGGACTTTCTCTGCCCTCTACACTCACCTGCTGGGAA
 TGGGGTCATCTTGGGATTATCTGCCCTGGACTGTAAGCTTACACACCCATGTACTTCTCC
 TCTCACACCTGCCATTGTTGACATATCCTATGCTTCAACTATGCTCCCAAGATGCTGACG
 AATCTTATGAACCAGGAAAGCACCACATCCTTTTCCATGCATAATGCAGACATTCTGT
 ATTGGCTTGTCTACGTAGAGTGTCTGATTGGTGTGATGCTCTATGATCGCTATGCG
 GACATCTGCCACCCCTACGTTACAATATCCTATGAGCTGGAGAGTGTGCACTGCTGG
 40 CTGTTGGCTTCTGGGTGTTGACGTTCTCTGCCCTGGCTCTGGTCCCTTAGTTCTCATCCTGAGG
 CTGCCCTTCTGCCGGCTCATGAAATCAACCACTTCTGTGAAATCCTGCTGCTCTCAAGTT
 GGCCTGTGCTGACACCTGGCTCAACCAGGTGGTCATCTTGAGCCTGCGTGTTCATCCTG
 GTGGGGCCACTCTGCCCTGGTGTCTCTACTTGCCTACCTGCTCTCCACCTTGCCTGGT
 TCCAGTCTGGGAGGGCCGAGAAAGGCCCTCTCCACCTGCTCTCCACCTTGCCTGGT
 45 GGGACTCTCTTGGCAGGCCATTGTCACGTACATGGCCCCCAAGTCCCACATCCTGAG
 GAGCAGCAGAAAGTTCTTCCCTGTTTACAGCCTTTCAATCCAATGCTGAACCCCTGA
 TATATAGCTTAAGGAATGCAGAGGTCAAGGGGCCCTGAGGGAGGGACTGAGGAAGGAG
 AGGCTGACGTGA (SEQ ID NO: 472).

AOLFR252 sequences:

50 MRLANQTLGGDFLLGIFSQISHPGRCLLIFSIFLMAVSWNITLILLIHDSSLHTPMYFFINQLSL
 IDLTYISVTPKMLVNQLAKDKTISVLGCGTQMYFYLQLGGAECCLLAAMAYDRYVAICHPLR
 YSVLMSHRVCLLLASGCWFVGSVDGFMLTPIAMSPFCRSHEIQHFFCEVPAVLKLSCSDTSLY
 KIFMYLCCVIMLLIPVTVISVSYYYIILTIIKMNNSVEGRKKAFTCSSHITVVSFLFYGAIIYNML
 PSSYQTPEKDMMSFFYTLTPVLPNPIYSLFRNKDVTRALKKMLSVQKPPY (SEQ ID NO: 473).

ATGCGGCTGGCCAACCAGACCCCTGGGTGGTGACTTTCTGTTGGGAATCTTCAGCCAGA
 TCTCACACCCCTGGCCGCCTCTGCTTATCTTCAGTATATTTGATGGCTGTGCTTGG
 AATAITACATTGATACTTCTGATCCACATTGACTCCTCTGCATACTCCCATGACTTCTT
 5 TATAAACCGACTCTCACTCATAGACTTGACATATATTCCTGCACTGTCCCCAAAATGCTG
 GTGAACCAGCTGGCCAAGAGACAAGACCATCTCGGTCTGGGTGGCACCCAGATGTAC
 TTCTACCTGCAGTTGGGAGGGTGCAGAGTGCTGCCTCTAGCCGCATGGCCTATGACCGCT
 ATGTGGCTATCTGCCATCCTCTCCGTTACTCTGTGCTCATGAGCCATAGGGTATGTCTCCTC
 CTGGCATTAGGCTGCTGGTTGTGGGCTCAGTGGATGGCTCATGCTCACTCCCATCGCCA
 10 TGAGCTTCCCCTCTGCAGATCCCAGATGAGATTGACACTTCTGAGGTCCTGCTGTT
 TTGAAGCTCTCTGCTCAGACACCTCACTTACAAGATTTCATGACTTGTGCTGTGTCAT
 CATGCTCCTGATACCTGTGACGGTCATTCACTGCTTACTACTATATCATCCTCACCATCC
 ATAAGATGAACACTAGTTGAGGGTGGAAAAAGGCCTCACCACCTGCTCCTCCCACATTAC
 AGTGGTCAGCCTCTCTATGGAGCTGCTATTACAACATGCTCCCCAGCTCCTACCAA
 15 ACTCCTGAGAAAGATATGATGTCATCCTTTCTACACTATCCTACACCTGCTTGAATCC
 TATCATTACAGTTCAAGGATAAGGATGTCACAAGGGTTGAAAAAAATGCTGAGCGT
 GCAGAAACCTCCATATTAA (SEQ ID NO: 474).

AOLFR253 sequences:

MTFFSSGGNCEPMCSGNQTSQNQASTDFLTGLFAESKHAALLYTVTFLFLMALTGNALL
 20 ILLIHSEPRLHTPMYYFISQLALMDLMYLCVVPKMLVGQVTGDDTISPSGCGIQMFHHTLAG
 AEVFLLAAMAYDRYAAVCRPLHYPLMNQRVCQLLVSACWVLMGVDLLTPITMSFPFCQS
 RKILSFFCETPALLKLSCSDVSLYKMLTYLCCILMLTPIMVISSYTLILHIIHRMNSAAGRKA
 LATCSSHMIIVLLLFGASFYTYMLRSSYHTAEQDMMMVSAYTIFTPVNLPIYSLRNKDVTRAL
 RSMMQSRMNQEK (SEQ ID NO: 475).

25 ATGACTTTTTCTCAGGGGAAACTGTGAGCCAGTCATGTGCTCAGGGAAATCAGACTT
 CTCAGAACACAGCAAGCACTGATTTCACCCCTCACGGGACTCTTGCTGAGAGCAAGCA
 TGCTGCCCTCTACACCGTGACCTTCTTCTTGATGGCCCTCACTGGGAATGCC
 30 TCCTCATCCTCCTCATCCACTCAGAGCCCCGCCACACCCCCATGTAATTCTCATCAGC
 CAGCTCGCGCTCATGGATCTCATGTACCTATGCGTACTGTGCCAAGATGCTTGTGGGCC
 AGGTCACTGGAGATGATACCATTCCTCCCGTCAGGCTGTGGATCCAGATGTTCTCCACCT
 GACCCCTGGCTGGAGCTGAGGTTTCTCTGGCTGCCATGGCTATGACCGATATGCTGCT
 GTTGCAACCTCTCATTACCCACTGCTGATGAACCAGAGGGTGTGCCAGCTCCTGGTGT
 35 CAGCCTGCTGGTTTGGGAATGGTTGATGGTTGTGCTCACCCCCATTACCATGAGCTT
 CCCCTTGGCAAGTCTAGGAAATCCTGAGTTTCTGTGAGACTCTGCCCTGCTGAAGC
 TCTCCTGCTCTGACGTCTCCCTATAAGATGCTCACGTACCTGTGCTGCATCCTCATGCTT
 CTCACCCCCATCATGGTCATCTCAGCTATACACCCCTCATCCTGCATCTCATCCACAGGAT
 GAATTCTGCCGGGGCGAGAAGGCCCTGGCACCTGCTCCTCCCACATGATCATAGTG
 40 CTGCTGCTCTGGTCTGCTTCTACACCTACATGCTCCGGAGTTCTACCACACAGCTGA
 GCAGGACATGATGGTGTCTGCCCTTACACCATCTCACTCCTGTGCTGAACCCCTCATTT
 ACAGTCTCCGCAACAAAGATGTCACCAGGGCTTGAGGAGCATGATGCAAGAATGA
 ACCAAGAAAAGTAG (SEQ ID NO: 476).

AOLFR254 sequences:

45 MTNTSSDFTLGLLVNSEAAGIVFTVILAVFLGAVTANLVMIFLIQVDSRLHTPMVFLLSQLSI
 MDTLFICTTVPKLLADMVSKEKIIISFVACGIQIFLYLTMIGSEFLLGLMAYDCYVAVCNPLRYP
 VLMNRKKCLLAAGAWFGGSLDGFLTPITMVNPYCGSRSHFFCEIPAVLKLACADTSLYET
 LMYICCVLMLLIPISIISTSYSLILLTIIHRMPSAEGRKKAFTCSSHLLTVSIFYGAAFYTYVLPQS
 FHTPEQDKVVSAYTIVTPMLNPLIYSLRNKDVGAFKKVFACCSAQKVATSDA (SEQ ID NO:
 50 477).

55 ATGACGAACACATCATCCTCTGACTTCACCCCTGGGGCTTCTGGTGAACAGTGAGGCTG
 CCGGGATTGTATTACAGTGATCCTGCTGTTCTGGGGCCGTGACTGCAAATTGGT
 CATGATATTCTGATTCAAGTGGACTCTGCCTCCACACCCCCATGTAATTCTGCTCAGTC
 AGCTGTCCATCATGGACACCCTTTCATCTGTACCAACTGTCCAAAATCCTGGCAGACAT
 GGTTCTAAAGAGAAGATCATTCTTGTGGCCTGTGGCATCCAGATCTTCCTACCTG

5 ACCATGATTGGTTCTGAGTTCTCCTGGGCCTCATGGCCTATGACTGCTACGTGGCTGT
 CTGTAACCCCTCTGAGATACCCAGTCCTGATGAACCGCAAGAAGTGTCTTGTGGCTGCT
 GGTGCCTGGTTGGGGCTCCCTCGATGGCTTCTGCTCACTCCCACCATGAATGTCC
 CTTACTGTGGCTCCCGAAGTATCAACCATTCTGTGAGAGATCCCAGCAGTCTGAAACT
 10 5 GCCCTGTGCAGACACCGTCCTGTATGAAACTCTGATGTACATCTGCTGTGCTCATGTG
 CTCATCCCCATCTCTATCATCTCCACTCCCTCATCTGTTAACCATCCACCGCAT
 GCCCTCTGCTGAAGTCGCAAAAGGCCTTCACACTGTTCTCCACTTGACTGTAGTT
 AGCATCTTCTATGGGGCTGCCCTACACATACCGTGCCTGCCAGTCTCCACACCCCCG
 AGCAGGACAAAGTAGTGTCAGCCTCTATACCATGTCACGCCATGCTTAATCCTCTCAT
 15 10 CTACAGCCTCAGAAACAAGGACGTATAGGGGATTAAAAAGGTATTGCAATGTTGCTCA
 TCTGCTCAGAAAGTAGCAACAAGTGTGCTTAG (SEQ ID NO: 478).

AOLFR255 sequences:

15 MEQSNSVYADFILLGLFSNARFPWLLFALILLVFLTSIASNVVKIILIHIDSRLHTPMYFLLSQLS
 LRDILYISTIVPKMLVDQVMSQRAISFAGCTAQHFLYLTLAGAEFFLLGLMSYDRYVAICNPLH
 YPVLMRSRKICWLIVAAWLGGSIDGFLTPVTMQFPFCASREINHFFCEVPALLKLSCTDTSA
 ETAMYVCCIMMLLIPFSVISGSYTRILITVYRMSEAEGRGKAVATCSSHMVVVSLFYGAAMYT
 YVLPHSYHTPEQDKAVSAFYTILTPMLNPLIYSLRNKDVTGALQKVVGRCVSSGKVTTF (SEQ
 ID NO: 479).

20 20 ATGGAGCAGAGCAATTATTCCGTGTATGCCGACTTTATCCTCTGGGTTTGTTCAGCAACG
 CCCGTTTCCCTGGCTTCTCTTGCCTCATCTCCTGGCTTTGACCTCCATAGCCAGC
 AACGTGGTCAAGATCATTCTCATCCACATAGACTCCCCTCCACACCCCCATGTACTCT
 GCTCAGCCAGCTCTCCCTCAGGGACATCCTGTATATTCCACCATGGTCCAAAATGCTG
 25 25 GTCGACCAGGTGATGAGCCAGAGGCCATTCCCTTGCTGGATGCACTGCCAACACTTCC
 TCTACTTGACCTTAGCAGGGGCTGAGTTCTCCTCTAGGACTCATGTCCTATGATCGCTAC
 GTAGCCATCTGCAACCCCTCTGCACTATCCTGTCCTCATGAGCCGAAGATCTGCTGGTTGA
 TTGTGGCGGCAGCCTGGCTGGAGGGTCTATCGATGGTTCTTGCTCACCCCCGTACCAT
 30 30 GCAGTTCCCTCTGTGCTCTCGGGAGATCAACCACTTCTCTGCGAGGTGCCCTGCCCCTC
 TGAAGCTCTCTGCA CGGACACATCAGCCTACGAGACAGCCATGTATGTCCTGTATTAT
 GATGCTCTCATCCCCCTCTGTCTCATCTCGGGCTCTACACAAGAATTCTCATTACTGTT
 ATAGGATGAGCGAGGCAGAGGGGAGGGAAAGGCTGTGCCACCTGCTCTCACACATGG
 TGGTTGTCAGCCTCTATGGGGCTGCCATGTACACATACGTGCTGCTCATCTTACAC
 35 35 ACCCCTGAGCAGGACAAAGCTGTATCTGCTCTACACCATCTTACTCCCAGTCTCAATC
 CACTCATTACAGCCTAGGAACAAGGATGTACAGGGCCCTACAGAAGGTTGGGGA
 GGTGTGTGCTCTCAGGAAAGGTAACCACCTTCTAA (SEQ ID NO: 480).

AOLFR256 sequences:

40 40 MGGKQPWVTEFILVGFQVGPALAILCGLFSVFYTLTLLNGVIFGIICLDSLKLHTPMYFFLSHL
 AIDMSYASNNVPKMLANLMNQKSTISFVPCIMQTFLYLAFAVTECLILVVMSYDRYVAICHPF
 QYTVIMSWRVCTILASTCWIIISFLMALVHITHILRPPFCGPQKINHFIGQIMSVFKLACAGPRLNQ
 VVLYAGSAFIVEGPLCLELVSNLHILSRHLEDPVMGRAADRLTLPAPSHLCMVGLLFGSTMVM
 YMAPKSRHPEEQKVLSFYSLNPMLNPLIYSLRNAEVKGALKRVLWKQRSK (SEQ ID NO:
 481).

45 45 ATGGGAGGCAAGCAGCCCTGGGTACAGAATTCTCCTGGTGGGATTCCAGGGTTGGTCCA
 GCACTGGCGATTCTCCTCTGTGGACTCTCTGTCTTCTATACACTCACCCCTGCTGGGAA
 TGGGGTCATCTTGGGATTATCTGCTGGACTCTAACGCTTCACACACCCATGTACTCTCTCC
 TCTCACACCTGGCCATCATTGACATGTCCTATGCTTCCAACAATGTCCAAGATGTTGGC
 50 50 AAACCTAATGAACCAGAAAAGCACCCTCCTTGTCCATGCATAATGCAGACTTTTTG
 TATTGGCTTGTGCTTACAGAGTGCCTGATTTGGTGGTGTGATGTCCTATGATAGGTATGT
 GGCCATCTGCCACCCCTTCCAGTACACTGTCATCATGAGCTGGAGAGTGTGCAAGATCTG
 GCCTCAACATGCTGGATAATTAGCTTCTCATGGCTCTGGCCATATAACTCATATTCTGAG
 GCCGCCTTTGTGGCCACAAAAGATCAACCACCTTATCTGTCAAATCATGTCCTATTCA
 55 55 AATTGGCCTGTGCTGGCCCTAGGCTCAACCAGGTTGGTCTATATGCGGGTTCTGCGTTCAT
 CGTAGAGGGGCCGCTCTGCCTGGAGCTGGTCTCCAACATGTCACATCCTGCGGCCATCTT

5 GAGGATCCAGTAATGGGGAGGGCCGCAGACCGACTTACTCTTCTGCTCCCTCCCCACCTT
 GCATGGTGGGACTCCTTTGGCAGCACCATGGTCAATGTACATGGCCCCAAGTCCCGCCA
 CCCTGAGGAGCAGCAGAAGGCTCTTACAGCCTTTCAACCCGATGCTGAAC
 CCCCTGATCTACAGCCTGAGGAACGCAGAGGTCAAGGGTGCCTGAAAAGAGTGTGTTGG
 AAACAGAGATCAAAGTGA (SEQ ID NO: 482).

AOLFR257 sequences:

10 MESNQTWITEVILLGFQVDPALELFLEFGFLLFYSLTLMGNGLIYLDTRLHTPMYVFLSHL
 AIVDMSYASSTVPKMLANLVMHKKVISFAPCILQTFLYLAFAITECLILVMMCYDRYVAICHPL
 QYTLIMNWRVCTVLAUTCWIFSFLALVHITLILRLPFCGPQKINHFFCQIMSVFKLACADTRLN
 QVVLFAGSAFLVGPLCLVLVSYLHILVAILRIQSGEGRKAFSTCSSHLCVVGLFFGSAIVMYM
 APKSSHSQERRKILSLFYSLFNPLIYSLRNAEVKGALKRVLWKQRSM (SEQ ID NO: 483).

15 ATGGAAAGCAATCAGACCTGGATCACAGAAGTCATCCTGTTGGATTCCAGGTGGACCCA
 GCTCTGGAGTTGTTCTCTTGGGTTTCTGCTATTCTACAGCTAACCCCTGATGGGAAA
 TGGGATTATCCTGGGCTCATCTACTTGGACTCTAGACTGCACACACCCATGTATGTCITC
 CTGTCACACCTGGCCATTGTGGACATGTCTATGCCTCGAGTACTGTCCTAAGATGCTAG
 CAAATCTGTGATGCACAAAAAGTCATCTCCTTGCTCCTGCATACTTCAGACTTTTG
 TATTGGCGTTGCTATTACAGAGTGTGATTTGGTGTATGATGTGCTATGATCGGTATG
 20 TGGCAATCTGTCACCCCTGCAATACACCCCTCATTATGAACGGAGAGTGTGCACGTCTCCT
 GGCTCAACTGCTGGATATTAGCTTCTCTGGCTCTGGCCATATTACTCTTATTCTGA
 GGCTGCCTTTGTGGCCCACAAAAGATCAACCACCTTCTGTCAAATCATGTCCGTATTC
 AAATTGGCCTGTGCTGACACTAGGCTCAACCAGGGTGTCTATTGCGGGTTCTGCGTTCA
 25 TCTTAGTGGGGCCGCTCTGCCTGGTGTGGCTCTTACTTGACATCTGCACTCCTGGTGGCCATCTTG
 AGGATCCAGTCTGGGGAGGGCCGCAGAAAGGCCTCTACACCTGCTCTCCACCTCTGCG
 TGGTGGGGCTTTCTTGGCAGCGCATTGTCAATGATGGCCCCAAGTCAGCCATT
 TCAAGAACGGAGGAAGATCCTTCCCTGTTACAGCCTTTCAACCCGATCTGAACCC
 CTCATCTACAGCCTAGGAATGCAGAGGTGAAAGGGCTCTAAAGAGAGTCCTTGGAAA
 CAGAGATCAATGTGA (SEQ ID NO: 484).

30 **AOLFR259 sequences:**
 MGDNQSRVTEFILVGFQLSVEMEVLLFWIFSLLYLFSSLANGMILGLICLDPLRLRTPMYFFLSHL
 AVIDIYYASSNLLNMLENLVKHKTISFISCIMQMAYLTFAAAVCMILVVMYSYDRFVAICHPL
 35 HYTVIMNWRVCTVLAUTSWACGFSLALINLILLRLPFCGPQE VNHFGEILSVKLACADTWIN
 EIFVFAGGVFVLVGPLSLMLISYMRILLAIKIQSKERKKAFSTCSSHLCVVGLYFGMAMVVY
 LVPDNSQRKQQKILTLFYSLFNPLIYSLRNAQVKGALYRALQKKRTM (SEQ ID NO:
 485).

40 ATGGGGACAACCAATCACGGGTACAGAATTACATCCTGGTGGATTCCAGCTCAGTGTG
 GAGATGGAAGTGCTCCTCTTCTGGATCTCTCCCTGTTATCTCCTCAGCCTGCTGGCAA
 TGGCATGATCTGGGGCTCATCTGCTGTGGATCCCAGACTGCGCACCCCCATGTACTTCTC
 TGTACACTGGCGTCATTGACATATACTATGCTCCAGCAATTGCTCAACATGCTGGA
 AACCTAGTGAACACAAAAAAACTATCTGTTCACTCTGCTTGTGATTATGCAGATGGCTTG
 TATTGACTTTGCTGCTGCAGTGTGATTTGGTGGTGTATGCTCTATGACAGATTGT
 45 GCGATCTGCCATCCCCGCATTACACTGTCACTCATGAACGGAGAGTGTGCACAGTACTG
 GCTATTACTCCTGGCATGTGGATTCCCTGGCCCTCATAAAATCTAATTCTCTTCTAAG
 GCTGCCCTCTGTGGGCCCCAGGAGGTGAACCACTCTCGGTGAAATTCTGCTGTGCTC
 AAACCTGGCGTGTGAGACACCTGGATTATGAAATTGCTTGTGCTGGTGGTGTGTTG
 TCTTAGTCGGGCCCTTCTTGTGATGCTGATCTCTACATGCGCATCCTCTGGCCATCCTG
 50 AAGATCCAGTCAAAGGAGGGCCGCAAAAAGCCTTCCACCTGCTCCTCCACCTCTG
 TGGTGGGCTTACTTGGCATGGCCATGGTGGTTACCTGGTCCCAGACAACAGTCACAG
 ACAGAACGAGCAGAAAATTCTCACCCCTGTTACAGCCTTTCAACCCATTGCTGAACCC
 CTCATCTACAGCCTGCGGAATGCTCAAGTGAAGGGTGCCTTACAGAGCACTGCAGAAA
 AAGAGGACCATGTGA (SEQ ID NO: 486).

AOLFR24B sequences:

5 MPSINDTHFYPPFFLLGIPGLDTLHIWISFPFCIVYLIAIVGNMTILFVIKTEHSLHQPMFYFLAM
 LSMIDLGLSTSTIPKMLGIFWFNLQEISFGGCLLQMFIIHMFCTGMETVLLVVMAYDRFVAICNP
 LQYTMILTNKTISLASVVVGRNLVLVTPFVFLRLPFCGHNIVPHTYCEHRLAGLACAPIKIN
 IIYGLMVISYIIVDVILASSYVLILRAVFRLPSQDVRKAFNTCGSHVCVMLCFYTPAFFSFMTH
 RFGQNIPHYSIHILLANLYVVVPPALNPVITYGVRTKQIREQIVKIFVQKE (SEQ ID NO: 487)

10 ATGCCCTCATCAATGACACCCACTTCTATCCCCCCTCTTCCCTCGTAGGAATACCAAGG
 ACTGGACACTTACATATCTGGATTCTTCCCATTCTGTATTGTGTACCTGATTGCCATTG
 TGGGAATATGACCATTCTCTTGTGATCAAAACTGAACATAGTCTACACCAGCCATGTT
 CTACTTCCGCCATGTTGCTATGATTGATCTGGGCTGTCCACATCCACTATCCCCAAAA
 TGCTAGGAATCTTCTGGTCAACCTCCAAGAGATCAGCTTGGGGATGCCCTCTTCAGAT
 GTTCTTATTACACATGTTACAGGCATGGAGACTGTTCTGTTGGTGTATGGCTTATGACC
 GCTTGTGTCATCTGCAACCCCTCCAGTACACCATGATCCTACCCAATAAAACCATCAG
 15 TATCCTAGCTCTGTTGTTGGAAGAAATTAGTTCTGTAACCCCATTGTGTTCTCA
 TTCTGCGCTGCCATTCTGTGGGCATAACATCGTACCTCACACATACTGTGAGCACAGGGG
 TCTGGCCGGGTTGGCCTGTGCACCCATTAAAGATCAACATAATCTATGGCTCATGGTGATT
 TCTTATATTATTGTGGATGTTGATCTTAATTGCCCTTCCTATGTGCTTATCCTTAGAGCTGT
 20 TTTGCCCTCCCTCAAGATGTCCGACTAAAGGCCTCAATACCTGTGGTCTCATGTCT
 GTGTTATGCTGTGCTTACACACCAGCATTTTTCTTTATGACACATGTTGGCCAA
 AACATTCCCCACTATATCCATATTCTTTGGCTAACCTGTATGTGGTTGCCCACCTGCCCT
 TAACCCTGTCATTATGGAGTCAGGACCAAGCAGATCCGAGAGCAAATTGTGAAAATT
 GTACAGAAAGAATAA (SEQ ID NO: 488)

AOLFR33B sequences:

25 MLHTNNTQFHPSTFLVVGVPGLEDVHVWIGPFFAVYLALLGNIIILFVIQTEQSLHQPMFYFL
 AMLAGTDLGLSTATIPKMLGIFWFNLGEIAFGACITQMYTIHICLGEVVLTVTGDYRVAICNP
 LRYSMILTNKVIAILGIVIIVRTLVLVTPFTLRLPFCGVRIIPHTYCEHIMGLAKLACASINVY
 30 GLIAFSVGYIDISVIGFSYVQILRAVFHLPAWDARKALSTCGSHVCVMLAFYLPALFSFMTHRF
 GHNPYIHIILLANLYVVFPALNSVITYGVTKQIREQVRLNPKSFWHFDPKRIFHNNNSVRQ
 (SEQ ID NO: 489)

35 ATGCTTCATACCAACAATACACAGTTCACCCCTCACCTCCGTAGTGGGGGTCCAG
 GGCTGGAAGATGTGATGTGATTGGCTTCCCTCTTGCCTGTATCTAACAGCCCT
 TCTAGGGAACATCATTATCCTGTTGTGATACAGACTGAACAGAGCCTCCACCAACCCATG
 TTTACTCCTAGCCATGTTGCCGGCACTGATCTGGCTTGTCTACAGCAACCATCCCCA
 AGATGCTGGAAATTCTGGTTAATCTGGAGAGATTGCAATTGGTGCCTGCATCACACA
 GATGTATACCATTATGCACTGGCCTGGAGTCTGTGTTACTGACAGTCACGGGATA
 GATCGCTATATTGCCATCTGCAACCCCTGAGATAAGCATGATCCTACCAACAAGGTA
 40 TAGCCATTCTGGCATAGTCATCATTGTCAGGACTTGGTATTGTGACTCCATTACATT
 CTCACCCCTGAGATTGCCATTCTGTGGTGTCCGGATTATCCTCATACCTATTGTGAACACAT
 GGGCTGGCAAAGTTAGCTTGCCAGTATTAAATGTTATATGGATTGATTGCCCTCTCA
 GTGGGATACATTGACATTCTGTGATTGGATTCTCTATGTCCAGATCCTCCGAGCTGTCTT
 45 CCATCTCCAGCCTGGATGCCGGCTTAAGGCACATGTGGCTCTCACGTCTGT
 GTTATGTTGGCTTCTACCTGCCAGCCCTTCTTCCATGACACACCGCTTGGCCACAA
 CATCCCTCATTACATCCACATTCTGCCAATCTGTATGTGGTTTCTCCCTGCTCTA
 ACTCTGTTATCTATGGGTCAAAACAAAAGATACGAGAGCAGGTAATTAGGATACTCA
 ACCCTAAAAGCTTGGCATTGACCCCAAGAGGATCTCCACAAACAATTAGTAA
 ATAA (SEQ ID NO: 490)

50

AOLFR112B sequences:

55 MKNKTVLTEFILLGTDVPELQVAVFTFLFLAYLLSILGNLTILTLDSHLQTPMYFFLRNFSF
 LEISFTNIFIPRVLISITGNKSISFAGCFTQYFFAMFLGATEFYLLAAMSYDRYVAICKPLHYTTI
 MSSRICIQLIFCSWLGGLMAIPTITLMSQQDFCASNRLNHYFCDYEPLLELSCSDTSLIEKVVFL
 VASVTLVVTLVLVILSYAFIUKTILKPSAQQRKAFSTCSSHMIVISLSYGSCMFMYINPSAKEG
 DTFNKGVALITSVAPLLNPFIYTLRNQQVKQPFKDMVKLLNL (SEQ ID NO: 491)

5 ATGAAAAATAAAACCGTGTAACTGAGTTATCCTCTGGGTCTAACAGATGTCCTGAAC
 TCCAGGTGGCAGTTTACCTTCTTTCTTGCCTGCTGACTTACTCAGCATCCTGGAAATCTG
 ACTATCCTCATCCTCACCTGCTGGACTCCCACCTCAGACTCCCATGTATTCCTTCTCCG
 GAACCTCTCCTCTGGAAATTCTTACAAACATCTTCACTTCAAGGGCTGATTAGCA
 TCACAACAGGGAAACAAGAGTATCAGCTTGCCTGCTGCTCACTCAGTATTCCTTGCCT
 GTTCCTTGGGGCTACAGAGTTACCTTCTGGCTGCCATGCCTATGACCGCTATGTGGCC
 ATCTGCAAACCTCTGATTACACCACCATGAGCAGCAGAATCTGCATCCAGCTGATT
 10 TCTGCTCTGGCTGGGCTAATGGCTATTATACCAACAATCACCCGTATGAGTCAGCA
 GGACTTTGTGCATCCAACAGACTGAATCATTACTTCTGTGACTATGAGCCTCTGGAA
 CTCTCATGTTACAGACACAAGCCTCATAGAGAAGGGTGTCTTCTGTGGCATCTGTGACCC
 TGGTGGTCACTCTGGTCTAGTGATTCTCTCATGCATTATCAAGACTATTCTGAAG
 CTCCCTCTGCCAACAAAGGACAAAAGCCTTTCCACATGTTCTCCACATGATTGTAT
 15 CTCCCTCTTACGGAAGCTGCATGTTATGTACATTAATCCCTCTGAAAAGAAGGGAT
 ACATTCAACAAGGGAGTAGCTACTCATTACTTCAGTTGCTCTTGTGAACCCCTTAT
 TTACACCCTAAGGAACCAACAGGTAACAAACACCCTCAAGGATATGGTCAAAAAGCTTCT
 GAATCTTAA (SEQ ID NO: 492)

AOLFR130B sequences:

20 MEGKNQTAPSEFIILGFDHLNELQYLLFTIFLTYICLGGNVFIIVVTIADSHLHTPMYYFLGNL
 ALIDICYTTNPQMMVHLLSEKKIISYGGCVTQLFAFIFFVGSECLLAAMAYDRYIAICKPLR
 YSFIMNKALCSWLAASCWTGFLNSVLHTVLTFLPFCGNQINYFFCDIPPLLILSCGDTSLNE
 LALLSIGILISWTPFLCIILSYIISTILRIRSSEGRHKAFSTCASHLIVLYYGSIAFTYVRPISSYS
 LEKDRLISVLYSVVTPMLNPVIYTLRNKDIKEAVKAIGRKWQPPVFSSDI (SEQ ID NO: 493)

25 ATGGAAGGAAAGAACAAACAGCTCCATCTGAATTACATCATCTTGGGGTTCGACCACCTGA
 ATGAATTGCAGTATTACTCTCACCATCTTCTGACCTACATATGCACTTTAGGAGGC
 AATGTTTTATCATTGTGGTACCATAGCTGATTCCACCTACACACACCCATGTATTATT
 30 CCTAGGAAATCTGCCCTTATTGACATCTGCTACACTACTAATGCCCCAGATGATG
 GTGCATCTCTGTCAAGAGAAGAAAATCATCTCATGGAGGCTGTGACCCAGCTTTG
 CATTCACTTCTTGTGGCTCAAGAGTGTCTCCTCTGGCAGCAATGGCATATGATCGATAT
 ATTGCTATCTGTAAGCCGTTAAGGTACTCATTTATTATGAACAAGGCCCTGTGAGCTGGT
 TAGCAGCCTCATGCTGGACATGTGGTTCTCAACTCAGTGTGACACCCGTTCTGACCTT
 35 CCACCTGCCCTCTGTGGTAACAATCAGATCAATTATTCTCTGTGACATACCCCTTGC
 TCATCTGTCTGTGGTACATTCCCTCAATGAACCTGGCTTGTGTCATTGGGATCCCT
 ATAAGCTGGACTCTTCTGTGCATCATCCTTACCTTACATCATCTCCACCATCCT
 GAGGATCCGTTCTGTGAGGGGAGGCACAAAGCCTTCCACCTGTGCCTCCACCTGCTC
 ATTGTTATTCTTATTATGGCAGTGTCTACAGTGTGACATGTGAGGCCATCTCATCTTACTC
 40 TCTAGAGAAAGATAGATTGATCTCAGTGTGACATGTGAGGCCATCTCATCTTACTC
 GTAATTATACGCTAAGGAATAAGGACATCAAAGAGGCTGTGAAGGCCATAGGGAGAAAG
 TGGCAGGCCACCAGTTCTCTGTATATAA (SEQ ID NO: 494)

AOLFR142B sequences:

45 MARKDMAHINCTQATEFILVGLTDHQELKMPFLVFLSIYLFTVVGNLGLILLIRADTSNTPM
 YFFLSNLAFVDFCYSSVTPKMLGNFLYKQNVISFDACATQLGCFITFMISESLLASMAYDRY
 VAICNPPLLYMVMTPGICQLVAVPYSYSFLMALFHTILTFRLSYCHSNIVNHFYDDMPLLRL
 TCSDTRFKQLWIFACAGIMFISSLLIVFVSYMFIISAIRMHSAGRQKAFSTCGSHMLAVTIFYG
 TLIFMYLQPSSSHALDTDKMASVFYTVIIPMLNPLIYSLQNKEVKEALKKIIINKN (SEQ ID NO:
 495)

50 ATGGCCAGAAAAGATATGGCTCACATCAATTGCACCCAGGGCAGAGAGTTATTCTGTGG
 GCCTCACAGACCATCAGGAGTTGAAGATGCCCTTTGTGCTATTCTTATCCATCTACCTC
 TTCACAGTGGTAGGCAACTTGGTTGATCCTACTCATTAGAGCGGGATACAAGTCTCAACA
 CACCAATGTACTTCTTCTAGCAACCTAGCTTGTGGATTCTGTTACTCTCTGTCTATT
 55 ACACCCAAAATGCTGGAAATTCTGTACAAACAAAATGTTATATCCTTGATGCTGATGTG
 CTACTCAACTGGCTGCTTCTCACCTCATGATATCAGAATCCTGCTACTGGCTTCCATG

5 GCCTATGACCGATA TGTGGCCATTGTAACCCTTATTGTATATGGTTGTAATGACTCCAG
 ACCATCTCACCTTCCGCCTCTCTATTGCCACTCCAACATGTCAACCATTCTATTGTGA
 TGACATGCCTCTCCTCAGGCTAACCTGCTCAGACACTCGCTCAAACAGCTCTGGATCTT
 10 GCCTGTGCTGGTATCATGTTATTCCCTCCCTCTGATTGCTTTGCTCTACATGTTCATC
 ATTTCTGCCATCCTGAGGATGCATTAGCTGAGGGAAAGACAGAAGGCTTCTGACGTGTG
 GCTCTCACATGCTGGCAGTCACCATATTCTATGGGACCTCATTITATGTAACAGCCT
 AGCTCTAGCCATGCCCTGGACACAGACAAGATGGCCTCTGCTCTACACAGTGTACATTC
 CCATGTTGAATCCCTTAATCTATAGCCTCCAGAATAAGGAGGTGAAAGAAGCTCTGAAGA
 AAATCATTATCAATAAAACTAG (SEQ ID NO: 496)

15 **AOLFR171C sequences:**
 MAEVNIIYVTVFILKGITNRPELQAPCFGVFLVIYLTVLGNLGLITLIKIDTRLHPTMYYFLSHL
 AFVDLCYSSAIPKMMVNFFVERNTIPFHACATQLGCFLTFMITECFLLASMAVDCYVAICSP
 HYSTLMSRRVCICQLVAVPYIYSLFLVALFHTVITFRLTYCGPNLINVHFYCDDLPFLALSCSDTHMK
 EILIFAFAGFDMISSSSIVLTSYIFIAAILRIRSTQGQHKIASTCGSHMVTVTIFYGTLIFMYLQPKS
 NHSLDTDKMASVFYTVVIPMLNPLIYSLRNKEVKDASKKALDKGCENLQILTFLKIRKLY (SEQ
 ID NO: 497)

20 ATGGCTGAAGTTAATATCATTATGTCAGTATTCACTGAAAGGAATTACCAACCGGC
 CAGAGCTCAGGCCCGTGCTTGGGGTTTTAGTTATCTATCTGGTCACAGTGTG
 CAATCTTGGGTTGATTACTTTAATCAAGATTGATACTCGACTCCACACACCTATGTACTATT
 TCCCTAGCCACCTGGCCTTGTGACCTTGTACTCCTCTGCTATTACACCGAAGATGATG
 GTGAATTITGTTGTGGAACGCAACACCATTCTTCCATGCTGTGCAACCCAACGGTT
 25 GTTTCTCACCTCATGATCACTGAGTGTCTCTAGCTCCATGGCCTACGATTGCTAT
 GTCGCCATCTGTAGTCCCCTGCATTATTCAACACTGATGTCAGAAGAGTCTGCAATTCAAC
 TGGTGGCAGTTCCATATATACAGCTCCTGGTGCCTTCCACACCGTTATCACTTC
 CGTCTGACTTACTGTGGCCAAACTTAATTACCAATTCTATTGTGATATTGCTTGTGGCTT
 30 AGCTCTGCTCTGCTCAGACACACACATGAAGGAAATTCTGATATTGCTTGTGGCTT
 GATATGATCTCTCCCTTCCATTGTCCTCACCTCTACATCTTATTATTGCCCTATCTTA
 AGGATCCGCTCTACTCAGGGCAACACAAAGCCATTCCACCTGTGGCTCCATATGGTGA
 CTGTCACTATTCTATGGCACACTGATCTTATGTACCTACAGCCAAATCAAATCACTCC
 TTGGACACAGACAAGATGGCTCTGATTACACAGTGGTATCCCCATGTTAAACCCCC
 TAATCTATAGTCTAAGGAACAAAGAAGTGAAGATGCCCTAAAGAAAGCCTGGATAAAAG
 35 GTTGTGAAAACCTACAGATATTAACATTAAAAATAAGAAAACCTTATTAA (SEQ ID NO:
 498)

40 **AOLFR225B sequences:**
 MKNRTMFGEFILLGLTNQPELQVMIFIFLTYMLSILGNLTITLTLDPHLQTPMYFFLRNFSF
 LEISFTSIFIPRFLTSMTGNKVISFAGCLTYFAIFLGFATEFYLALASMSYDRYVAICKPLHYLTI
 MSSRVCICQLVFCWSLGGFLAILPPILMTQVDFCVSNILNHYYCDYGPLVELACSDTSLELMVI
 LLA VVTLMVTLVLTLSYTYIIRTLIRPSAQQRKAFSTCSSHMIVISLGSCKMFYINPSAKE
 GGAFNKGIAVLITSVTPLNPFIYTLRNQQVKQAFKDSVKIVKL (SEQ ID NO: 499)

45 ATGAAAAACAGAACCATGTTGGTGAGTTATTCTACTGGCCTTACAAATCAACCTGAAC
 TCCAAGTGTGATATTCACTTCTGTTCTCACCTACATGCTAAGTATCCTAGGAAATCTG
 ACTATTATCACCCCTCACCTACTAGACCCCCACCTCCAGACCCCCATGTATTCTCTCCG
 GAATTCTCCTCTAGAAATTCTCACATCCATTATTCCCAGATTCTGACCAGCA
 TGACAACAGGAAATAAGTTACAGCTTGTGGCTGCTGACTCAGTATTCTTGTCTAT
 50 ATTCTTGGAGCTACCGAGTTTACCTCTGGCCTCATGCTTATGATCGTTATGTGGCCA
 TCTGCAAACCCCTTGCATTACCTGACTATTATGAGCAGCAGAGTCTGCATACAACACTAGTGT
 CTGCTCTGGTGGGGATTCTTAGCAATCTACCAACATCCTGATGACCCAGGTA
 GATTCTGTGTCTCCAACATTCTGAATCACTATTACTGTGACTATGGCCTCTGGAGCT
 TGCCTGCTCAGACACAAAGCCTCTAGAAACTGATGGTATCCTCTGGCCGTTGACTCTC
 55 ATGGTTACTCTGGTGTGGTGACACTTCTACACATACATTCTGAGGACTATTCTGAGGAA
 TCCCTCTGCCAGCAAAGGACAAAGGCCATTCCACTTGTCTCCCACATGATTGTCATC

TCCCTCTCTTATGGCAGCTGCATGTTATGTACATTAATCCTCTGAAAAGAAGGAGGTG
 CTTCAACAAAGGAATAGCTGACTCATTACTCGTTACTCCCTACTGAATCCCTCATA
 TAACTTTAAGAAATCAGCAAGTGAAACAAGCTTCAAGGACTCAGTCAAAAAGATTGTG
 AAACTTAA (SEQ ID NO: 500)

5

AOLFR274B sequences:

MEVFVFLAYPSCPELHILSFLGVSLVYGLIITGNILIVVSIHETCLCTSMYYFLGSLSGIEICYTAV
 VVPHILANTLQSEKTITLLGCATQMAFFLALGSADCFLAAMA YDRYVAICHPLQYPLLMTLTL
 10 CVHLVVAVSISGLFLSQLVAFIFSLPFCQAQGIEHFFCDVPPVMHVCAQSHIHEQSVLVAAIL
 AIAVPFFLITTSYTFIVAALLKIHSAAAGRHRAFSTCSHLTVVLLQYGCCAFMYLCPSSSYNPKQ
 DRFISLVYTLGTPLLNPLIYALRNSEMKGAVGRVLTRNCLSQNS (SEQ ID NO: 501)

15 ATGGAATTGTGTTCTGGCTATCCCTCCTGCCAGAACGTGATATTCTGCTCTCCCTGG
 GGTCAAGCCTGGTTATGGTTGATCATCACTGGAAACATTCTCATTGTGGTGTCCATTCAAC
 ACAGAAACCTGTCTATGCACATCCATGACTATTCCCTGGCAGCCTTCTGGGATTGAAA
 TATGCTACACTGCAGTGGTGGCCCCATATCCTGGCCAACACCCCTACAGTCAGAGAAC
 CATCACTCTCCTGGGCTGTGCCACCCAGATGGCTTCTTCATTGCACGGCAGTGCTGAT
 TGCTTCTCTGGCTGCCATGGCTATGACCGCTATGTGGCCATTGCCACCCGTTGAGTA
 20 CCCCTCCTCATGACATTGACTCTTGTGTCACCTGGTTGTGGCATCAGTCATCAGTGGC
 TGGTCTGCTCTTACAACACTGGTGGCCTCATCTCTCTGCCATTGCCAGGGCTAGGGC
 ATTGAGCACTCTTTGTGATGTGCCACCGACTGATGCTGCTGCTGCTCAGAGTCACAT
 TCATGAGCAGTCAGTGCTGGTGGCAGCCATACTAGCCATTGCTGTGCCATTCTCCTC
 25 ACCACCTCCTACACCTTCATAGTGGCTGCTGCTCAAGATCCACTGGCTGCTGGCC
 ACCGGGCCTCTCCACCTGCTCTCCCACCTCACTGTGGTGTGCTGAGTATGGCTGCTGT
 GCCTTCATGTACCTGTGCCCCAGCTCCAGCTACAACCCCAAGCAAGATCGGTTCATCTC
 TGTTGTACACATTGGAAACCCACTGCTCAACCCACTATCTATGCCCTGAGGAACAGTGA
 GATGAAAGGGGCCGTAGGGAGAGTTCTACCAGGAACGCCCTTCCCAGAACAGCTAG
 (SEQ ID NO: 502)

30

AOLFR276B sequences:

MGGFGTNISSTSFTLTGFPEMKGLEHWLAALLLLY AISFLGNILILFIKEEQSLHQPMYYFLS
 LFSVNDLGVSFSTLPTVLAACVCFHAPETTFDACLAMQFFIHFSWTEFGILLAMSFDHYVAICNP
 LRYATVLTDRVVAHNGISIVIRSFCAVFLPFLKRLPCKASVVLAHSYCLHADLRLPWGDT
 35 TINSMYGLFIVISAFGVDSLLLSSYVLLHSVLAIASRGERLKTNTCVSHIYAVLIFYVPMVSVS
 MVHRFGRHAPEYVHKFMSLCTSNAALPNYLFHQD (SEQ ID NO: 503)

40 ATGGGGGGCTTGGACTAACATCTCAAGTACTACCAGCTTCACTCTAACAGGCTTCCCTG
 AGATGAAGGGTCTGGAGCACTGGCTGGCTGCCCTCTGCTGCTGCTTATGCTATTCCCT
 CCTGGCAACATCCTCATCCTCTTATCATAAAGGAAGAGCAGAGCTGACCAGCCAATG
 TACTACTTCTGTCTCTTTCTGTTAATGACCTGGGTGTGCTCTTCTACATTGCCACT
 GTACTGGCTGCTGTGTTTCTGCCACAGAGACAACCTTGTGCTGCTGCTGGCC
 45 TGTTCTCATCCACTTTCTCTGGACAGAGTTGGCATCCTACTGCCATGAGTTTGAC
 CACTATGTGGCATCTGTAACCCGCTGCGCTATGCCACAGTGCTCACTGATGTCCGTG
 CCCACAATGGCATATCCATTGTCATCCGAGCTCTGCTGATGGTATTCCACTTCCCT
 CTGAAGAGACTGCCCTCTGTAAGGCCAGTGTGGTACTGCCATTCTACTGTCATG
 CAGACCTGATCGGCTGCCCTGGGAGACACTACCATCAACAGCATGTATGCCCTGTT
 50 TGTCACTCTGCTTGGGTAGATTCACTGCTCATCCTCTCTATGTGCTCATCTAC
 ATTCTGTGCTGGCATTGCTCCAGGGGTGAGAGGCTTAAGACACTCAACACATGTGTC
 ACATATCTATGCACTGCTGATCTCTATGTGCTATGGTTAGTGTGCTCATGGTTCATCGAT
 ACCCAATTATCTATTCCATCAAGACTAA (SEQ ID NO: 504)

AOLFR311B sequences:

55 MDWENCSSLDFFLGITNNPEMKVTLFAVFLAVIINFSANLGMIVLIRMDYQLHTPMYFFLS
 HLSFCDCLCYSTATGPKMLVDLLAKNSIPFYGCALQFLVFCIFADSECLLSSVMAFDRYKAIINP
 LLYTVNMSSRVCYLLLTGVYLVGIADALIHMTLAFLRCFCGSNEINHFFCDIPPLLLSRSRSDTQV

NEVLVFTVFGFIELSTISGVFISYCYIILSVLEIHSAGRFKALSTCTSHLSAVAIFQGTLLFMYFRP
SSSYSLDQDKMTSLFYTLVVPMLNPLIYSLRNKDVEALKKLKNILF (SEQ ID NO: 505)

5 ATGGACTGGGAAAATTGCTCCTCATTAACGTATTTCTCTGGGAATTACCAATAACCC
AGAGATGAAAGTGACCCATTGCTGATTCTGGCTGTTATATCATTAAATTCTCAGCAA
ATCTTGGAAATGATAGTTAACAGAATGGATTACCAACTTCACACACCAATGTATTCCT
CCTCAGTCATCTGCTTCTGTGATCTGCTATTCTACTGCAACTGGGCCAAGATGCTGG
TAGATCTACTGCCAAGAACAGTCATACCCATTCTATGGCTGTGCTGCAATTCTGGT
CTTCTGTATCTTGAGATTCTGAGTGTACTGCTGTCAGTGATGCCATTGATCGGTACA
10 AGGCCATCATCAACCCCTGCTCTATACAGTCACATGTCTAGCAGAGTGTGCTATCTACT
CTTGACTGGGTTATCTGGTGGAAATAGCAGATGCTTGATACATATGACACTGGCCTTC
CGCCTATGCTCTGTGGTCTAATGAGATTAACTATTCCTCTGTGATATCCCTCCTCTT
ATTACTCTCGCTCAGATACACAGGTCAATGAGTTAGTGTATTCAACCGCTTGGTTTA
15 TTGAACGTGAGTACCATTCAGGAGTTTCATTCTTATTGTTATATCATTCTACAGTC
GAGATACACTCTGCTGAGGGAGGTTCAAAGCTCTCTACATGCACTTCCCACCTATCTG
CGGTTGCAATTTCAGGGAACTCTGCTCTTATGTATTCCGGCCAAGTTCTCCTATTCT
CTAGATCAAGATAAAATGACCTCATTGTTACACCCCTGGTCCATGTTGAACCCCT
GATTATAGCCTGAGGAACAAGGATGTGAAAGAGGCCCTGAAAAAAACTGAAAAAATAAAAT
TTTATTTAA (SEQ ID NO: 506)

20

AOLFR314 sequences:

MEVKNCMVTEFILLGIPHTEGLEMTLFVLFLPFYACTLLGNVSILVAVMSSARLHTPMYFFLG
NLSVFDMGFSSVTCPKMLLYLMGLSRLISYKDCVCQLFFFHFLGSIECFLETVMAYDRFTAICY
PLRYTVIMNPRICVALAVGTWLLGCIHSSILTSLTFLPYCGPNEVDHFCDIPALLPLACADDSL
25 AQRVSFTNVGLISLVCFLILLSYTRITISLIRSIRTEGRRRAFSTCSAHLIAILCAYGPIITVYLQPT
PNPMLGTVVQILMNLVGPMLNPLIYTLRNKEVKTALKTILHRTGHVPES (SEQ ID NO: 507)

30 ATGGAGGTGAAGAACTGCTGCATGGTACAGAGTTACCTTTGGGAATCCCACACACA
GAGGGGCTGGAGATGACACTTTGTCTTATCTTGCCTCTATGCCACTCTACTGGG
AAATGTGCTATCCTGTTGCTGTTATGCTCTGCTGCCCTCACACACCTATGTATTCT
TCTCTGGAAACTTGTCTGTGTTGACATGGGTTCTCCTCAGTGACTTGTCCAAAATGCT
GCTCTACCTTATGGGGCTGAGCCACTCATCCTACAAAGACTGTGTCTGCCAGCTTCT
TCTTCCATTCTCGGGAGCATTGAGTGCTCTGTTACGGTGATGCCCTATGACCGCTTC
ACTGCCATCTGTTATCCTCTGCGATACACAGTCATCATGAACCCAAGGATCTGTGTGGCCC
35 TGGCTGTGGGCACATGGCTGTTAGGGTCATTCACTCCAGTATCTGACCTCCACCTTC
ACCTTGCCTACTGTGGTCCCAATGAAGTGGATCACTCTCTGTGACATTCCAGCACTGTT
GCCCTTGGCCTGTGCTGACACATCCTAGCCCAGAGGGTGAGCTTCAACACGTTGGCCTC
ATATCTCTGTCTGCTTCTGCTAATTCTTATCCTACACTAGAAATACAATATCTATCTT
40 AAGCATTCGTACAACGTGAGGGCCGTCGCCGTGCCCTCTCCACCTGCACTGCTCACCTCATT
GCCATCCTCTGTGCCATGGGCCCATCATCACTGTCTACCTGCAAGCCCACACCCAACCCCA
TGCTGGGAACCGTGGTACAAATTCTCATGAATCTGGTAGGACCAATGCTGAACCCCTTGAT
CTATACCTTGAGGAATAAGGAAGTAAAAACAGCCCTGAAAACAATATTGCACAGGACAGG
CCATGTTCTGAGAGTTAG (SEQ ID NO: 508)

45

AOLFR324B sequences:

MPIANDTQFHTSSFLLGIPGLEDVHIGFPFFSVYLIALLGNAIAFFVIQTEQSLHEPMYYCLA
MLDSIDLSSLSTATIPKMLGIFWPNIKEISFGGYLSQMFFIHFFTVMESIVLVAAMFDYIAICKPL
WYTMILTSKJISLIAJIAVRLSLYMVPLVFLRLPFCGHRIIPHTYCEHMGIAIRLACASIKVNIM
50 FGLGSISLLLLDVLLIILSHIRILYAVFCLPSWEARLKALNTCGSHIGVILAFSTPAFFSFFTHCFGH
DIPQYIHIFLANLYVVVPTLNPVITYGVRTKHIRETVLRIFFKTDH (SEQ ID NO: 509)

55 ATGCCTATAGCTAACGACACCCAGTTCCATACCTCTCATTCTACTGCTGGTATCCCAGG
GCTAGAAGATGTGCACATCTGGATTGGATTCCCTTTCTCTGTGATCTTATTGCACTCC
TGGGAAATGCTGCTATCTTCTGTGATCCAAACTGAGCAGAGTCTCCATGAGGCCATGTA
CTACTGCCTGGCCATGTTGGATTCCATTGACCTGAGCTTGCTACGCCACCATTCCAAA
ATGCTGGCATCTCTGGTCAATATCAAGGAAATATCTTTGGAGGCTACCTTCTCAGA

5 TGTTCTTCATCCATTCTTCACTGTCATGGAGAGGCATCGTATTGGTGGCCATGCCCTTGAC
 CGCTACATTGCCATTGCAAACCTCTTGGTACACCATGATCCTCACAGCAAATCATCA
 GCCTCATTGCAGGCATTGCTGCTGAGGAGCTGTACATGGTCATTCCACTGGTGTCT
 CCTCTTAAGGTTGCCCTCTGTGGACATCGTATCATCCCTACACTTACTGTGAGCACATGG
 10 GCATTGCCCTGTGCCAGCATCAAAGTCAACATTATGTTGGCTGGCAGTAT
 TTCTCTTGTATTGGATGTGCTCCTATTATTCTCTCCATATCAGGATCCTATGCTGT
 CTTCTGCCTGCCCTCTGGGAAGCTCGACTCAAAGCTCTAACACACCTGTGGCTCTCACATT
 GGTGTTATCTTAGCCTTCTACACCAGCATTTCTCTTACACACTGCTTGGCCAT
 GATATTCCCCAATATATCCACATTCTGGCTAATCTATATGTGGTGTCCCTCCACCC
 15 CAATCCTGTAATCTATGGGTCAAGACCAAACATTAGGGAGACAGTGCTGAGGATTT
 TTCAAGACAGACACTAA (SEQ ID NO: 510)

AOLFR328 sequences:

15 MALGNHSTITEFLLLGLSADPNIRALLFVLFLGIYLLTIMENLMLLVIRADSCLHKPMYFFLSH
 LSFVDLCFSSVIVPKMILENLLSQRKTISVEGCLAQVFFVFTAGTEACLLSGMAYDRHAAIRRP
 LLYQIMGKQLYMHLVWGSWGLGFLDALINVLLAVNMVFCEAKIHHYSYEMPSLLPLSCSDI
 SRSLIVLLCSTLLHGLGNFLVFLSYTRIISTLSISSTSRSKAFSTCSAHLTAVTLYYGSGLLRHL
 MPNSGSPIELIFSVQYTVVTPMLNSLIYSLKNKEVKVALKRTLEKYLQYTRR (SEQ ID NO: 511)

20 ATGGCCTTGGGAATCACAGCACCATCACCGAGTTCCCTCCCTGGGCTGTCGCCGACC
 CCAACATCCGGCTCTGCTCTTGTGCTGTCCTGGGATTACCTCTGACCATATAATGGA
 AACACCTGATGCTGCTCGTGATCAGGGCTGATTCTGTCCTCCATAAGCCCATGTATTCT
 TCCTGAGTCACCTCTCCTTGTGATCTGCTCTTCAGTCATTGTGCCAAGATGCTG
 25 GAGAACCTCCTGTCACAGAGGAAACATTTCAGTAGAGGGCTGCCCTGGCTCAGGTCTCT
 TTGTGTTGTCACTGCAGGGACTGAAGCCTGCCCTCTCAAGGGATGCCCTATGACCGCCA
 TGCTGCCATCCGCCGCCCCACTACTTATGGACAGATCATGGTAAACAGCTGTATATGCAC
 CTTGTGTTGGCTCATGGGACTGGCTTCTGGACGCACTCATCAATGTCCTCCTAGCTG
 TAAACATGGCTTTGTGAAGCCAAATCATTCAACACTACAGCTATGAGATGCCATCCCT
 30 CCTCCCTCTGCTCTGCTGATATCTCAGAACGCTCATCGTTTGCTCTGCTCCACTCTCC
 TACATGGCTGGAAACTCCTTGTGCTTCTATCCTACACCCGTATAATCTTACCATC
 CTAAGCATCAGCTCACCTCGGGCAGAACGCAAGGCCCTCTCCACCTGCTCTGCCAACCTCA
 CTGCACTGACACTTACTATGGCTCAGGTTGCTCCGCCATCTCATGCCAAACTCAGGTT
 CCCCATAGAGTTGATCTCTGTGCACTATACTGTAGTCACCTCCATGCTGAATTCCCTCA
 TCTATAGCCTGAAAAATAAGGAAGTGAAGGTAGCTGAAAGAAACTTTGGAAAAATATT
 35 TGCAATATACCAAGACGTTGA (SEQ ID NO: 512)

CLAIMS

What is Claimed:

1. An isolated nucleic acid sequence selected from the group consisting of:
 - 5 (i) an isolated nucleotide sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID

NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID 5 NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, 10 SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID 15 NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, 20 SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID 25 NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510; and SEQ ID NO: 512, or a fragment thereof which comprises at least 75 nucleotides;

30 (ii) an isolated cDNA or an insoluble RNA transcribed therefrom that encodes a polypeptide having an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ

ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ 5 ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, 10 SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID 15 NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, 20 SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID 25 NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, 30 SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325,

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. (iii) a nucleic acid sequence that comprises at least 30% sequence identity with an isolated nucleic acid sequence selected from the group consisting of: SEQ ID NO: 2, 25 SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, 30 SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92,

SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, 5 SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID 10 NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, 15 SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID 20 NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, 25 SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID 30 NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID

NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,
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NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,
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5 NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,
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SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID
NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,
SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512, or to a fragment thereof
15 which comprises at least 100 contiguous nucleotides thereof;

(iv) a nucleic acid sequence that encodes a polypeptide having at least 40%
sequence identity at the amino acid level with a polypeptide having an amino acid
sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ
ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID
NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID
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NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID
NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID
NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID
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NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131,
SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID
NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149,

SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, 5 SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID 10 NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, 15 SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID 20 NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, 25 SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID 30 NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID

NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455,
SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID
NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473,
SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID
5 NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491,
SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID
NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509
and SEQ ID NO: 511 or a nucleic acid sequence encoding at least 50 contiguous
amino acid residues thereof;

10 (v) an isolated nucleic acid sequence which encodes an olfactory receptor or a
fragment thereof that specifically hybridizes and exhibits at least 30% sequence
identity under stringent conditions to a nucleic acid sequence selected from the group
consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID
NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID
15 NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID
NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID
NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID
NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID
NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID
20 NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID
NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID
NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID
NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108,
SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID
25 NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126,
SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID
NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144,
SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID
NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162,
30 SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID
NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180,
SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID
NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198,

SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, 5 SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID 10 NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, 15 SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID 20 NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, 25 SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID 30 NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID

NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512;

(vi) an isolated nucleic acid sequence that specifically hybridizes to (i) or a portion thereof under stringent hybridization conditions that is at least 20-30 nucleotides in
5 length; and

(vii) a naturally occurring allelic or synthetic variant of a nucleic acid sequence according to (i) or (ii), containing at least one substitution, deletion or addition mutation in the coding region.

10 2. The isolated nucleic acid sequence of Claim 1 which is selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214,

SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250,
5 SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340,
10 SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430,
15 SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID

NO: 512 or a fragment thereof which comprises at least 75 contiguous nucleotides thereof.

3. The isolated nucleic acid sequence of Claim 1 which encodes a
5 polypeptide having an amino acid sequence selected from the group consisting of:
SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ
ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ
ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ
ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ
10 ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ
ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ
ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ
ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ
ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ
15 ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ
ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109,
SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID
NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127,
SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID
20 NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145,
SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID
NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163,
SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID
NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181,
25 SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID
NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199,
SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID
NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217,
SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID
30 NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235,
SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID
NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253,
SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID

NO.; 263, SEQ ID NO.; 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof encoding at least 25 contiguous amino acid residues of said polypeptide.

30

4. An isolated nucleic acid sequence having at least 30-60% sequence identity with a nucleic acid sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID

NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID 5 NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ 10 ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ 15 ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID 20 NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ 25 ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID 30 NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID

NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, 5 SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, 10 SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512; or a fragment thereof 15 comprising at least 100 contiguous nucleotides of any of said sequences.

20

25 5. An isolated nucleic acid sequence having at least 60-80% sequence identity with a nucleic acid sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID

30

NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,
5 SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID
10 NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,
15 SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID
20 NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,
25 SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID
30 NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID

NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID
NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,
SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID
5 NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,
SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID
NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,
SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID
NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,
10 SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID
NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,
SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID
NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,
SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID
15 NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,
SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a fragment thereof
comprising at least 100 contiguous nucleotides of any of said sequences.

6. An isolated nucleic acid sequence having at least 80-90% sequence
20 identity with a nucleic acid sequence selected from the group consisting of: SEQ ID
NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID
NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID
NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID
NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID
25 NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID
NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID
NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID
NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID
NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID
30 NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ
ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,
SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID
NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,

SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,
5 SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID
10 NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,
15 SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID
20 NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,
25 SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID
30 NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID

NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,
SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID
NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,
SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID
5 NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,
SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID
NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,
SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID
NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,
10 SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a fragment thereof
comprising at least 100 contiguous nucleotides of any of said sequences.

7. An isolated nucleic acid sequence having at least 85% sequence
identity with a nucleic acid sequence selected from the group consisting of: SEQ ID
15 NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID
NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID
NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID
NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID
NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID
20 NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID
NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID
NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID
NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID
NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ
25 ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,
SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID
NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,
SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID
NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,
30 SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID
NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,
SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID
NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,

SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,
5 SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,
10 SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,
15 SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID

NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512, or a fragment thereof 5 comprising at least 100 contiguous nucleotides of any of said sequences.

8. An isolated nucleic acid sequence having at least 90% sequence identity with a nucleic acid sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID 10 NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID 15 NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, 20 SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID 25 NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, 30 SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,

SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,
5 SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,
10 SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,
15 SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,
20 SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a fragment thereof comprising at least 100 contiguous nucleotides of any of said sequences.

9. An isolated nucleic acid sequence according to Claim 1 which encodes a polypeptide having at least 40-60% sequence identity with a polypeptide having an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID

NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof that comprises at least 40 contiguous amino acids thereof.

10. An isolated nucleic acid sequence according to Claim 1 which encodes a polypeptide having at least 60-70% sequence identity with a polypeptide having an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID

NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID 5 NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, 10 SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID 15 NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, 20 SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID 25 NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, 30 SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327,

SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363,
5 SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453,
10 SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof that comprises at least 40 contiguous amino acids thereof.

11. An isolated nucleic acid sequence according to Claim 1 which encodes
25 a polypeptide having at least 70-80% sequence identity with a polypeptide having an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID

NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111,
5 SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201,
10 SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291,
15 SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID

NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381,
SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID
NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399,
SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID
5 NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417,
SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID
NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435,
SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID
NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453,
10 SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID
NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471,
SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID
NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489,
SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID
15 NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507,
SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof that comprises at least
40 contiguous amino acids thereof.

12. An isolated nucleic acid sequence according to Claim 1 which encodes
20 a polypeptide having at least 80-90% sequence identity with a polypeptide having an
amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID
NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID
NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID
NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID
15 NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID
NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID
NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID
NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID
NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID
25 NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID
NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ
ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111,
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30 NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129,
SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO:
139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID
NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157,
SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO:
167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID
NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185,
SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO:
195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID
NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213,
SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID
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241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID
NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259,
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269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID
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297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID
NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315,
SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO:
325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID
NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343,
SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO:
353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID
NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371,
SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO:
381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID
NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399,
SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID
NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417,
SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID
NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435,
SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID
NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453,
SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID
NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471,
SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID
NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489,
SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID
15 NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507,
SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof that comprises at least
40 contiguous amino acids thereof.

NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129,
SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID
NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147,
SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID
5 NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165,
SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID
NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183,
SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID
NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201,
10 SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID
NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219,
SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID
NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237,
SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID
15 NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255,
SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID
NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273,
SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID
NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291,
20 SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID
NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309,
SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID
NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327,
SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID
25 NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345,
SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID
NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363,
SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID
NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381,
30 SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID
NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399,
SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID
NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417,

SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453,
5 SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID
10 NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof that comprises at least 40 contiguous amino acids thereof.

13. An isolated nucleic acid sequence according to Claim 1 which encodes
15 a polypeptide having about 90-99% sequence identity with a polypeptide having an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129,
20 SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165,

SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, 5 SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, 10 SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, 15 SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, 20 SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, 25 SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, 30 SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID

NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID 5 NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof that comprises at least 40 contiguous amino acids thereof.

14. An isolated nucleic acid sequence which exhibits at least 50% sequence identity with a nucleic acid sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ 15 ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ 20 ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, 25 SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID 30 NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID

NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226,
SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID
NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244,
SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID
5 NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262,
SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID
NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280,
SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID
NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298,
10 SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID
NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316,
SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID
NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334,
SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID
15 NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352,
SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID
NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370,
SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID
NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388,
20 SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID
NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406,
SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID
NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424,
SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID
25 NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442,
SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID
NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460,
SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID
NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478,
30 SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID
NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496,
SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID
NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid

sequence which exhibits at least 50% sequence identity to a fragment comprising at least 100 contiguous nucleotides of said nucleic acid sequence.

15. An isolated nucleic acid sequence which exhibits at least 60%
5 sequence identity with a nucleic acid sequence selected from the group consisting of:
SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ
ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ
ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ
ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ
10 ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ
ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ
ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ
ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ
ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ
15 ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100,
SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID
NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118,
SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID
NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136,
20 SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID
NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154,
SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID
NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172,
SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID
25 NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190,
SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID
NO: 200, SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208,
SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID
NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226,
30 SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID
NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244,
SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID
NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262,

SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298,
5 SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388,
10 SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478,
15 SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence which exhibits at least 60% sequence identity to a fragment comprising at
20 least 100 contiguous nucleotides of said nucleic acid sequence.

16. An isolated nucleic acid sequence that exhibits at least 70% sequence identity with a nucleic acid sequence selected from the group consisting of: SEQ ID

NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,

SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, 5 SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID 10 NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, 15 SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID 20 NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence having at least 70% sequence identity with a fragment thereof comprising at least 100 25 contiguous nucleotides thereof.

17. An isolated nucleic acid sequence that exhibits at least 80% sequence identity with a nucleic acid sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID 30 NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID

NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID 5 NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID 10 NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, 15 SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID 20 NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, 25 SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID 30 NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID

NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence having at least 80% sequence identity with a fragment thereof comprising at least 100 contiguous nucleotides thereof.

18. An isolated nucleic acid sequence that exhibits at least 85% sequence identity with a nucleic acid sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ

ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,
SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID
NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,
SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID
5 NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,
SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID
NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,
SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID
NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,
10 SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID
NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,
SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID
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SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,
20 SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,
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SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID
25 NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,
SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID
NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,
SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID
NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,
30 SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID
NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,
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NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,

SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, 5 SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID 10 NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence having at least 85% sequence identity with a fragment thereof comprising at least 100 15 contiguous nucleotides thereof.

19. An isolated nucleic acid sequence that exhibits at least 90% sequence identity with a nucleic acid sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID 20 NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID 25 NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, 30 SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,

SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,
5 SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,
10 SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,
15 SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,
20 SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID

NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID 5 NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence having at least 90% sequence identity with a fragment thereof comprising at least 100 10 contiguous nucleotides thereof.

20. An isolated nucleic acid sequence that exhibits at least 95% sequence identity with a nucleic acid sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID 15 NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID 20 NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, 25 SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID 30 NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID

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5 NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,
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10 SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID
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30 SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID
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SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID
NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,

SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence having at least 95% sequence identity with a fragment thereof comprising at least 100

5 contiguous nucleotides thereof.

21. An isolated nucleic acid sequence that exhibits about 96-99% sequence identity with a nucleic acid sequence encoding an olfactory receptor selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID

NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID 5 NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, 10 SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID 15 NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, 20 SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID 25 NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, 30 SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a fragment having at least 96-99% sequence identity with a fragment thereof comprising at least 100 contiguous nucleotides thereof.

22. A nucleic acid sequence which encodes for a functional olfactory receptor polypeptide, wherein said nucleic acid sequence comprises a portion which is at least 100 nucleotides in length and exhibits at least 40% sequence identity with at least 100 contiguous nucleotides of a portion of an olfactory receptor encoding a nucleic acid sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256,

SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292,
5 SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382,
10 SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472,
15 SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512.

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23. The nucleic acid sequence of Claim 22 which is a chimeric nucleic acid sequence, wherein said nucleic acid sequence is produced by combining portions of at least two different G protein-coupled receptors.

24. The chimeric nucleic acid sequence of Claim 23 wherein said two different G protein-coupled receptors are olfactory receptors.

5 25. The chimeric nucleic acid sequence of Claim 23 wherein said chimeric sequence contains at least 200 contiguous nucleotides that are at least 40% identical to a portion of one of said olfactory receptor encoding nucleic acid sequences.

10 26. An isolated nucleic acid sequence according to Claim 1, wherein said isolated nucleic acid sequence is directly or indirectly attached to a nucleic acid sequence that encodes a detectable polypeptide.

15 27. The nucleic acid sequence of Claim 26, wherein said detectable polypeptide is green fluorescent protein, or a fragment or variant thereof.

28. An isolated nucleic acid sequence which encodes a polypeptide that exhibits at least 40% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID

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30 SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID
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SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID
NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449,

SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, 5 SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof comprising at least 40 contiguous amino acids thereof that optionally is directly or indirectly attached to a sequence that facilitates the expression and/or 10 translocation of said polypeptide on the surface of a cell.

29. An isolated nucleic acid sequence which encodes a polypeptide that exhibits at least 50% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID 15 NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID 20 NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID 25 NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID 30 NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID

NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197,
SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID
NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215,
SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID
5 NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233,
SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID
NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251,
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NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269,
10 SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID
NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,
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SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID
NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341,
SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID
NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359,
20 SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID
NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377,
SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID
NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395,
SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID
25 NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413,
SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID
NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431,
SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID
NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449,
30 SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID
NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467,
SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID
NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485,

SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof comprising at least 40 contiguous amino acids thereof that optionally
5 is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of said polypeptide on the surface of a cell.

30. An isolated nucleic acid sequence which encodes a polypeptide that exhibits at least 60% sequence identity with a polypeptide selected from the group
10 consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID

NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof comprising at least 40 contiguous amino acids thereof that optionally

is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of said polypeptide on the surface of a cell.

31. An isolated nucleic acid sequence which encodes a polypeptide that

5 exhibits at least 70% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID

NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof comprising at least 40 contiguous amino acids thereof that optionally is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of said polypeptide on the surface of a cell.

32. An isolated nucleic acid sequence which encodes a polypeptide that exhibits at least 80% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,

SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,
5 SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413,
10 SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503,
15 SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof comprising at least 40 contiguous amino acids thereof that optionally is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of said polypeptide on the surface of a cell.
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25
30

33. An isolated nucleic acid sequence which encodes a polypeptide that exhibits at least 85% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID

NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,

SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359,
5 SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449,
10 SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof comprising at least 40 contiguous amino acids thereof that optionally is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of said polypeptide on the surface of a cell.
25

34. An isolated nucleic acid sequence which encodes a polypeptide that exhibits at least 90% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID

NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359,

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5 SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485,
10 SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof comprising at least 40 contiguous amino acids thereof that optionally is directly or indirectly attached to a sequence that facilitates the expression and/or
15 translocation of said polypeptide on the surface of a cell.
20

35. An isolated nucleic acid sequence which encodes a polypeptide that exhibits about 90-99% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID

NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107,
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20 SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID
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25 NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,
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NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395,

SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, 5 SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, 10 SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof comprising at least 40 contiguous amino acids thereof that optionally 15 is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of said polypeptide on the surface of a cell.

36. The isolated nucleic acid sequence according to Claim 26, wherein said isolated nucleic acid sequence is operably linked to a constitutive promoter.

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37. The isolated nucleic acid sequence according to Claim 1, wherein said isolated nucleic acid sequence is operably linked to a regulatable promoter.

25 38. The isolated nucleic acid sequence of Claim 1, wherein said isolated nucleic acid sequence is directly or indirectly attached to a nucleic acid sequence encoding a mammalian rhodopsin polypeptide or a fragment thereof.

30 39. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes a fragment of at least 60 contiguous amino acids of a polypeptide having an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID

NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID

NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, 10 SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, 15 SEQ ID NO: 509, and SEQ ID NO: 511.

40. The isolated nucleic acid molecule of Claim 39, wherein the nucleotide sequence encodes at least 100 amino acids.

25 41. The isolated nucleic acid molecule of Claim 39, wherein the nucleotide sequence encodes at least 150 amino acids.

42. The isolated nucleic acid molecule of Claim 39, wherein the nucleotide sequence encodes at least 200 amino acids.

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43. The isolated nucleic acid molecule of Claim 39, wherein the nucleotide sequence encodes at least 250 amino acids.

44. The isolated nucleic acid molecule of Claim 39, wherein the polypeptide is an olfactory G protein-coupled receptor.

45. The isolated nucleic acid molecule of Claim 39, wherein the expression 5 product binds an odorant.

46. The isolated nucleic acid molecule of Claim 1 comprising a nucleotide sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID 10 NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID 15 NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, 20 SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID 25 NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, 30 SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240,

SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276,
5 SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366,
10 SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456,
15 SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510
20 and SEQ ID NO: 512.

47. An expression vector that comprises a nucleic acid sequence according to Claim 1.

48. The expression vector of Claim 47, wherein said vector is a 5 mammalian, yeast, bacterial or insect expression vector.

49. A cell which is transfected or transformed with at least one nucleic acid sequence according to Claim 1.

10 50. A mammalian cell according to Claim 49.

51. A human cell according to Claim 50.

52. A yeast or insect cell according to Claim 49.

15 53. The mammalian cell according to Claim 49 which is selected from the group consisting of: an olfactory cell, Chinese hamster ovary cell, baby hamster kidney cell, and a myeloma cell.

20 54. A solid phase comprising at least one isolated nucleic acid sequence according to Claim 1.

25 55. A solid phase comprising at least one isolated nucleic acid sequence according to Claim 1, wherein the solid phase is attached to an array comprising at least one additional nucleic acid sequence.

56. The solid phase according to Claim 55 which comprises an array of at least 4 different nucleic acid sequences that encode olfactory receptors or fragments or variants thereof.

30 57. The solid phase according to Claim 55 which comprises at least 10 different nucleic acid sequences that encode olfactory receptors or fragments or variants thereof.

58. The solid phase according to Claim 55 which comprises at least 50 different nucleic acid sequences that encode olfactory receptors or fragments or variants thereof.

5

59. The solid phase according to Claim 55 which comprises at least 100 different sequences that encode olfactory receptors or fragments or variants thereof.

60. An isolated polypeptide that is selected from the group consisting of:

10 (i) a polypeptide comprising an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215,

SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, 5 SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID 10 NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, 15 SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID 20 NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, 25 SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID 30 NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511;

(ii) a polypeptide comprising an amino acid sequence that exhibits at least 40% sequence identity with an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289,

SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, 5 SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID 10 NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, 15 SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID 20 NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, 25 SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511;

(iii) a polypeptide comprising an amino acid sequence that exhibits at least 60% sequence identity with a fragment of a polypeptide according to (i) which fragment is at least 40 amino acids in length;

(iv) a chimeric polypeptide that comprises a portion of a polypeptide according to 30 (i) or (ii) that is at least 40 amino acids in length and a portion of at least one other G protein-coupled receptor; and

(v) a variant of a polypeptide according to (i) which differs by said polypeptide by at least one substitution, addition or deletion modification.

61. An isolated polypeptide according to Claim 60 wherein such polypeptide exhibits at least 70% sequence identity with a polypeptide having a sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ
5 ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ
10 ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149,
15 SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID
20 NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239,
25 SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275,

SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311,
5 SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401,
10 15 SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491,
20 25 SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

62. An isolated polypeptide according to Claim 60 wherein said polypeptide exhibits at least 80% sequence identity with a polypeptide having a sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 30

NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329,

SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, 5 SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, 10 SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, 15 SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID 20 NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

63. An isolated polypeptide according to Claim 60 wherein said polypeptide exhibits at least 90% sequence identity with a polypeptide having a 25 sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID 30 NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID

NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383,

SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419,
5 SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509
10 and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.
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64. An isolated polypeptide according to Claim 60 wherein said polypeptide exhibits about 80-90% sequence identity with a polypeptide having a sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID

NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149,
SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID
NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167,
SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID
5 NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185,
SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID
NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203,
SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID
NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221,
10 SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID
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SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID
NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257,
SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID
15 NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275,
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20 SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID
NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329,
SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID
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SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID
NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401,
30 SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID
NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419,
SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID
NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437,

SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, 5 SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

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65. An isolated polypeptide according to Claim 60 wherein said polypeptide exhibits at least 90-95% sequence identity with a polypeptide having a sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, 25 SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID 30 NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID

NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203,
SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID
NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221,
SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID
5 NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239,
SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID
NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257,
SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID
NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275,
10 SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID
NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293,
SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID
NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311,
SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID
15 NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329,
SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID
NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347,
SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID
NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365,
20 SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID
NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383,
SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID
NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401,
SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID
25 NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419,
SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID
NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437,
SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID
NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455,
30 SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID
NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473,
SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID
NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491,

SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

5 66. An isolated polypeptide according to Claim 60 wherein said polypeptide exhibits about 95-99% sequence identity with a polypeptide having a sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID

NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID 5 NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, 10 SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID 15 NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, 20 SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID 25 NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 30 and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

67. A variant according to Claim 60(v) which comprises at least 5 conservative amino acid substitutions.

68. A variant according to Claim 60(v) which comprises at most 5 conservative amino acid substitutions.

5 69. A variant according to Claim 60(v) which comprises 5 to 7 conservative substitution modifications.

70. A variant according to Claim 60(v) which comprises 3 to 4 conservative substitution modifications.

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71. A variant according to Claim 60(v) which comprises 1 or 2 conservative substitution modifications.

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72. A solid phase comprising at least one directly or indirectly immobilized isolated polypeptide according to Claim 60, or a cell which expresses said polypeptide on the surface thereof.

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73. The solid phase of Claim 72 comprising at least 4 different immobilized polypeptides according to Claim 60, or a cell which expresses said polypeptide on the surface thereof.

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74. The solid phase of Claim 72 comprising at least 16 different immobilized polypeptides according to Claim 60, or a cell which expresses said polypeptide on the surface thereof.

30

75. The solid phase of Claim 72 comprising at least 25 different immobilized polypeptides according to Claim 60 or a cell which expresses said polypeptide on the surface thereof.

76. A method of detecting expression of an olfactory receptor gene comprising (a) hybridizing at least one sample with a nucleic acid according to Claim 1 and (b) detecting expression of the olfactory receptor gene by a positive hybridization signal.

77. A method of screening a library comprising (a) hybridizing the library with a nucleic acid according to Claim 1 and (b) detecting one or more olfactory receptor clones in the library by a positive hybridization signal.

5

78. A recombinant polynucleotide comprising a nucleic acid according to Claim 1 attached directly or indirectly to a heterologous nucleic acid.

79. An expression vector comprising the nucleic acid of Claim 1 and an 10 operably linked heterologous nucleic acid that drives expression thereof.

80. A transfected or transformed cell comprising the recombinant polynucleotide of Claim 78 introduced into a host cell, or a progeny thereof.

15 81. A transgenic non-human organism comprising the recombinant polynucleotide of Claim 78 introduced into a cell of a host non-human organism, or a progeny thereof.

20 82. A method of making a recombinant polynucleotide comprising ligating the nucleic acid of Claim 1 to a heterologous nucleic acid.

83. The method of Claim 82 wherein the heterologous nucleic acid comprises a translational and/or transcriptional regulatory region.

25 84. A method of making a transfected cell comprising introducing the recombinant polynucleotide of Claim 79 into a host cell, and propagating the host cell in which the recombinant polynucleotide has been introduced.

30 85. A method of detecting specific binding of a putative ligand to an olfactory receptor comprising (a) contacting the putative ligand with a cell in which the expression vector of Claim 79 has been introduced, wherein the olfactory receptor is expressed by the cell thereby, and (b) directly or indirectly detecting specific binding between the putative ligand and the olfactory receptor.

86. A method of making transgenic non-human organism comprising introducing the recombinant polynucleotide of Claim 78 into a cell of a host non-human organism, or propagating the host non-human organism in which the 5 recombinant polynucleotide has been introduced.

87. An isolated protein molecule comprising a fragment of at least 60 contiguous amino acids of a polypeptide having an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID 10 NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID 15 NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ 20 ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ 25 ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID 30 NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID

NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241,
SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID
NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259,
SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID
5 NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277,
SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID
NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295,
SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID
NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313,
10 SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID
NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331,
SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID
NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349,
SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID
15 NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367,
SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID
NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385,
SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID
NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403,
20 SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID
NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421,
SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID
NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439,
SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID
25 NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457,
SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID
NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475,
SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID
NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493,
30 SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID
NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO:
511.

88. The isolated protein molecule of Claim 87, wherein the fragment contains at least 100 amino acids.

89. The isolated protein molecule of Claim 87, wherein the fragment 5 contains at least 150 amino acids.

90. The isolated protein molecule of Claim 87, wherein the fragment contains at least 200 amino acids.

10 91. The isolated protein molecule of Claim 87, wherein the fragment contains at least 250 amino acids.

92. The isolated protein molecule of Claim 87, which is a functional olfactory receptor polypeptide.

15 93. The isolated protein molecule of Claim 87, wherein the fragment specifically binds an odorant molecule.

20 94. A recombinant polypeptide comprising the protein molecule of Claim 87 and a heterologous peptide domain.

95. The recombinant polypeptide of Claim 94, wherein the heterologous peptide domain comprises a G protein-coupled receptor transmembrane domain.

25 96. The recombinant polypeptide of Claim 94 comprising a seven-transmembrane receptor with an olfactory receptor ligand-binding domain, wherein the olfactory receptor ligand-binding domain is a chimera of at least two different olfactory receptors.

30 97. A method of detecting specific binding of a ligand to an olfactory receptor comprising (a) contacting the ligand with the protein of Claim 86, and (b) directly or indirectly detecting specific binding between the ligand and the olfactory receptor.

98. An antibody or antibody fragment that specifically binds a polypeptide having an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ 5 ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ 10 ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID 15 NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ 20 ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID 25 NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ 30 ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281,

SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, 5 SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID 10 NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, 15 SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID 20 NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, 25 SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

99. A method of detecting specific binding of the antibody of Claim 98 to an olfactory receptor comprising (a) contacting the antibody with a sample comprising the olfactory receptor and (b) detecting specific binding therebetween. 30

100. The method of Claim 99, wherein specific binding of the antibody to a cell in the sample identifies the cell as an olfactory cell.

101. A method of screening a library of chemical compounds for compounds that are involved in olfactory sensation comprising contacting compounds in said library with at least one polypeptide according to Claim 87 and identifying 5 compounds that specifically bind to at least one of said polypeptides.

102. The method of Claim 101 wherein said library is a combinatorial chemical library.

10 103. The method of Claim 101 wherein said library is a peptide library.

104. The method of Claim 101 wherein said library is a peptide, encoded peptide, benzodiazepine, diversomer, vinylogous polypeptide, nonpeptidal peptidomimetic, or small molecule organic compound library.

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105. The method of Claim 101 wherein said library is a random combination of compounds.

20 106. The method of Claim 101 wherein said compounds are screened by high turning point screening.

107. The method of Claim 101 wherein said screening is effected using animal cells or tissues that express at least one of said polypeptides.

25 108. A cell-based assay for identifying molecules that interact with an olfactory receptor comprising:

obtaining a cell that expresses at least one polypeptide according to Claim 60 or a chimeric protein comprising a portion of said protein and that of another G protein-coupled receptor, and which optionally expresses at least one functional G protein;

30 contacting said cell with a molecule to be screened for its ability to modulate an olfactory receptor; and

detecting whether modulation occurs.

109. The method of Claim 108 wherein modulation is detected based on changes in intracellular calcium.

110. The method of Claim 108 wherein modulation is detected by 5 measuring the transfer of 32P from gamma-labeled GTP to the olfactory receptor polypeptide.

111. The method of Claim 108 wherein modulation is determined based on 10 a comparison to a control compound known to modulate the particular olfactory receptor protein.

112. The method of Claim 108 wherein the G protein is G α 15 or G α 16 or another promiscuous G protein.

15 113. The method of Claim 108 wherein modulation is determined by detecting whether a change in the level of intracellular cyclic nucleotides occurs.

114. The method of Claim 108 wherein modulation is determined based on the level of transcription of said olfactory polypeptide after contacting the cell with the 20 screened compound.

115. The method of Claim 108 when said screened compounds are synthesized by computer assisted drug devices based on the predicted or actual three-dimensional structure of the amino acid sequence of the olfactory protein or a 25 fragment thereof.

116. The method of Claim 108 wherein compounds that modulate olfactory receptor are identified based on whether they specifically bind to a olfactory receptor polypeptide.

30 117. The method of Claim 108 wherein modulation refers to the inhibition of olfactory receptor function.

118. The method of Claim 108 wherein modulation refers to the enhancement of olfactory receptor function.

119. A method for representing the olfactory perception of one or more odors in one or more mammals, comprising:

5 providing values X₁ to X_n representative of the quantitative stimulation of each of n odor receptors of said mammals; and

generating from said values a quantitative representation of odor perception, wherein at least one of said odor receptors is an odor receptor polypeptide having a sequence

10 that is at least about 40% identical to a sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID

NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225,
SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID
NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243,
SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID
5 NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261,
SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID
NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279,
SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID
NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297,
10 SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID
NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315,
SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID
NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333,
SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID
15 NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351,
SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID
NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369,
SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID
NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387,
20 SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID
NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405,
SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID
NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423,
SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID
25 NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441,
SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID
NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459,
SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID
NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477,
30 SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID
NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495,
SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID
NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

120. The method of claim 119, wherein said representation constitutes a point or a volume in n-dimensional space.

5 121. The method of claim 119, wherein said representation constitutes a graph or a spectrum.

122. The method of claim 119, wherein said representation constitutes a matrix of quantitative representations.

10

123. The method of claim 119, wherein said providing step comprises contacting a plurality of recombinantly produced olfactory receptors with a test composition, and quantitatively measuring the interaction of said composition with said receptors.

15

124. A method for predicting the odor perception in a mammal generated by one or more molecules or combinations of molecules comprising:

providing values X_1 to X_n representative of the quantitative stimulation of each of n odor receptors of said mammal, for one or more molecules or combinations of

20 molecules yielding known odor perception in a mammal,

generating from said values a quantitative representation of odor perception in a mammal for the one or more molecules or combinations of molecules yielding known odor perception in a mammal;

providing values X_1 to X_n representative of the quantitative stimulation of each of n

25 odor receptors of said mammal, for one or more molecules or combinations of molecules yielding unknown odor perception in a mammal;

generating from said values a quantitative representation of odor perception in a mammal for the one or more molecules or combinations of molecules yielding unknown odor perception in a mammal; and

30 predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown odor perception in a mammal by comparing the quantitative representation of odor perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown odor

perception in a mammal to the quantitative representation of odor perception in a mammal for the one or more molecules or combinations of molecules yielding known odor perception in a mammal, wherein at least one of said odor receptors is a odor receptor polypeptide having a sequence that is at least about 40% identical to a sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO:

267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, 5 SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID 10 NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, 15 SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID 20 NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, 25 SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

* 20 * 40 * 60 * 80
 AOLFR01 .PR : * --- MMVLR- --- T- --- FSSFLQIGRMHQGNOTTI- --- TTEFLING
 AOLFR02 .PR : --- MMVLR- --- T- --- NLSMPEPTFALLC
 AOLFR03 .PR : --- LLTDR- --- ENQNN- --- VTEFLIC
 AOLFR04 .PR : --- GKE- --- NCTTVREFILIC
 AOLFR05 .PR : --- GKE- --- NOSSTPTFILIC
 AOLFR06 .PR : --- GKE- --- ATSNHSSGAEFILAC
 AOLFR07 .PR : --- GKE- --- LARNNSLVTETILAC
 AOLFR08 .PR : --- GKE- --- LARNNSLVTETILAC
 AOLFR09 .PR : --- GKE- --- LARNNSLVTETILAC
 AOLFR10 .PR : --- GKE- --- TLRNSSSVTEFLIC
 AOLFR11 .PR : --- GKE- --- LARNNSLVTETILAC
 AOLFR12 .PR : --- GKE- --- LARNNSLVTETILAC
 AOLFR13 .PR : --- GKE- --- TLRNSSSVTEFLIC
 AOLFR14 .PR : --- GKE- --- LARNNSLVTETILAC
 AOLFR15 .PR : --- GKE- --- RR - NCTLVTEFLIC
 AOLFR16 .PR : --- GKE- --- L- --- NFTDVTEFLIC
 AOLFR17 .PR : --- GKE- --- SNTNGSAITETILAC
 AOLFR18 .PR : --- GKE- --- ETYKNYSSTSSTGELIC
 AOLFR19 .PR : --- GKE- --- ENHTMKNEFILE
 AOLFR20 .PR : --- GKE- --- EPRKN- --- VTDDEVIL
 AOLFR21 .PR : --- GKE- --- ROKNN- --- XTEFVL
 AOLFR22 .PR : --- GKE- --- KNNLTRVT- --- EFLIL
 AOLFR23 .PR : --- GKE- --- ETGNLITW- --- VSDFVFL
 AOLFR24 .PR : --- GKE- --- AAKNS- --- VTEFILE
 AOLFR25 .PR : --- GKE- --- ONYSLISENILE
 AOLFR26 .PR : --- GKE- --- P- --- NFTDVTEFLIC
 AOLFR27 .PR : --- GKE- --- P- --- SHSPVFLFL
 AOLFR28 .PR : --- GKE- --- GV- --- EH- L- --- LNRT- --- E-VSEEFFL
 AOLFR29 .PR : --- GKE- --- MSFAPNA- --- GT- --- SPVNGEVFL
 AOLFR30 .PR : --- GKE- --- GV- --- EH- L- --- LNRT- --- E-VSEEFFL
 AOLFR31 .PR : --- GKE- --- NSLK- --- ANET- --- GVKNHSTVTEFLIS
 AOLFR32 .PR : --- GKE- --- LE- --- DGNHTALTGFILIC
 AOLFR34 .PR : --- GKE- --- EP- --- SNATLITTAFILE
 AOLFR35 .PR : --- GKE- --- EP- --- NPENWTQVTSFLV
 AOLFR36 .PR : --- GKE- --- EP- --- NPANHSQ- --- VAGEVFL
 AOLFR37 .PR : --- GKE- --- EP- --- IATSNGNLVH- --- PAYFLV
 AOLFR38 .PR : --- GKE- --- EP- --- SSCNETH- --- A-TFLV
 AOLFR39 .PR : --- GKE- --- EP- --- ST- --- H-PAVEFLV
 AOLFR40 .PR : --- GKE- --- EP- --- PSNIT- --- H-PAVEFLV
 AOLFR41 .PR : --- GKE- --- EP- --- KPQLL- --- LT- --- H-PTAFLV
 AOLFR42 .PR : --- GKE- --- EP- --- VPI- --- VDNGNESSA- T- YFLV
 AOLFR43 .PR : --- GKE- --- EP- --- PSSEWFL- --- PSEWFLV
 AOLFR44 .PR : --- GKE- --- EP- --- ALNSNSWRLP- --- QPSEFLV
 AOLFR45 .PR : --- GKE- --- EP- --- LGPAYNHTMETPASELLV- --- LGPAYNHTMETPASELLV
 AOLFR46 .PR : --- GKE- --- EP- --- QILRDCILLHLCINRKKVSLV- --- QILRDCILLHLCINRKKVSLV
 AOLFR47 .PR : --- GKE- --- EP- --- M-
 AOLFR48 .PR : --- GKE- --- EP- --- LTFFHN- --- VCSV
 AOLFR49 .PR : --- GKE- --- EP- --- LDSEFFSFLL- --- KSLIM
 AOLFR50 .PR : --- GKE- --- EP- --- AOLFR51 .PR : --- GKE- --- AOLFR52 .PR : --- GKE-

Figure 1

Figure 1

Figure 1

* 340 * -FSTGCSHTVY- LIEPCTI- YCQFPEST- * 360 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 320 * * 400 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 325
 AOLFR01.PR : TOGKWC- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 340 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 325
 AOLFR02.PR : VSPHRC- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 360 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 314
 AOLFR03.PR : VSGRPR- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 340 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 313
 AOLFR04.PR : SKGRHC- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 360 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 309
 AOLFR05.PR : AEGPHC- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 340 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 311
 AOLFR06.PR : ASGRRC- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 360 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 311
 AOLFR07.PR : ACKRRC- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 340 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 314
 AOLFR08.PR : TEQOSG- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 360 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 347
 AOLFR09.PR : TQRSQG- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 340 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 311
 AOLFR10.PR : TQRSQG- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 360 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 313
 AOLFR11.PR : AEGRSQ- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 340 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 313
 AOLFR12.PR : AACRKR- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 360 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 314
 AOLFR13.PR : ATQQRK- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 340 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 314
 AOLFR14.PR : AACRKR- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 360 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 314
 AOLFR15.PR : VEGRRC- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 340 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 312
 AOLFR16.PR : TEGRCR- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 360 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 312
 AOLFR17.PR : AEGRCR- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 340 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 312
 AOLFR18.PR : AEGRCR- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 360 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 312
 AOLFR19.PR : AACRKR- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 340 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 305
 AOLFR20.PR : AACRKR- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 360 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 311
 AOLFR21.PR : QKGRQD- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 340 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 316
 AOLFR22.PR : QKGRQD- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 360 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 316
 AOLFR23.PR : SGGRAC- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 340 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 315
 AOLFR24.PR : GEARPR- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 360 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 314
 AOLFR25.PR : TEGRRC- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 340 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 307
 AOLFR26.PR : AEGRCR- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 360 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 310
 AOLFR27.PR : AEGRCR- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 340 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 310
 AOLFR28.PR : ADGRRC- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 360 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 316
 AOLFR29.PR : AGRRCR- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 340 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 310
 AOLFR30.PR : TEGRSQ- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 360 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 318
 AOLFR31.PR : TKGRCR- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 340 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 326
 AOLFR32.PR : AEGRCR- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 360 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 311
 AOLFR33.PR : ADGRRC- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 340 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 322
 AOLFR34.PR : AGRRCR- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 360 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 332
 AOLFR35.PR : ARRCR- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 340 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 310
 AOLFR36.PR : SDGKRC- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 360 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 312
 AOLFR37.PR : AEGRCR- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 340 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 312
 AOLFR38.PR : SDRKSC- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 360 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 319
 AOLFR39.PR : KKGRCR- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 340 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 294
 AOLFR40.PR : SEGRRC- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 360 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 314
 AOLFR41.PR : AAERRC- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 340 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 311
 AOLFR42.PR : REGSSC- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 360 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 323
 AOLFR43.PR : RRAJRC- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 340 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 318
 AOLFR44.PR : KSEPRC- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 360 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 324
 AOLFR45.PR : QEARRC- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 340 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 320
 AOLFR46.PR : EGAVRA- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 360 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 314
 AOLFR47.PR : QEARRA- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 340 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 384
 AOLFR48.PR : REAQRA- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 360 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 314
 AOLFR49.PR : PEASRA- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 340 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 316
 AOLFR50.PR : NEARFA- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 360 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 317
 AOLFR51.PR : KTRQRA- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 340 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 319
 AOLFR52.PR : KTAQRA- FSTGCSHTVY- LIEPCTI- YCQFPEST- * 360 * -HPEPDTKGATL- VTPMTHFSYSHM- DFGATPKLNUKISS- : 350

Figure 1

440

AOLFR01.pr	:	-----	:	-
AOLFR02.pr	:	-----	:	-
AOLFR03.pr	:	-----	:	-
AOLFR04.pr	:	-----	:	-
AOLFR05.pr	:	-----	:	-
AOLFR06.pr	:	-----	:	-
AOLFR07.pr	:	-----	:	-
AOLFR08.pr	:	-----	:	-
AOLFR09.pr	:	-----	:	-
AOLFR10.pr	:	-----	:	-
AOLFR11.pr	:	-----	:	-
AOLFR12.pr	:	-----	:	-
AOLFR13.pr	:	-----	:	-
AOLFR14.pr	:	-----	:	-
AOLFR15.pr	:	-----	:	-
AOLFR16.pr	:	-----	:	-
AOLFR17.pr	:	-----	:	-
AOLFR18.pr	:	-----	:	-
AOLFR19.pr	:	-----	:	-
AOLFR20.pr	:	-----	:	-
AOLFR21.pr	:	-----	:	-
AOLFR22.pr	:	-----	:	-
AOLFR23.pr	:	-----	:	-
AOLFR25.pr	:	-----	:	-
AOLFR26.pr	:	-----	:	-
AOLFR27.pr	:	-----	:	-
AOLFR28.pr	:	-----	:	-
AOLFR29.pr	:	-----	:	-
AOLFR30.pr	:	-----	:	-
AOLFR31.pr	:	-----	:	-
AOLFR32.pr	:	-----	:	-
AOLFR34.pr	:	-----	:	-
AOLFR35.pr	:	-----	:	-
AOLFR36.pr	:	HSIPTSANPAP	:	305
AOLFR37.pr	:	-----	:	-
AOLFR38.pr	:	EKGQPH-----	:	300
ACLFR39.pr	:	-----	:	-
AOLFR40.pr	:	-----	:	-
AOLFR41.pr	:	-----	:	-
AOLFR42.pr	:	-----	:	-
AOLFR43.pr	:	-----	:	-
AOLFR44.pr	:	-----	:	-
AOLFR45.pr	:	-----	:	-
AOLFR46.pr	:	-----	:	-
AOLFR47.pr	:	-----	:	-
AOLFR48.pr	:	-----	:	-
AOLFR49.pr	:	-----	:	-
AOLFR50.pr	:	-----	:	-
AOLFR51.pr	:	-----	:	-
AOLFR52.pr	:	-----	:	-

Figure 1

Figure 2

Figure 2

AOLFR54 · PR	* 120 * * 140 * * 160 * * 180 * * 200 *	YIAMDNA-PIAEMMLECUTSITDIALS--STVPEKETAILIMIHLAG-ETSEPGCCLAOH-CVHSIYALESSILAT-PIRIVATIUNHAVIGR- SIITCTO-LIHOENWYERLNLVYLSLDYCYTSTVT-BKEMVDDLAERK-TIISUNNMOLH-TIIFGGLIIFD-TGMA-ADRVYATICKPLHHTT- AOLFR57 · PR
AOLFR58 · PR	ITSSPAL-IVSPDREBPSGFSFEDACSEVT-BKEMVDDLAERK-TIISUNNMOLH-TIIFGGLIIFD-TGMA-ADRVYATICKPLHHTT- AOLFR59 · PR	
AOLFR60 · PR	VIWIESS-PIHOMMEYDLS-PIHOMMEYDLS-PIHOMMEYDLS-PIHOMMEYDLS-PIHOMMEYDLS-PIHOMMEYDLS-PIHOMMEYDLS- AOLFR61 · PR	
AOLFR62 · PR	VIKTEPS-PIREMPYR2IAPISTEDIALS-ATSVRPIV2IAPISTEDIALS-PIREMPYR2IAPISTEDIALS-PIREMPYR2IAPISTEDIALS- AOLFR63 · PR	
AOLFR64 · PR	VIKCTDAS-PICTEDIALS-PICTEDIALS-PICTEDIALS-PICTEDIALS-PICTEDIALS-PICTEDIALS-PICTEDIALS- AOLFR65 · PR	
AOLFR66 · PR	VIOTEQS-PIEENZDAMDSIDEGLS-PIEENZDAMDSIDEGLS-PIEENZDAMDSIDEGLS-PIEENZDAMDSIDEGLS-PIEENZDAMDSIDEGLS- AOLFR67 · PR	
AOLFR68 · PR	VYCDEA-PIHRENNV2IAPISTEDIALS-PIHRENNV2IAPISTEDIALS-PIHRENNV2IAPISTEDIALS-PIHRENNV2IAPISTEDIALS- AOLFR69 · PR	
AOLFR70 · PR	VWLDQS-PIWLDQS-PIWLDQS-PIWLDQS-PIWLDQS-PIWLDQS-PIWLDQS-PIWLDQS- AOLFR71 · PR	
AOLFR72 · PR	VIKLDLQ-PIHRLDQ-PIHRLDQ-PIHRLDQ-PIHRLDQ-PIHRLDQ-PIHRLDQ-PIHRLDQ- AOLFR73 · PR	
AOLFR74 · PR	VIKLDVSR-PITKLDVSR-PITKLDVSR-PITKLDVSR-PITKLDVSR-PITKLDVSR-PITKLDVSR- AOLFR75 · PR	
AOLFR76 · PR	VIKLDSDH-PILLDSH-PILLDSH-PILLDSH-PILLDSH-PILLDSH-PILLDSH- AOLFR77 · PR	
AOLFR78 · PR	VIKRDVSR-PIVARDVSR-PIVARDVSR-PIVARDVSR-PIVARDVSR-PIVARDVSR- AOLFR79 · PR	
AOLFR80 · PR	VIKLDSDH-PIVARDVSR-PIVARDVSR-PIVARDVSR-PIVARDVSR-PIVARDVSR- AOLFR81 · PR	
AOLFR82 · PR	VIKLDSDH-PIVARDVSR-PIVARDVSR-PIVARDVSR-PIVARDVSR-PIVARDVSR- AOLFR83 · PR	
AOLFR84 · PR	VIKLDSDH-PIVARDVSR-PIVARDVSR-PIVARDVSR-PIVARDVSR-PIVARDVSR- AOLFR85 · PR	
AOLFR86 · PR	VIKLDSDH-PIVARDVSR-PIVARDVSR-PIVARDVSR-PIVARDVSR-PIVARDVSR- AOLFR87 · PR	
AOLFR88 · PR	VIKLDSDH-PIVARDVSR-PIVARDVSR-PIVARDVSR-PIVARDVSR-PIVARDVSR- AOLFR89 · PR	
AOLFR90 · PR	VIKLDSDH-PIVARDVSR-PIVARDVSR-PIVARDVSR-PIVARDVSR-PIVARDVSR- AOLFR91 · PR	
AOLFR92 · PR	VIKWAEPR-PIVWAEPR-PIVWAEPR-PIVWAEPR-PIVWAEPR-PIVWAEPR- AOLFR93 · PR	
AOLFR94 · PR	VIKLYMDPH-PIVLYMDPH-PIVLYMDPH-PIVLYMDPH-PIVLYMDPH-PIVLYMDPH- AOLFR95 · PR	
AOLFR96 · PR	VIKTSVDA-PIVTSVDA-PIVTSVDA-PIVTSVDA-PIVTSVDA-PIVTSVDA- AOLFR97 · PR	
AOLFR98 · PR	VIKIVSAT-PIVIVSAT-PIVIVSAT-PIVIVSAT-PIVIVSAT-PIVIVSAT- AOLFR99 · PR	
AOLFR101 · PR	VIKLDRA-PIVLDRA-PIVLDRA-PIVLDRA-PIVLDRA-PIVLDRA- AOLFR102 · PR	
AOLFR103 · P	VIKLDHQ-PIVLDHQ-PIVLDHQ-PIVLDHQ-PIVLDHQ-PIVLDHQ- AOLFR105 · P	
AOLFR106 · P	VIWNSERS-PIWNSERS-PIWNSERS-PIWNSERS-PIWNSERS-PIWNSERS- AOLFR107 · P	
AOLFR108 · P	VIKFLDSR-PIVFLDSR-PIVFLDSR-PIVFLDSR-PIVFLDSR-PIVFLDSR- AOLFR109 · P	

Figure 2

Figure 2

AOLFR110.P : C-----	20 *-----	40 *-----	60 *-----	80 *-----	100 *-----
AOLFR111.P : C-----	-----	-----	-----	-----	-----
AOLFR113.P : C-----	-----	-----	-----	-----	60
AOLFR114.P : E-----	-----	-----	-----	-----	87
AOLFR115.P : D-----	-----	-----	-----	-----	82
AOLFR116.P : D-----	-----	-----	-----	-----	61
AOLFR117.P : D-----	-----	-----	-----	-----	77
AOLFR118.P : A-----	-----	-----	-----	-----	60
AOLFR119.P : P-----	-----	-----	-----	-----	108
AOLFR120.P : P-----	-----	-----	-----	-----	60
AOLFR121.P : KR-----	-----	-----	-----	-----	60
AOLFR122.P : EWENQ-----	-----	-----	-----	-----	60
AOLFR123.P : YRFIDEDVSN-----	-----	-----	-----	-----	60
AOLFR124.P : AL-----	-----	-----	-----	-----	60
AOLFR125.P : A-----	-----	-----	-----	-----	60
AOLFR126.P : FLYLCFIFORTCSEE-----	-----	-----	-----	-----	60
AOLFR127.P : SNED-----	-----	-----	-----	-----	60
AOLFR128.P : A-----	-----	-----	-----	-----	60
AOLFR129.P : A-----	-----	-----	-----	-----	60
AOLFR130.P : A-----	-----	-----	-----	-----	60
AOLFR131.P : A-----	-----	-----	-----	-----	60
AOLFR132.P : V-----	-----	-----	-----	-----	60
AOLFR133.P : TTI-----	-----	-----	-----	-----	60
AOLFR134.P : -TFPSHDGQAFSYDME-----	-----	-----	-----	-----	60
AOLFR135.P : A-----	-----	-----	-----	-----	60
AOLFR136.P : -TM-----	-----	-----	-----	-----	60
AOLFR137.P : S-----	-----	-----	-----	-----	60
AOLFR138.P : L-----	-----	-----	-----	-----	60
AOLFR139.P : L-----	-----	-----	-----	-----	58
AOLFR140.P : L-----	-----	-----	-----	-----	46
AOLFR141.P : SSTIGHN-----	-----	-----	-----	-----	62
AOLFR143.P : A-----	-----	-----	-----	-----	62
AOLFR144.P : A-----	-----	-----	-----	-----	62
AOLFR145.P : SYOYSLSPQMLLSNTOF-----	-----	-----	-----	-----	60
AOLFR146.P : S-----	-----	-----	-----	-----	72
AOLFR147.P : PSA--SA-----	-----	-----	-----	-----	62
AOLFR148.P : PTV-----	-----	-----	-----	-----	62
AOLFR149.P : S-----	-----	-----	-----	-----	62
AOLFR150.P : EL-----	-----	-----	-----	-----	58
AOLFR151.P : F-----	-----	-----	-----	-----	60
AOLFR152.P : DQ-----	-----	-----	-----	-----	60
AOLFR153.P : S-----	-----	-----	-----	-----	60
AOLFR154.P : CAMPSPPTGSSTN-----	-----	-----	-----	-----	58
AOLFR157.P : KA-----	-----	-----	-----	-----	76
AOLFR158.P : KA-----	-----	-----	-----	-----	60
AOLFR159.P : A-----	-----	-----	-----	-----	60
AOLFR160.P : PMOLLTT-----	-----	-----	-----	-----	60
AOLFR161.P : E-----	-----	-----	-----	-----	81
AOLFR162.P : MRLMGEVRG-----	-----	-----	-----	-----	60
AOLFR163.P : QRSNHT-----	-----	-----	-----	-----	67

Figure 3

Figure 3

Figure 3

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Figure 4

Figure

Figure 5

Figure 7

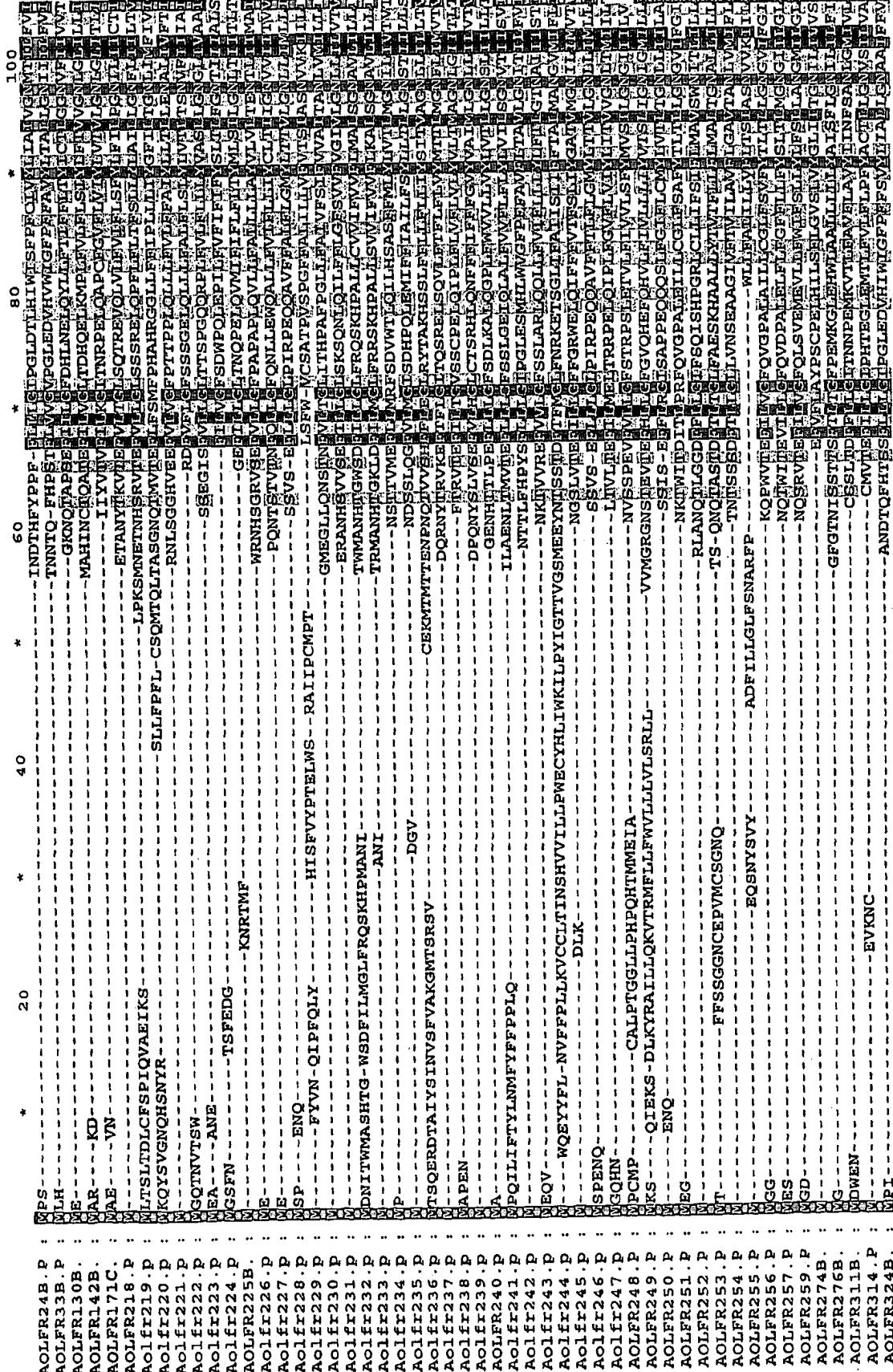


Figure 5 1/5

Figure 5

Figure 5
4/5

Figure 5



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(57) Abstract:

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DECLARATION OF NON-ESTABLISHMENT OF INTERNATIONAL SEARCH REPORT (PCT Article 17(2)(a), Rules 13ter and 39)

Applicant's or agent's file reference 978005PCT	IMPORTANT DECLARATION	Date of mailing (day/month/year) 05 SEP 2001
International application No. PCT/US01/07771	International filing date (day/month/year) 13 MARCH 2001	(Earliest) Priority Date (day/month/year) 13 MARCH 2000
International Patent Classification (IPC) or both national classification and IPC Please See Continuation Sheet.		
Applicant SENONYX, INC.		

This International Searching Authority hereby declares, according to Article 17(2)(a), that **no international search report will be established** on the international application for the reasons indicated below.

1. The subject matter of the international application relates to:
 - a. scientific theories.
 - b. mathematical theories.
 - c. plant varieties.
 - d. animal varieties.
 - e. essentially biological processes for the production of plants and animals, other than microbiological processes and the products of such processes.
 - f. schemes, rules or methods of doing business.
 - g. schemes, rules or methods of performing purely mental acts.
 - h. schemes, rules or methods of playing games.
 - i. methods for treatment of the human body by surgery or therapy.
 - j. methods for treatment of the animal body by surgery or therapy.
 - k. diagnostic methods practiced on the human or animal body.
 - l. mere presentations of information.
 - m. computer programs for which this International Searching Authority is not equipped to search prior art.
2. The failure of the following parts of the international application to comply with prescribed requirements prevents a meaningful search from being carried out:

the description the claims the drawings
3. The failure of the nucleotide and/or amino acid sequence listing to comply with the standard provided for in Annex C of the Administrative Instructions prevents a meaningful search from being carried out.

the written form has not been furnished or does not comply with the standard.

 the computer readable form has not been furnished or does not comply with the standard.
4. Further comments:

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**DECLARATION OF NON-ESTABLISHMENT OF
INTERNATIONAL SEARCH REPORT**

International application No
PCT/US01/07771

The International Patent Classification (IPC) or National Classification and IPC are as listed below:

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